ASSESSMENT OF GENETIC VARIABILITY FOR GRAIN YIELD AND ITS COMPONENTS IN FINE 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

CHENDAKE SHUBHAM ANNASO
(ADPM/20/2748)

DEPARTMENT OF AGRICULTURAL BOTANY
COLLEGE OF AGRICULTURE, DAPOLI

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NOVEMBER, 2022

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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 **"ASSESSMENT OF GENETIC VARIABILITY FOR GRAIN YIELD AND ITS COMPONENTS IN FINE 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, **“Assessment of genetic variability for grain yield and its components in fine Rice (*Oryza sativa* L.)”** submitted for the degree of M. Sc. (Agri.) in 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. Chendake Shubham Annaso (ADPM/20/2748)** 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 and has submitted one research paper from his M. Sc. Work.

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

Place: Dapoli
Date: / /

Chairman
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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, **“Assessment of genetic variability for grain yield and its components in fine Rice (*Oryza sativa* L.*)*”** submitted by **Mr. Chendake Shubham Annaso (ADPM/20/2748)** to the College of Agriculture, Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli, in partial fulfillment of the requirements for the degree of M.Sc. (Botany) 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 / /

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Place: Dapoli
Date: / / **(Chendake Shubham Annaso)**

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List of Abbreviations

% : Percentage
* : Significant at 5% level of significance
** : Significant at 1% level of significance
ha : hectare
i.e. : That is
cm : Centimeter
d.f. : Degree of freedom
Viz., : Namely
°C : Degree Celsius
et al. : And others
Kg : Kilogram
g : Grams
N : Nitrogen
P_2O_5 : Phosphorus
K : Potassium
RBD : Randomized Block Design
@ : At the rate of
m : Meter
C.D. : Critical Difference
EMSS : Error mean sum of squares
MSS : Mean sum of squares
Err. : Error
S.E. : Standard error
Sig. : Significant
mg : Milligram
< : Less than
> : Greater than
= : Equal to
Fig. : Figure
GA : Genetic advance
GAM : Genetic advance as per cent of mean
GCV : Genotypic coefficient of variation
PCV : Phenotypic coefficient of variation
h^2 : Heritability
mm : millimeter
σ^2p : Phenotypic variance
σ^2g : Genotypic variance
σ^2e : Environmental variance

Glossary

Correlation: Correlation is a statistical measure that indicates the extent to which two or more variables fluctuate in relation to each other.

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

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

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

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

Konkan: Konkan is the 720 km long rugged section of the western coastline of Arabian Sea which extends from Damon in the North to western side land of Maharashtra and Goa.

CHAPTER I : INTRODUCTION

1.1 Background information

Rice (*Oryza sativa* L.) is one of the world's most important cereal crop, providing the major staple food for 50 per cent of the world population. It supplies two third of the calories for the two billion people of Asia and one third of calorie intake of nearly one billion people in Africa and Latin America. It belongs to family 'Poaceae' and genus include 24 species out of which '*Oryza sativa*' and '*Oryza glaberrima'* are cultivated. *'Oryza sativa'* has three subspecies *viz*; India, Japonica and Javanica. However, the chromosome number (2n=2x=24). It is self pollinated and short day plant.

The cultivated rice has round and jointed culms, flat leaves and a terminal flower. The plant's root system is fibrous. Nodes and hollow internodes make form the stem. The rice is divided into two parts: subsurface and aerial. The blade and the leaf sheath are both part of the leaf. The flag leaf is the highest leaf below the panicle. The auricle is a paired structure on either side of the leaf blade's base. The rice inflorescence is made up of spikelets and is called a panicle. The rachilla and the floret are two sterile lemmas that make up a spikelet. The floret consists of the lemma, palea and flower. Six stamens make up the bloom. Caryopsis is the rice fruit, which is surrounded by the lemma and palea.

Rough rice is mature rice that has been collected as covered grain. Rice is typically a high-calorie or high-energy meal. It has a lower protein content than wheat. Milled rice typically has a protein level of 6 to 7%. Rice, on the other hand, has a higher amino acid concentration than other grains. Its protein has a great biological value. Rice has a modest fat content (2.0 to 2.5%) and much of the fat is lost during milling. Rice has a very low calcium content. Rice has the same amount of B vitamins as wheat. Milled rice loses important proteins, vitamins and minerals when the embryo and aleurone layer are lost during the milling process. The parboiling procedure can prevent a significant amount of nutritional loss. Rice milling by-products are utilized for a number of purposes. Cattle and poultry feed are made from rice bran. Rice hulls may be used to make insulating materials, cement and card board, as well as a litter for poultry. During the winter, rice straw may be utilized as both cow feed and litter. Rice is the only cereal crop that can thrive in standing water for lengthy periods of time. Rice is farmed on irrigated land in 57% of cases, rainfed lowlands in 25%, uplands in 10%, deep water in 6% and tidal wetlands in 2% of cases. (Kumar *et al*., 2018)

Due to its commercial and nutritional worth, rice is a significant food crop. About 345 calories per 100 grams are found in rice. In addition to carbohydrates, proteins and lipids, rice is an excellent source of minerals, including phosphorus, calcium, manganese, iron and zinc. Additionally, it has vitamins E and B-complex. It has very little fiber and no vitamin A or C. According to the amino acid profile of rice, glutamic and aspartic acids are abundant, with lysine serving as the limiting amino acid.

In India the area under rice cultivation is about 45.07 million hectares and production 122.3 million tons with an average productivity of 2713 kg ha^{-1}(Anonymous, 2021a). In Maharashtra, rice is the second most important food grain crop of the people grown on an area of 15.61 lakh ha with an annual rice production of 32.91 lakh tons. The average productivity of the Maharashtra state is 2109 kg ha^{-1} (Anonymous, 2021b). Konkan region is a major rice producing area of Maharashtra. Nearly 3.57 lakh ha area of Konkan is under rice crop with production of 8.52 lakh tons. The average productivity of Konkan region is 2386.01 kg ha^{-1}(Anonymous, 2021c).

1.2 Importance of study

The breeding methods to be adopted for improvement of a crop depend on the nature of gene action involved in the inheritance of economically important traits. Besides its use in selection of potential parents and superior crosses, combining ability studies also provide information on the nature and magnitude of gene effects involved in the expression of quantitative traits. Such information is of practical values in formulating as well as executing the efficient breeding programme for obtaining maximum gain with minimum resource and time.

To alleviate some of the constraints in rice production to develop improved variety researcher's must have studied the genetic variability in rice which is the pre-requisite for rice breeding programme hence development of an effective rice breeding programme is dependent upon the existence of genetic variability and characters association. Therefore, before initiation of any breeding programme survey of genetic variability with the help of suitable parameters such as genotypic coefficient of variation, heritability estimates and genetic advance are absolutely necessary to begin the any efficient breeding programme.

Genetic variation is one of the difference occurs among the individuals rice genotype due to differences in their genetic composition and the environment factors in which they were grow. The difference of the genetic variability having in the introduced rice genotype is much more essential to rice improvement programme which must be exploited by the rice breeders for its yield improvement to achieve the demands of the rice producers.

It is vital to understand the genetic architecture of genotypes in order to develop effective breeding methods. It is critical to determine the relative amount of additive and non-additive genetic variations, heritability and genetic gain in relation to the breeder's target characteristics.

To generate promising kinds, a systematic breeding programme includes processes such as creating genetic heterogeneity, performing selection and utilizing selected genotypes. The wide range of genetic variability in segregating populations, which is dependent on genotype genetic variation, provides more selection opportunities. Estimates of GCV, PCV, heritability and genetic progress will be crucial in utilizing future rice improvement research estimates.

The nature and extent of genetic variability are critical to the success of any crop improvement initiative. The degree of genetic variability in the plant population determines the effectiveness of selection. Due to the polygenic nature of characteristics like yield and its components, the breeder must separate desirable genotypes from the knowledge of components of variance. The essential element is the partitioning of total variation into phenotypic and genotypic components, with the amount of these components for distinct characteristics serving as a measure of the kind of gene action that aids in the selection of a breeding technique for genetic improvement of a trait. High heritability numbers alone may not indicate the amount of genetic advancement that would be made if the best genotype were chosen. (Bhargavi *et al.*, 2021)

Due to a variety of socio-economic obstacles, there is a slim likelihood of expanding rice agriculture. As a result, increasing rice output per unit area is required to meet the aim of increased rice production. The focus has shifted to maximising land usage by generating a higher rice yield per unit area per unit time, which necessitates the improvement of various grain production features.

1.3 Objectives of study

Grain yield is a complicated characteristic that is determined by several factors, including the number of spikes per plant, spike length, number of grains per spike and grain weight per 1000-grains. These components are also dependent on a number of morphological and developmental traits that are interrelated, so the parents chosen for breeding programmes aimed at increasing seed yield should have a wide range of genetic variation for the morphological and developmental characters mentioned above. Furthermore, knowing the extent of variance attributable to heritable component could be useful as a guide for population improvement selection. To put it another way, understanding of genetic variability for traits is essential for crop development in any species. Keeping in view the above important aspects, the existing investigation will carried out under the following objectives.

1. To estimate the genetic variability for yield and yield attributing characters.
2. To estimate the genotypic and phenotypic correlation coefficient of different characters.

1.4 Hypothesis

Fine grain rice are categorized into two types medium slender (TW14-18gm) and short slender grain (TW10-14gm). They are known for their unique grain texture, palatability, fineness, cooking quality and taste. It having highest preference among consumers for different preparations. The demand for fine grain rice in urban area is increasing day by day. Because of its premium grain quality and high demand it fetches more price which help to farmer to increase their profit.

1.5 Scope and Limitations

Yield is the end outcome of a number of morphological, physiological and biological factors. In a hybridization scheme, several cultivars with more genetic variability might be used to increase yield. The availability of sufficient genetic variability is considered a necessary precondition for launching any crop improvement effort and its size in a specific species determines its success. The magnitude of genetic variability is measured by the genotypic coefficient of variation. It does so because it represents the heritable component of variability. (Bandi *et al*., 2018)

The demand for fine rice is increasing day by day, both at home and abroad, after significant yields in high yielding types have been achieved. Although fine grain rice has a poor yield, it is in high demand in the market and sells for a premium price. On exceptional occasions, it's also employed in the preparation of unique foods. Rice millers choose cultivars that have a high milling and head rice out-turn, while consumer's value quality. Variety, grain type, chalkiness, cultural practice, drying, storage and milling conditions all influence head rice yields. Rice's appearance, which is determined by the shininess and chalkiness of the kernel, is significant in attracting consumers' attention. Size and shape are also crucial considerations for customers. Consumer preferences regarding grain size and shape differ from one group to the next.

The amylose content of rice is the most important criterion for cooking and eating quality. Many of rice's starch qualities are influenced by amylose concentration, volume expansion and water absorption. Cooking time is crucial since it impacts the tenderness and stickiness of cooked rice to a large extent. The energy content per unit volume or weight of cooked rice will be decreased as the imbibition ratio of rice rises, since they will contain more water and solid elements. Working-class people still view high-volume cooking growth to be of superior quality, regardless of whether the expansion is lengthwise or transverse. People in cities, on the other hand, favour kinds that are longer than they are wide. Fine rice can be classified as export quality rice with a good nutritional profile. (Dipti *et al*., 2002)

In Konkan region, rice is common staple food, it contains carbohydrates than any other micronutrients. Which can be need to be improved. Variability helps among the population to enhance the plant breeder to study source and come out with new cultivars. By using genetic variability as source material which brings very specific changes in existing rice genotype. This plant genotypes developed using these new tools will improved for nutrition value and other morphological traits.

The collecting of superior alleles into a single production is referred to as an efficient and cost-effective crop enhancement method. Selection of desirable parents for hybridization has been found to be an efficient operating implement in producing high yielding crop varieties on which contemporary agriculture may rely throughout the last century. Though it is a challenging task for a plant breeder, different biometric procedures presented by various individuals from time to time have proven to be effective in selecting parents, which in turn affects crosses and eventually develops a population true to the breeding value. The availability of the aforesaid data substantially assists in the creation of a breeding programme as well as the selection of the most appropriate selection procedure.

More the genetic variability unable to maintain the genetic purity of the rice genotypes. Rarely, variation lead to the development of new alleles and so new phenotypes are develop and if they do, most only have a small effect on the genotypes.

With these considerations in mind, the proposed research titled "Assessment of genetic variability for grain yield and its components in fine Rice (*Oryza sativa* L.)" is scheduled to take place at the Education and Research farm, Department of Agriculture Botany, College of Agriculture Dapoli, Dr. B.S. Konkan Krishi Vidyapeeth, Dapoli during the *Kharif* 2021.

CHAPTER II : REVIEW OF LITERATURE

The present study had undertaken to evaluate variability, genotypic and phenotypic correlation coefficient for yield and yield attributing characters in 32 genotypes of Rice. The relevant literatures related to various aspects of present study entitled “**Assessment of genetic variability for grain yield and its components in fine Rice (*Oryza sativa* L.*)*” are reviewed under the following heads.

2.1. Genetic variability, heritability and genetic advance

2.2. Correlation coefficient

2.1. Genetic variability, heritability and genetic advance

Variability describes the existence of variances among plant population members that are brought about by variations in either the genetic make-up of population members or the environments in which they grew.

Variation is the degree of difference between individuals within a population. Fisher (1930) divided the entire phenotypic variance into genotypic variance and environmental variance. He further differentiated the effects of additive, dominance, and epistasis on genotypic variance. However, it is simply the extent of genetic variability present within the population. Therefore, for plant breeders to begin a breeding programme in any crop, including rice, understanding the degree of genetic diversity existing in a population is of the utmost significance.

Prasad *et al.* (2001) studied eight fine rice genotypes to detect the genetic variability and selection of some yield contributing characters through correlation and path analysis. Reported that high genetic coefficient variation and high genetic advance along with high variability for 1000-grain weight, no. of effective tillers per plant, number of fertile grains per panicle and yield per plant showed that there was further scope for genetic gain through selection process.

Mustafa and Elsheikh (2007) was conducted experiment to evaluate genetic variability in 14 rice genotypes and found that majority of the features studied had a larger range of genetic variability among genotypes. Grain yield, unfilled grains per panicle, and number of grains per panicle all had the greatest GCV.

Padmaja *et al*. (2008) evaluated 150 rice genotypes including five check varieties, for eleven features to study the genotypic and phenotypic coefficient of variation, heritability and genetic advance. The genotypes had extremely significant variations in all of the parameters except leaf breadth and 100-seed weight, according to the analysis of variance. For all of the parameters except days to 50 per cent flowering and panicle length, the estimations of GCV and PCV were high. All of the traits exhibited high heritability and genetic advance, with the exception of days to 50 per cent flowering and panicle length, which had moderate genetic advance but high heritability, showing the role of additive gene action in influencing these features.

Chandra *et al.* (2009) conducted an experiment on 49 rice germplasm to estimate genetic variability, heritability and genetic advance for yield and its quality traits. The results were revealed that high value of GCV and PCV were observed for the number of productive tillers per plant, number of grains per panicle, 1000-grain weight and grain yield per plant.

Veerabadhiran *et al.* (2009) carried out an experiment to study the genetic variability by using fifteen rice hybrids and five checks for seventeen different qualitative characters along with grain yield. The difference between PCV and GCV were low for all the characters under study indicating that less environmental effect. Highest (20%) PCV and GCV were observed for gelatinization temperature and gel consistency.

Anjaneyulu *et al.* (2010) carried out an experiment to study genetic variability among the fifty rice germplasm. The results were shown that the highest GCV and PCV were recorded for number of grains per panicle, fertility percentage and grain yield per plant. The traits like number of grains per panicle, plant height and fertility percentage recorded high heritability along with high genetic advance showed that suitability for further selection process.

Jayasudha *et al.* (2010) used forty seven rice cultivar including thirty three hybrids and fourteen parents to investigate grain yield and other physiological characters. ANOVA showed that there is little variability among the tested cultivar for all the characters under study. Grain yield per plant, harvest index, pollen fertility (%), spikelet fertility (%) showed the high genotypic and phenotypic coefficient of variation.

Krishna *et al.* (2010) tested 97 rice genotypes along with three checks by using RBD to study the genetic variability, heritability and genetic advance. The high PCV and GCV were recorded for the characters like number of unfilled spikelet per plant, and number of total spikelet per plant. The study revealed that high heritability along with high genetic advance were recorded for total spikelet per plant and number of spikelet per plant specifying that they can be upgraded through selection.

Prasad *et al.* (2011) conducted an experiment during Rabi, 2010 at Directorate of Rice Research (DRR) farm, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) Campus Patancheru, Hyderabad, (India) with fifty two rice cultivar to study the genetic variability for yield and its component traits in diverse rice germplasm lines, as well as the interrelationship between different yield contributing features and their relationship to grain yield. The results were revealed that eight superior genotypes, including Ujala Depama, IR-64, Bhurma Bhuqi, Malida, Tella Hamsa, Kavya, Vldhan-221, and Krishna Hamsa, may be employed as parents in heterosis breeding.

Idris *et al.* (2012) reported the highest values of phenotypic and genotypic variance by yield kg/ha and also the grain yield has been recorded to the highest value of GCV and PCV. Positive PCV and GCV was found in the grain yield, no. of filled grains per panicle, panicle length, no. of grains per panicle and harvest index. Results shown that there was a high genetic variability was found between the tested genotypes.

Aditya *et al.* (2013) evaluated the eighteen rice genotype under rainfed condition for fifteen qualitative traits. They observed GCV and PCV was high for the grain yield per plot along with fertile grains per panicle and grains per panicle. The high genetic heritability and high genetic advance for no. of grains per panicle and fertile grains per panicle.

Dhurai *et al.* (2014) evaluated genetic variability for all the five quality traits and nine quantitative traits among the different germplasm of the rice. It is showed that the difference between the PCV and GCV were very low for all traits under the evaluation and very little effect of environment in the expression of these traits. The high value of PCV and GCV were recorded for no. of grains per panicle and grain yield per plant.

Gokulkrishnan *et al.* (2014) evaluated heritability, genetic advance, phenotypic and genotypic coefficients of variation among yield, quality, and its component characters in twenty three genotypes of rice. For all of the traits studied, there was a lot of variation among the tested genotype. Moderate phenotypic and genotypic coefficients of variation were found for panicle weight, number of grains per panicle, grain L/B ratio, plant height, 1000-grain weight, and grain width. Grain breadth, grain L/B ratio, plant height, number of grains per panicle, and grain yield per plant all had strong heritability and genetic advance as a per cent of mean, showing that the features were regulated by additive gene action. As a result, phenotypic value selection will be critical for successful improvement in these traits.

Paikhomba *et al.* (2014) evaluated thirty F_1 rice hybrids for variability, heritability and genetic advance in different yield and yield contributing characters. The results were showed that mean sum of squares for 14 traits stretches significant differences, specifying that presence of high genetic variability among the tested genotypes.

Gamphala *et al.* (2015) evaluated 80 different genotypes for yield and quality attributing characters. Days to 50 per cent flowering, plant height, flag leaf length, flag leaf width, number of tillers per hill, number of panicles per hill, panicle length, number of spikelet's per panicle, days to maturity, biological yield per hill, harvest index, test weight, grain yield per hill all showed considerable differences in yield and quality attributing traits, indicating the presence of massive genetic variability.

Islam *et al.* (2015) conducted experiment to estimate genetic variability of twenty three rice germplasm including three check varieties for yield and yield contributing traits in rice. For the traits like plant height, number of filled grains per panicle, days to 50 per cent flowering, thousand grain weight, grain width and grain yield observed that genotypic and phenotypic coefficient of variation is high. Generally, the PCV is higher than the GCV for all the characters showed that effect of environmental factors on these characters under study. High heritability was observed for grain width, days to 50 per cent flowering, thousand grain weight, grain length, days to maturity and number of filled grains per panicle.

Kishore *et al.* (2015) used seventy-three rice varieties to estimate their variability with regards to yield and yield components. Evaluation of heritability and genetic advance in per cent of mean were also obtained for the above traits. The results were showed that high heritability, variability and genetic advance in per cent of mean for grain yield where high heritability along with low genetic advance as per cent of mean for panicle bearing tillers and 1000-grain weight. In addition to yield it was observed to be positively associated with panicle bearing tillers and number of filled grains per panicle and these characters were noticed to show highly direct effects on grain yield per plant.

Sameera *et al.* (2015) investigates the nature and extent of variability, heritability, and genetic progress. Twenty-five rice genotypes were tested in a randomized block design with three replications. For all of the traits tested, analysis of variance indicated substantial variations between genotypes. In addition, the attributes number of tillers per plant, productive tillers per plant, number of grains per panicle, and number of filled grains per panicle all had higher estimates of genotypic and phenotypic coefficients of variance, as well as high estimates of heritability. Number of tillers per plant, productive tillers per plant, number of grains per panicle, and number of full grains per panicle all had high heritability and genetic progress as a percent of mean, indicating that these variables were more relevant for targeted yield development programmes in rice.

Rukminidevi *et al.* (2016) used twenty seven rice variety to estimate genetic variability for grain yield and quality characters in rice. Analysis of variance revealed highly substantial differences among 27 cultivars for all the yield components and most of the kernel quality characters except hulling percent, volume expansion ratio and water uptake signifying that sufficient variability is present in the tested material.

Sameera *et al*. (2016) carried out an experiment to study genetic variability, heritability and genetic advance as per cent of mean in twenty-five rice varieties. The traits like productive tillers per plant, number of tillers per plant, number of grains per panicle, number of filled grains per panicle recorded the high variability, heritability and genetic advance as per cent of mean. However high heritability, along with low genetic advance as per cent of mean recorded for days to maturity. The traits like number of tillers per plant, productive tillers per plant, number of grains per panicle, number of filled grains per panicle stretches the optimistic relation with yield.

Abebe *et al.* (2017) analysed genetic variability, heritability and genetic advance for grain yield and 13 yield associated characters in thirty six different rice genotypes at two diverse locations, namely Fogera and Pawe. The investigation was carried out by using 6 X 6 simple lattice design at two locations with two replications. The analysis of variance showed that significant difference existed among the tested genotypes for all the characters. The traits like days to maturity, plant height and panicle length showed significant Genotype X location interaction.

Ajmera *et al*. (2017) tested thirty-seven rice genotypes for yield and yield component variability. For the variables mentioned above, estimates of heritability and genetic progress in per cent of mean were also derived. Except for days to 50 per cent flowering, all of the features studied had high heritability and strong genetic progress as a percentage of mean, indicating that these traits were governed by additive gene action in the inheritance of these characters. By using a simple selection technique, these characters may be enhanced even further. The high heritability estimates combined with the low genetic progress as a per cent of mean for days to fifty per cent blooming suggested the presence of non-additive gene effects, as well as some environmental impact, implying a poor response to selection.

Khaire *et al.* (2017) evaluated twenty four rice genotypes, which were taken from local area of Maharashtra along with two check varieties. It was observed that a wide range of variability was found in the local lines of the rice under study. The estimation was showed that phenotypic variances were higher for all the characters under study. The evaluated GCV and PCV were high for the number of filled spikelets per panicle and number of spikelets per panicle.

Rashid *et al*. (2017) carried out the investigation to study the genetic variability of ten rice varieties using RBD. In this investigation the highest PCV recorded than the GCV indicating that the influence of environmental factors on the expression of the traits studied. Result was showed that the highest PCV and GCV was found for number of filled grains per panicle, no. of unfilled grains per panicle and plant height and lowest for days to 50 % flowering, days to maturity, panicle length, no. of effective tillers per plant, 1000 seed weight, fertility per cent showed that selection based on these traits helps to develop variability by the hybridization or mutation.

Ram *et al*. (2017) used hundred rice genotypes to evaluate the genetic parameters for yield and yield contributing traits in rice. ANOVA for the traits under study showed the significant difference among the genotype. The results were showed that low PCV and GCV noted for the days to 50 per cent flowering, plant height, days to maturity, spikelet fertility, and harvest index. Grain yield and biological yield recorded high estimates of GCV and PCV. The small estimates of GCV and PCV were noted for the ear bearing tillers, number of grains per panicle, biological yield, test weight and grain yield per plant. The results were showed that simple selection process effective for the improvement of these traits.

Rashmi *et al*. (2017) studied sixty-five rice germplasms to study the variability, heritability, genetic advance, correlation coefficient and path correlation with regards to yield and yield contributing traits. The results were showed that analysis of variance have significant differences for the characters under study, gives that presence of very high genetic variability among the tested genotypes. Traits like days to maturity, days to 50 per cent flowering and panicle weight showed high heritability with moderate genetic advance as per cent of mean.

Srujana *et al.* (2017) studied the twenty nine rice genotype including one check for 13 different quantitative characters to estimate their genetic variability, heritability and genetic advance. The results were showed that high heritability was observed for spikelet’s per panicle, days to maturity, biological yield, grain yield per hill, panicles per hill and tillers per hill. The traits like spikelet per panicle, seed yield per plant, tillers per plant, panicles per plant and biological yield per hill showed high heritability coupled with moderate to low estimates of genetic advance.

Sumanth *et al.* (2017) assessed twenty three rice varieties for the study of genetic variability, heritability, genetic advance, correlation coefficient analysis and path analysis for 13 different quantitative characters. The highest GCV and PCV were found in seed yield per plant coupled with flag leaf length, number of spikelet’s per panicle, biological yield per plant and panicle per plant, which is useful for the further crop improvement.

Yadav *et al.* (2017) evaluated thirty five different rice germplasm along with two checks for twelve different quantitative traits under the sodic soil condition. The study shows that high PCV and GCV was detected for the biological yield per plant. While the moderate PCV and GCV were seen in plant height, grain yield per plant, effective tillers per plant, flag leaf area. The heritability estimates were observed in case of plant height, days to 50 per cent flowering, biological yield per plant, days to maturity, grain yield per plant, 1000-grain weight and spikelet per panicle and for the flag leaf area per plant, spikelet fertility and harvest index showed moderate heritability estimates. The high heritability along with high genetic advance as per cent of mean were seen in plant height and grain yield per plant, specify that involvement of additive gene action.

Bandi *et al*. (2018) studied thirty six varieties, which consist of ten yield contributing characters, six physical quality characters, eight cooking and chemical quality characters of the rice genotype. The ANOVA were shows that presence of significant difference among the genotype for all the characters studied. The presence high PCV compared to GCV were recorded for the gel consistency and alkali spreading value shows that wider variability for these traits. Moderate GCV and PCV were observed for the tillers per plant, number of grains per panicle, leaf area index at maximum tillering stage, volume expression ratio, amylose content, water uptake and the grain yield per plant.

Girma *et al*. (2018) reported presence of genetic variability among the different sixty four genotype, The experiment were conducted by using 8X8 simple lattice design. The results were showed that there is significant difference is present between the genotype under the study and observed GCV were lower than the PCV shows that presence of variability in all the studied genotypes. The genetic advance and heritability were present among traits under the study shows that presence of additive gene action, then these traits can be improved through the direct selection. The most of the evaluated traits are important for the development of the high yielding variety and contributing for the wider genetic variability of the genotypes.

Meena *et al*. (2018) conducted the experiment on thirty eight rice genotypes to evaluate the magnitude of variability for yield and yield contributing traits. Reported that the estimated GCV were lower than the respective PCV, showed that effect of environmental factors on the characters under study. The highest PCV and GCV were recorded for the unfilled grain per panicle, shows that further improvement of these traits through the selection process. The variety RP 5125-17-6-3-2-1 which were best for yield and yield contributing traits on the basis of per cent performance. The estimation showed that high heritability was observed for the days to 50 per cent flowering, days to maturity, total grain per plant and filled grain per panicle.

Pratap *et al.* (2018) used thirty eight rice variety to estimate the genetic variability, heritability, genetic advance, correlation and direct indirect effect for grain yield and yield contributing traits. The results were showed that analysis of variance revealed substantial differences for all the traits under study, signifying presence of enough variability among the tested genotype. On the basis of the genotype performance CRR599-4-1 genotype found to best for its grain yield, effective tillers per plant, panicle length, test weight and spikelet fertility per cent.

Kurmanchali *et al*. (2019) tested twenty four rice genotype to assess the magnitude of genetic variability for different seventeen important traits. The estimated value of GCV were smaller than the PCV for all the characters under study shows that influence of environment on all the characters. The results were showed that broad sense heritability was high for the grain breadth, L/B ratio, grain length, gel consistency, and 1000-grain weight. The high genetic advance was recorded for the gel consistency, plant height, days to 50 per cent flowering. Shows that presence of additive gene action and it can be further used for development of new genotype through the direct selection.

Saha *et al.* (2019) reported existence of genetic variability, nature of different characters association with yield and yield contributing characters. The main aim of that study to estimate the different genetical parameters which associated with its yield and yield attributing characters in forty landraces of the rice with view to select best superior yield attributes in rice. The high value of PCV for all genotypes compared with GCV showed that there was influence of the environment. Number of unfilled grains per panicle exhibited high estimates of PCV and GCV along with filled grains per panicle, no. of grains per panicle, flag leaf area.

Parimala *et al*. (2020) experiment was carried out to investigate the genetic variability in grain yield and its component features in seventy-seven rice genotypes. The material under investigation had a considerable level of variability, according to analysis of variance. For the traits tested, the magnitude of phenotypic coefficient of variation was found to be greater than genotypic coefficient of variation, indicating that the environment has an impact on the manifestation of these features. Characters with larger estimates of phenotypic and genotypic coefficients of variation, such as number of filled grains per panicle and 1000-seed weight, suggest that they might be enhanced by direct selection.

Sudeepthi *et al*. (2020) assessed 107 best rice genotypes to estimate their variability, heritability and genetic advance as per cent of mean with regards to yield and yield components. Furthermore, the character relationship between yield and yield component features, as well as their direct and indirect influences on grain yield, were investigated. The study revealed ear bearing tillers per plant had noted a high variability, heritability and genetic advance as per cent of mean.

Bhargavi *et al*. (2021) evaluated fifty two rice genotype for twelve different characters in Randomized Block Design to study the genetic variability, heritability (broad sense) and genetic advances as per cent of mean. Reported that high Phenotypic and Genotypic coefficient of variation were recorded for *viz.* Panicle number per plant, weight of 1000-grain, grain yield per plant revealed that high amount of variation is present among the selected genotypes. High heritability along with high genetic advance was recorded for time of heading (50% of plants with panicle), stem length (excluding panicle), panicle number per plant, weight of 1000-grains shows that these traits governed by additive gene effects and thus this may be useful for selection criteria for formulating breeding strategies in rice.

Nath and Kole (2021) used twenty six different rice varieties to estimate their genetic variation and the cause- effect relationship on the different quantitative characters on seed yield in rice. The estimated varieties show positive variation for all the characters. The observed genotypic and phenotypic coefficients of variation were high for the flag leaf area, test weight, grain yield and grain number, where it is moderate for days to flowering, number of panicle, primary branches per panicle and plant height.

Chavan *et al*. (2022) used fifteen genotypes of rice to estimate the genetic variability, heritability and genetic advance for yield and yield contributing characters. The analysis of variance gives highly efficient differences among the tested genotypes for all the characters studied. The results were showed that inclusive variation was noted for the characters like *viz*. days to 50 per cent flowering, plant height, number of tillers per plant, length of panicle, total number of grains per panicle, number of filled spikelet per panicle, number of unfilled spikelet per panicle, spikelet fertility, test weight, grain yield per plant, straw yield per plant, harvest index, amylose content.

2.2. Correlation coefficient

Jiang *et al.* (2007) evaluated 274 rice genotypes, to study the association among potassium (K), calcium (Ca), sodium (Na), magnesium (Mg), iron (Fe), zinc (Zn), copper (Cu), and manganese (Mn), and other rice quality traits like three cooking quality traits, 17 amino acid contents, and protein content. The findings indicated that most mineral element contents had statistically significant associations. Additionally, a connection between protein content and the amounts of Na, Mg, Zn, Cu, or Mn was discovered to be significant.

Sabesan *et al.* (2009) conducted an investigation under coastal saline low lands, 54 rice cultivars from various origins were examined for genetic diversity and association analyses. The PCV values were slightly higher than GCV, indicating that the environment had minimal impact on how characters expressed themselves. For grain yield per plant, grain weight per 100-grains, productive tillers per plant, grain per panicle, grain length, grain width, kernel length, panicle length, and plant height, high heritability values were found along with genetic advance. At both the genotypic and phenotypic levels, the relationship between grain yield per plant and plant height and the number of productive tillers per plant was positively significant. Plant height, grains per panicle, and grain width all showed a substantial positive correlation with the 100-grain weight.

Anandan *et al*. (2011) evaluated the magnitude of genotypic variations in unpolished rice varieties for grain size, milling quality, cooking qualities, protein, and the mineral concentrations of Fe, Zn, Mn, and Cu. The findings demonstrated that among the examined rice genotypes, the most noticeable variation could be seen in the mineral content. Traditional genotypes have much greater Fe and Zn concentrations than improved cultivars. Grain yield and mineral content have a negative relationship. However, it seemed that the contents of Fe, Zn, Mn, and Cu were positively associated.

Basavaraja *et al.* (2011) conducted the experiment on 100 local rice genotypes to study the association of yield components and their direct indirect effects on grain yield. The correlation analysis showed that grain yield was significantly associated with number of tillers per plant, number of productive tillers per plant, panicle length, test weight, number of spikelet per panicle and amylose percent. Results showed that selection based on these traits helps in to bring improvement in the yield and yield attributes.

Immanual *et al*. (2011) observed the results of the phenotypic correlation coefficient (PCV) were substantially larger than those of the genotypic correlation coefficient (GCV), indicating a minor environmental effect on the development of character. Grain yield was significantly positively correlated with traits including plant height, number of tillers per plant, number of productive tillers per plant, panicle length, filled grains per panicle, and test weight. They contributed mostly to yield and could be trusted to enhance rice's genetic yield potential through genotype selection.

Venkata Lakshmi *et al*. (2014) evaluated 70 genotypes of rice (*Oryza sativa* L.) to determine the type and degree of correlation between yield and yield-related characteristics, including days to 50 per cent flowering, days to maturity, effective tillers per plant, plant height, panicle length, grains per panicle, grain yield per plant, kernel length, breadth, and L/B ratio. The findings showed that days to maturity, the number of productive tillers per plant, plant height, and kernel length were all positively and substantially related to grain production per plant, demonstrating the significance of these features as selection criteria in yield development programmes.

Bhati *et al.* (2015) conducted an experiment on thirty advanced rice genotypes, to study the genetic variability, correlation and path coefficient analysis. For all of the traits tested, analysis of variance revealed substantial differences across the 30 genotypes. The high GCV and PCV was found for the grain yield per hill along with harvest index demonstrating that these traits could be used as selection for crop improvement. At both the genotypic and phenotypic levels, correlation analysis found that grain production per hill was positively connected with harvest index, biological yield per hill, test weight, and plant height.

Vijaykumar *et al*. (2015) found substantial variations across genotypes for each of the 10 quality parameters, showing that the study's material had enough diversity. In land races and new plant types, grain length showed a significant positive correlation with the L/B ratio, grain elongation and amylose content whereas in japonica, it showed a significant positive correlation with the L/B ratio, 1000-grain weight and grain length. In land races, grain width was significantly correlated with test weight and protein content in new plant types and japonicas, grain width was significantly correlated with grain thickness and test weight. New plant kinds were predicted to have the greatest average iron content whereas land races had the highest zinc content. This demonstrated that grain width and length may be used to enhance the grain quality in rice.

Tulasi *et al.* (2016) conducted research in 58 germplasm lines, 20 indica genotypes, 25 tropical japonica genotypes, and 13 hybrids, a correlation coefficient and path analysis investigation were carried out for eleven component features, including grain yield. The collected data demonstrated that total dry matter during the flowering and harvesting stages, panicle number, length, weight, number of grains per panicle, number of filled grains per panicle, grain filling, and harvest index exhibited an extremely significant positive correlation with grain production per plant. Total dry matter at harvesting stage, harvest index, panicle weight, grain filling and total dry matter at flowering, number of grains per panicle were the key yield component features in path coefficient analysis that recorded the largest positive direct influence on grain yield.

Gour *et al*. (2017) current study used data from 83 rice genotypes to calculate genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance (GA), as well as correlations and path coefficients. For several morphological features, analysis of variance revealed substantial variations between genotypes. Grain yield per plant, panicle weight/plant, biological yield/plant, filled spikletes/plant, 1000-seed weight, harvest index, and number of tillers/plants all had high GCV and PCV, but Plant height had a moderate GCV and PCV. Grain yield per plant, panicle weight/plant, biological yield/plant, filled spikletes/plant, harvest index, 1000-seed weight, number of tillers/plants, and panicle length/plant all had high heritability coupled with high genetic advance as percent of mean, whereas days to 50 per cent flowering and days to maturity had high heritability coupled with moderate genetic advance as per cent of mean. Plant height had a negative correlation with grain production per plant, whereas positive correlations were seen with panicle weight per plant, biological yield per plant, number of tillers per plant, and harvest index. Grain yield per plant was most directly influenced by biological yield per plant, followed by harvest index, filled spikelets per plant, panicle length per plant, and days to maturity.

Kalyan *et al.* (2017) Studied 80 rice genotypes (*Oryza sativa* L.) to determine the type and degree of association between yield and yield-attributing traits. According to character association studies, plant height, the number of tillers per plant, the number of productive tillers per plant, the number of filled grains per panicle, and the test weight were significantly positively correlated with grain yield per plant. This suggested that choosing all of these qualities at once was crucial for increasing production.

Prasad *et al*. (2017) carried out a study on correlation and path analysis, 48 rice hybrids from various parents were examined at IIRR, Hyderabad. The correlation coefficients and path analysis for grain yield and their individual components were critically examined, and the results showed that panicle weight, the number of productive tillers per plant, the number of filled grains per panicle, and the weight of 1000-grains were found to be more significant factors in rice productivity. Panicle length and the total number of tillers per plant were other key variables to take into account for high grain output since they had a positive and stable relationship with the number of grains per panicle.

Thippani *et al*. (2017) conducted study to establish the degree of relationship between yield and its component features in rice. Forty F1 rice crosses were evaluated to determine the nature and extent of correlation between yield and yield attributing characters, such as days to 50 per cent flowering, days to maturity, plant height, total tillers per plant, productive tillers per plant, panicle length, number of filled grains per panicle, spikelet fertility, biomass, harvest index, 1000-grain weight, and grain yield per plant. The findings demonstrated that days to maturity, number of productive tillers per plant, plant height, and kernel length were all positively and substantially linked with grain production per plant, highlighting the usefulness of these features as selection criteria in yield development programmes.

Mourya *et al.* (2018) used thirty eight rice genotype to estimate the genetic variability, heritability, genetic advance, correlation and path coefficient analysis with regards to yield and yield components. The observation was recorded for the different eleven quantitative characters by selecting five plants randomly. The highest PCV over the GCV were observed for unfilled grain per panicle shows that expression of these traits influenced by the environmental factors. It is showed that high heritability was observe in total grains per panicle, days to 50 per cent flowering and panicle length. Grain yield is positively and significantly correlated with panicle length, test weight, filled grains per panicle, plant height, days to maturity, and spikelet fertility percentage. Days to maturity, panicle length, spikelet fertility, total grains per panicle, effective tillers per plant, test weight, and plant height all indicated positive direct effects on grain production per plant, according to a path coefficient analysis.

Dhavaleshwar *et al*. (2019) conducted the experiment on twenty seven advanced rice genotype along with four check to evaluate the nature and extent of genetic variability for yield and yield contributing traits. The results were found that all the thirteen characters under the study gives wide range of variation. Moderate to high genotypic and phenotypic correlation coefficient were observed in plant height, number of filled grains per panicle, number of spikelet per panicle, test weight and straw yield. Grain yield per plant showed the positive correlation with straw yield and harvest index therefore selection based on these traits helps to increase the grain yield per hectare.

Katiyar *et al.* (2019) used twenty seven rice genotypes to evaluate seed yield and its components for eighteen different characters. Tillers per plant showed a strong and positive phenotypic link with panicle bearing tillers per plant, seedling length showed a strong and positive phenotypic correlation with seedling vigour index. Because of the possibility of a correlation response, selection would be highly effective and efficient in improving these traits. Root length has a highly significant and positive phenotypic correlation with seedling length, and harvest index has a significantly positive phenotypic correlation with economic yield components.

Thorat *et al*. (2019) examines the type and degree of correlation between yield and the characteristics that contribute to yield, including days to 50 per cent flowering, days to maturity, productive tillers plant^{-1}, plant height (cm), panicle length (cm), total spikelets panicle^{-1}, fertile spikelets panicle^{-1}, and spikelet fertility (%). Additional variables to consider include 1000-grain weight (g), grain yield plant^{-1} (g), straw yield plant^{-1} (g), and harvest index (%). The findings showed that productive tillers plant^{-1}, panicle length, total spikelets panicle^{-1}, fertile spikelets panicle^{-1}, and straw yield plant^{-1} were all positively and significantly associated with grain yield plant^{-1}. This suggests the significance of these attributes as selection criteria in yield improvement programmes.

Ishwarya Lakshmi *et al*. (2020) examined variability, correlation, and path analysis for yield and yield-attributing variables, among the 31 rice accessions. According to the correlation, there is a positive correlation between grain production and the number of productive tillers per plant, panicle length, spikelets per panicle, 1000-seed weight, kernel length, and L/B ratio. However, it was shown that there was a negative correlation between plant height, days to 50 per cent flowering, and kernel width. Grain yield was determined by path analysis to have the most direct beneficial effects on L/B ratio, panicle length, and kernel breadth Therefore, the selection of accessions with longer panicles and earlier maturation would be ideal for programmes to increase yield.

Zeleke and Worede (2021) investigated twenty different varieties of upland rice to determine the correlation and path coefficient values between the grain yield and its constituent parts. Grain yield showed highly significant and favorable phenotypic and genotypic associations with yield per plant, number of filled grains per panicle, and biomass yield. Plant height, harvest index, days to maturity, and biomass output had the largest positive and statistically significant genotypic direct impacts on grain production. This suggests that indirect selection of these traits may increase the probability of increasing upland rice productivity. The number of filled grain per panicles, the number of fertile tillers per plant, the yield per plant and the harvest index all of these variables were strongly and favorably correlated with grain production.

CHAPTER III : MATERIALS AND METHODS

The present investigation, entitled "**Assessment of genetic variability for grain yield and its components in fine Rice (*0ryza sativa* L.)**", was conducted at the Education and Research farm, Department of Agriculture Botany, Dapoli. Dist. Ratnagiri, during the *Kharif*, 2021. The details of the material used and the methodology adopted during the course of investigation are given in this chapter under the following headings

1. To estimate the genetic variability for yield and yield attributing characters.
2. To estimate the genotypic and phenotypic correlation coefficient of different characters

3.1 Materials Required

3.1.1. Inputs used

The material for the present investigation comprised of 32 genotypes of rice. The experimental material is given below in Table 3.1.

Table 3.1. Experimental material

Sr. No.	Name of Genotype	Source
1	BARCKKV-13	RARS, Karjat
2	Sai	Nirmal seed
3	Sairam NR-9	Nirmal seed
4	Ratnagiri 6	ARS, Shirgaon
5	Palghar-1	ARS, Palghar
6	Wada kolam	Krishidhan seed
7	NR-212	Nirmal seed
8	NR-81	Nirmal seed
9	Komal-101	Krishidhan seed
10	Pusa 170-2-10-2-19	AICRP
11	WGL-14	AICRP
12	RP 6334-111-5-2-1	AICRP
13	CR 4069-111-1-1-4-5-7	AICRP
14	RP-6329-100-3-21-1	AICRP
15	CRAC-3998-41-2	AICRP
16	RP-6354-10-21-06	AICRP
17	NWGR-13052	AICRP
18	BPT-5204	AICRP

Sr. No.	Name of Genotype	Source
19	RNR-28362	AICRP
20	SKL-07-11-177-50-65-60-14	ARS, Sakoli
21	NWGR-15022	AICRP
22	BPT-2845	AICRP
23	AD-16163	AICRP
24	RP-6366 JBC 154-1-14	AICRP
25	MTU-1520	AICRP
26	GNV-1904	AICRP
27	Ankur Rupali	Ankur seed
28	Pusa-1702-10-289	AICRP
29	Karjat-8(ch)	RARS, Karjat
30	Ratnagiri-5(ch)	ARS, Ratnagiri
31	Karjat Shatabdi (ch)	RARS, Karjat
32	Karjat-4(ch)	RARS, Karjat

3.1.2 Machines and equipment used

Machines used

- Mould bold plough
- Rotovator
- Clod crusher
- Power tiller/ tractor
- Land leveler
- Tractor and Trolley
- Spectrophotometer
- Kjeldahl apparatus
- Atomic Absorption Spectrophotometer (AAS)

Equipment used

- Vaibhav sickle
- Measuring scale
- Hoe
- Weighing balance
- Meter tape
- Digital Vernier caliper

3.2 Methodology Adopted

The experiment was conducted in the Randomized Block Design (RBD) with two replications during *Kharif*, 2021 at Educational and Research farm Department of Agricultural Botany, College of Agriculture, Dapoli, The experimental details were as below

3.2.1 Experimental details

Table 3.2. Details of experimental plot

1	Crop	:	Rice
2	Spacing (cm)	:	20 x 15
3	Experimental design	:	Randomized Block Design (RBD)
4	No. of replications	:	2
5	No. of treatments / genotypes	:	32
6	No. of Lines	:	3
7	No of hills per lines	:	20
8	Plot size (m)	:	3.0 x 0.6
9	Recommended dose of fertilizer	:	100 : 50 : 50 Kg (N:P:K) kg ha^{-1}
10	Season	:	*Kharif* 2021
11	Date of sowing	:	21th June, 2021
12	Date of Transplanting	:	19 July, 2021

3.2.2 Cultural practices

The experiment was conducted at the normal fertility level on lateritic soil. The preliminary tillage operations were carried out properly in order to bring the soil at fine tilth. The total fertilizer dose applied @ 100 Kg N: 50 Kg P_2O_5: 50 Kg K_2O per hectare. Out of which half dose of nitrogen in the form of urea was applied at the time of sowing and remaining dose nitrogen was applied one month after transplanting, 26 days age seedling was transplanted with spacing of 20 x 15 cm. The operation like gap filling was done 10 days after transplanting so as to maintain one plant per hill and to maintain the plant population. Package of practices were carried out as and when required so as to maintain good stand of crop as per the standard recommendations.

3.2.3 Observations recorded

The observations on different growth parameters, yield and yield contributing traits were recorded by following standard procedures. Five plants per replication was selected for recording the following observations.

1. Days to first flowering

Number of days to first flower was recorded from date of sowing to the emergence of ear from main tiller.

2. Days to 50 per cent flowering

Days to 50 percent flowering were recorded on commencement of flowering in fifty per cent on plants in the plots from the date of sowing of the plot.

3. Days to maturity

The number of days were counted from the date of sowing to the date on which 95 per cent of the plants showed drying up, confined by the hardiness of the seeds.

4. Plant height (cm)

Plant height was measured in centimeter (cm) from base of the plant (at ground level) to the tip of the main panicle at maturity stage and calculated the average for randomly selected five plants.

5. Number of tillers plant^{-1}

At the time of maturity, number of tillers was counted from randomly selected five plants and calculated the average for those randomly selected five plants.

6. Length of panicle (cm)

The length of panicle was measured from base to the tip of panicle in centimeters at the time of maturity and calculated the average for randomly selected five plants.

7. Total number of grains panicle^{-1}

Total number of grains panicle^{-1} (both filled and unfilled) which are matured and fully developed were counted after harvesting of five plants and calculated the average for those randomly selected five plants.

8. Number of filled spikelets panicle^{-1}

Number of matured and fully developed filled spikelet's panicle^{-1} were counted after harvesting of each of the five plants under observation and mean was calculated.

9. Number of unfilled spikelets panicle^{-1}

Number of unmatured and not fully developed spikelet's panicle^{-1} were counted after harvesting of each of the five plants under observation and mean was calculated.

10. Spikelet fertility (%)

Spikelet fertility was obtained by using following formula.

$$\text{Spikelet fertility (\%)} = \frac{\text{Number of filled spikelets panicle}^{-1}}{\text{Total number of spikelets panicle}^{-1}} \text{ X } 100$$

11. Test weight (g)

The harvested fully filled, matured and clean dry seed of each treatment are collected. Then 1000 randomly selected grains weighted and recorded in grams.

12. Grain yield plant^{-1} (g)

The harvested fully filled, matured and clean dry panicles of the randomly selected five plants were threshed and cleaned. Then grains were weighted and recorded in grams and mean was calculated.

13. Straw yield plant^{-1} (g)

After removing the panicles, the dry matter (straw) obtained from five plants were dried in sunlight, weighted and recorded in grams and mean was calculated.

14. Harvest index (%)

Harvest index was calculated by using following formula given.

$$\text{Harvest Index (\%)} = \frac{\text{Total grain yield}}{\text{Biological yield}} \times 100$$

15. Grain length (mm)

Decorticated rice is taken for computing the grain shape and size. Minimum of 10 full grains per replication are taken and length measured with digital Vernier Caliper.

The International Rice Research Institute, Philippines, has given a classification for size and shape based on brown rice length and length-width ratio respectively.

16. Grain breadth (mm)

Decorticated rice is taken for computing the grain shape and size. Minimum of 10 full grains per replication are taken and breadth measured with Digital Vernier Caliper.

17. L/B ratio (mm)

The length/breadth ratio was obtained by dividing the length of a single grain by the corresponding breadth to determine the size and shape. The grain classification in India is being followed according to Ramaiah committee recommendation.

Table 3.3. Rice grain shape based on length and length/breadth ratio followed in Indian sub continent.

Grain Shape	Character
Long slender (LS)	Length 6 mm and above, length/breadth ratio 3 and above
Short slender (SS)	Length less than 6 mm, length/breadth ratio 3 and above
Medium slender (MS)	Length less than 6 mm, length/breadth ratio 2.5 to 3
Long Bold (LB)	Length greater than 6 mm and above, length/breadth ratio less than 3
Short Bold (SB)	Length less than 6 mm, length/breadth ratio less than 2.5

18. Amylose content (%)

Amylose contents of the milled rice samples were estimated by the method suggested by Juliano (1971) involving the spectrophotometer.

Determination of amylose Content

Materials: (1) Balance (mg); (2) Water bath; (3) Tri pod; (4) Gas burner; (5) 100 ml volumetric flask; (6) Pipettes (1 ml, 5 ml); (7) 1 ml and 10 ml automatic dispensing pipettes; (8) Absolute ethanol; (9) Methonol; (10) 1.0 N Sodium Hydroxide; (11) 1.0 Acetic acid; (12) Stock iodine solution (0.2% KI); (13) Amlysoe (Purified Potato, Sigma); (14) Wig-L-Amalgamator as UD Cyclone mill.

Reagents

(1) **1.0 N Sodium Hydroxide:** 40 gm of Anhydrous NaOH was dissolved in one liter distilled water.

(2) **1.0 N Acetic acid:** 57.75 ml of glacial acetic acid was dissolved in one liter of distilled water.

(3) **Iodine solution:** (0.2% I_2 in 2% KI) 2 grams of Iodine and 20 grams of KI dissolved one liter 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 min and make solution to 100 ml volumetric flask.

Preparation of amylose standard curve

Table 3.4. Protocol

H_2O	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 Acetic acid	0.0	0.2	0.4	0.6	0.8	1.0
I-KI reagent	2.0	2.0	2.0	2.0	2.0	2.0

Mix and after 20 minutes read at 620 nm

1. Take a 40 mg amylose add 1 ml of rectified spirit in a volumetric flask.
2. Then add 9 ml of 1.0 Sodium Hydroxide.
3. Shake well and boil over water bath for 15 minutes and make the solution to 100 ml volumetric flask.
4. Pipette out 1 ml, 2 ml, 3ml, 4 ml, 5 ml of the standard amylose into volumetric flask in three replicates

- For 1 ml standard amylose solution, add 0.2 ml of acetic acid and 2 ml Iodine+ KI,
- For 2 ml standard amylose solution, add 0.4 ml of acetic acid and 2 ml Iodine+ KI,
- For 3 ml standard amylose solution, add 0.6 ml of acetic acid and 2 ml Iodine+ KI,
- For 4 ml standard amylose solution, add 0.8 ml of acetic acid and 2 ml Iodine+ KI,
- For 5 ml standard amylose solution, add 1 ml of acetic acid and 2 ml Iodine+ KI,

5. After adding Iodine + KI solution makes up the solution to 100 ml and cover the flasks with a black cloth.
6. 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 the same room for at least 2 days to ensure equal moisture content. In choosing standard samples include a range of rices representing the low, intermediate and high amylose content
- Grind 20 lots of each sample to a fine powder in a Wig-L-Bug 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 long test tube (2 x 19.5 cm) add 1 ml of rectified spirit and add 9 ml of 1.0 N Sodium Hydroxide

3) Shake thoroughly and heat the test tube on water bath for 15 minutes. Pour the sample after digestion in a volumetric flask (100 ml) rinsed twice with hot distilled water and later make up to the samples to 100 ml.

4) Draw 5 ml solution in three replications into three 100 ml volumetric flasks.

5) For each 5 ml solutions add 1 ml of acetic acid and 2 ml of I_2- KI reagent and make it to 100 ml in a volumetric flask.

6) Cover the all flasks with black cloths as I_2- KI loses colour when exposed to light.

7) Adjust the spectrophotometer at 620 nm and take the readings.

8) Amylose content is assigned as per the presence of its given below.

Waxy : 1-2 %
Very Low : 2-9 %
Low : 9-20 %
Intermediate : 20-25 %
High : 25-33 %

19. Protein content (%)

The fat free oven dried 60 mesh flour sample of 0.5 g was digested with 15 ml concentrated H_2SO_4 (sp.gr.1.84) using 1g catalyst mixture K_2SO_4:$CuSO_4$ in 10:1 proportion respectively. Samples were kept on hot plate for heating at 150ºC for half an hour, 3ml of H_2O_2 was added in heated sample temperature was increased up to 200-250ºC. Again after half an hour 2-3 ml of H_2O_2 was added to avoid foaming while digestion of sample.

Samples were digested till the sample turns colourless from blackish brown. These digested samples were cooled at room temperature and 50ml volume was prepared from digested sample, by using volumetric flask. Out of 50ml sample prepared 5ml sample was taken for distillation and transferred to distillation unit for estimation of nitrogen by micro Kjeldahl method (A.O.A.C.). Percent nitrogen was multiplied with 6.25 as conversion factor to obtain protein content in percent.

20. Determination of micronutrient content from rice grain sample

Zinc (Zn) and Iron (Fe) content of rice grain samples were determined by using Atomic Absorption Spectrophotometer (AAS) as states by Lindsay and Norvell (1978). In this process the samples were digested by the application of di-acid mixture which includes nitric acid (HNO_2): and perchloric acid ($HCIO_2$) in 2:1 ratio.

Procedure for estimation of micronutrients

(A) Digestion of rice grain

- Before analysing the rice samples for estimation, the seeds were subjected to dehusking and grinding.
- The dehusked seeds were then grinded to make it powder with the help of a mechanical grinder. The rice grain powder of each genotype were then stored in the polythene bags. One gram of the rice grain powder for each genotype was weighed separately for the further use.
- The one gram powder from each genotype was taken in 150 ml conical flask and 10 ml of di-acid mixture (HNO, HCLO, 2:1) added to it. It was kept overnight at room temperature. (2.00 PM to 11.00 AM).
- Then the conical flask was placed the sand bath at temperature 180-200° C for 30-40 minutes. After a few minutes brown fumes were evolved. This indicated that the starting of digestion process. Finally white fumes were seen by clearing the solution. At the bottom of the conical flask about 2-3 ml solution was found.
- After heating was stopped and the digested sample was cooled for 20 minutes.
- Then about 20-30 ml distilled water was added to each conical flask. Then this solution was filtered into a 50 ml volumetric flask and the volume was made up to the mark (50 ml) by adding distilled water. The 50 ml solution was then transferred into a plastic bottle for each genotypes for further use. The plastic bottles stored at room temperature.

(B) Micronutrient content determination by AAS

It is based on the principle that atoms of Iron (Fe) which normally remain in ground state, under flame condition absorb energy which subjected to radiation is proportional to the specific wavelength. The absorption of radiation is proportional to the concentration of Iron. Iron content was estimated in the aliquot of seed extract by using Atomic Absorption Spectrophotometer (AAS) at 248.33 nm. The same procedure was followed for the estimation of Zinc (Zn) at 213.9 nm wavelength.

3.3 Statistical analysis

The statistical analysis will be done by the following methods

1. Statistical analysis of data on various parameters obtained during investigation will be carried out by using standard statistical method given by Panse and Sukhatme, (1985).
2. Estimation of genetic parameter includes variance; coefficient of variance will be done as per formula given by Burton and De Vane (1953).
3. Correlation among different character will be estimated as per procedure suggested by Johnson *et al*. (1955)

3.3.1 Analysis of variance (ANOVA)

Source of Variation	**D.F.**	**S.S.**	**M.S.S.**	**Expected M.S.S.**
Replication	(r-1)	RSS	RMS	$\sigma^2e + \sigma^2r$
Treatment	(g-1)	GSS	GMS	$\sigma^2e + \sigma^2g$
Error	(r-1) (g-1)	ESS	EMS	σ^2e
Total	(rg-1)	TSS		

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.

3.3.2 Estimation of mean and range

i. Mean

Mean value of each character was worked out by sum of given numbers by the total numbers of observations.

$$\bar{X} = \frac{\Sigma X_i}{n}$$

Where,

$\bar{X}$ = Mean of character

ΣX_i = summation of observations

n = total number of observations

ii. Range

The lowest and highest values from the mean of each character were recorded as range of that character.

Coefficient of variation (C.V) $= \frac{S.D}{\bar{X}} \times 100$

Where,

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

3.3.3 Estimation of components of variation

The environmental ($\sigma^2 e$), phenotypic ($\sigma^2 p$), genotypic ($\sigma^2 g$) variances were calculated as

i. Environmental variance

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

ii. Genotypic variances

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

iii. Phenotypic variances

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

Where,

GMS = Genotypic mean sum of squares

EMS = Error mean square

r = Number of replications

3.3.4 Estimation of standard error of mean and standard error of difference

a. Standard error of mean

$$\text{SEm} \pm = \sqrt{\sigma^2 e/r}$$

b. Standard error of difference

Standard error of difference between two means was calculated as S.E. of difference of mean (SEd).

$$(\text{SEd}) = \text{SE}_m \times \sqrt{2}$$

c. Critical difference

The critical difference between any two means was calculated as SEd x ‘t’ value at error degrees of freedom.

3.3.5 Estimation of Coefficient of Variation

The genotypic and phenotypic coefficient of variation were calculated as per the formula given by Burton and De Vane (1953).

1. Genotypic coefficient of variation (GCV)

$$\text{GCV (\%)} = \sqrt{\frac{\sigma^2 g}{\bar{X}}} \times 100$$

2. Phenotypic coefficient of variation (PCV)

$$\text{PCV (\%)} = \sqrt{\frac{\sigma^2 p}{\bar{X}}} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

$\bar{X}$ = Mean of characters

Categorization of range of variation as proposed by Shivasubramanian and Menon (1973)

<10(%) : Low

10 – 20 (%) : Moderate

>20 (%) : High

3.3.6 Estimation of Heritability

Heritability in broad sense were estimated for various characters by using the formulae suggested by Lush (1949). It is estimated from the total genetic variances.

$$h^2bs\ (\%) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variances

$\sigma^2 p$ = Phenotypic variances

Heritability in broad sense estimated by method, was suggested by Johnson *et.al* (1955), as given below

< 30(%) : Low

30 – 60 (%) : Medium

> 60 (%) : High

3.3.7 Estimation of genetic advance (GA)

Improvement in the mean genotypic value of selected plant over the parental population is known as genetic advance. The genetic variability is directly proportional to the genetic advance. The genetic advance is generally high with the characters having, high heritability and vice versa. It is calculated by the formula suggested by Johnson *et.al* (1955).

i. Genetic advance

$$\text{G.A.} = \frac{\sigma^2 g}{\sigma^2 p} \times \sigma p \times k$$

ii. GA as per cent of mean

$$\text{GAM} = \frac{GA}{\bar{X}} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

σp = Phenotypic standard deviation

k = Selection differential at 5% selection intensity

$\bar{X}$ = Mean of character

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

<10(%) : Low

10 – 20 (%) : Moderate

>20 (%) : High

3.3.8 Estimation of correlation coefficient

Analysis of co-variance was carried out by taking two characters at a time and error was used as environmental co-variance. The phenotypic and genotypic variances were derived as detailed below.

ANOVA for phenotypic and genotypic co-variances

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

Where,

r = Number of replication

g = Number of treatments

GMP = Genotype mean sum of products

EMP = Error mean sum of products

The genotypic and phenotypic co-variances were worked out as per the formulae given by Singh and Chaudhary (1977).

Environmental co-variance = (CoVe1.2) =EMP

Genotypic co-variance = (CoVg 1.2) = $\frac{\text{GMP}-\text{EMP}}{r}$

Phenotypic co-variance= (CoVp 1.2) = (CoVg1.2) + (CoVe 1.2)

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

1. Phenotypic correlation coefficient (r_p)

Phenotypic correlation coefficient was derived as

$$r_p 1.2 = \frac{\text{CoVp } 1.2}{\sqrt{(\sigma^2 p1)\,(\sigma^2 p2)}}$$

Where,

r_p1.2 = Phenotypic correlation between character 1 and 2

CoVp 1.2 = Phenotypic co-variance between character 1 and 2

σ^2p1 and σ^2p2 = Phenotypic variances of characters 1 and 2 respectively.

2. Genotypic correlation coefficient (r_g)

Genotypic correlation coefficient were obtained by the formula

$$r_g 1.2 = \frac{\text{CoVg } 1.2}{\sqrt{(\sigma^2 g1)\,(\sigma^2 g2)}}$$

Where,

r_g1.2 = Genotypic correlation between character 1 and 2

CoVg 1.2 = Genotypic co-variances between character 1 and 2

σ^2g1 and σ^2g2 =Genotypic variances of character 1 and 2 respectively.

The significance of genotypic and phenotypic correlation coefficient were tested by using ‘t’ test .

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

Where,

r = Correlation coefficient

n= Total number of observation

The calculated ‘t’ value is tested with table ‘t’ value for respective (n-2) degrees of freedom for significance.

3.4 Place / duration / seasons of experiment

The field experiment was carried out during *Kharif*, 2021 at Education and Research Farm, Department of Agricultural Botany, College of Agriculture, Dapoli.

Geographically, Dapoli is situated in the sub-tropical region on the $17^{0}45^{'}$ North latitude and $73^{0}12'$ East longitude having an elevation of 250 meters above the mean sea level with warm and humid conditions throughout the year. The soil of the experimental plot was lateritic in nature, the mean annual rainfall of this region ranges from 3500 to 4000 mm which is generally received from June to October.

The weather data from May 2021 to December 2021 of Dapoli collected from the Meteorological Observatory, Department of Agronomy, Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli are presented in Appendix.

CHAPTER IV : RESULTS AND DISCUSSION

The present study entitled "Assessment of genetic variability for grain yield and its components in fine Rice (*Oryza sativa* L.)" was undertaken at the Education and Research farm, Department of Agricultural Botany, College of Agriculture Dapoli during *Kharif,* 2021. The result were obtained on genetic variability and correlation coefficient aspects of rice and are presented below under the following headings.

4.1 Genetic variability, heritability and genetic advance

4.2 Correlation

4.1 Genetic variability, heritability and genetic advance

4.1.1 Analysis of variance

The analysis of variance are revealed that, mean sum of squares among all the genotypes were significant for all the twenty one characters under study. It suggests that there was considerable variability across all genotypes for every trait. Further estimation of genotypic and phenotypic variation was done using the computed genotype and error mean sum of squares.

4.1.2 Mean performance and range of variability

The statistical study of thirty two rice genotypes for twenty one traits yielded mean performance, range, general mean, standard error, coefficient of variance, and critical difference are presented in Table 4.2.

1. Days to appearance of first flower

The general mean for days to appearance of first flower was 96. Among the thirty two rice genotypes examined, the range for the first flowering's appearance was between 87 days (Karjat-4, Ratnagiri-5) to 105 days (BPT-5204). Seventeen genotypes required more days than the average, whereas fifteen genotypes required less days for the first flower appeared than the average.

2. Days to 50 per cent flowering

Days to 50 per cent flowering had a general mean of 98 days and a range of values between 89 days (Karjat-4) and 107 days (BPT-5204). For the days to 50 per cent flowering, twenty-one of the thirty-two rice genotypes evaluated required more days than the average, while eleven genotypes needed less days than the average.

3. Days to maturity

The mean values for days to maturity varied from 119 days (Ratnagiri – 5, Karjat - 4) to 139 days (BPT - 5204) with the general mean of 128 days. Twelve genotypes required less number days to maturity, while twenty genotypes required more days to maturity than the general mean.

Table 4.1. Analysis of variance for yield and yield attributing traits in rice

Sr. No.	Characters	Mean Sum of Squares		
		Replication (1)	Treatment (31**)	Error (31)
1	**Days to appearance of first flower**	1.891	25.564**	2.794
2	**Days to 50% flowering**	2.250	27.606**	2.315
3	**Days to maturity**	1.000	31.935**	2.839
4	**Plant height (cm)**	5.581	296.845**	4.612
5	**Number of tillers per plant**	0.345	21.539**	0.856
6	**Panicle length (cm)**	3.422	11.468**	1.788
7	**Number of filled spikelet's per panicle**	43.066	1329.955**	76.819
8	**Number of unfilled spikelet's per panicle**	2.402	262.669**	12.324
9	**Total number spikelet's per panicle**	65.813	1677.887**	90.207
10	**Spikelet fertility (%)**	0.021	65.08**	3.971
11	**Test weight (g)**	0.002	11.862**	0.072
12	**Straw yield per plant (g)**	5.881	51.631**	3.878
13	**Grain length (mm)**	0.001	0.203**	0.005
14	**Grain breadth (mm)**	0.001	0.14**	0.001
15	**Length / breadth ratio**	0.000	0.28**	0.003
16	**Harvest index (%)**	2.250	37.927**	17.243
17	**Amylose (%)**	0.092	4.467**	0.220
18	**Protein (%)**	0.236	3.32**	1.076
19	**Zinc (ppm)**	1.300	18.927**	1.739
20	**Iron (ppm)**	2.410	24.897**	3.049
21	**Grain yield per plant (g)**	1.891	18.015**	3.620

**=1% significance

Table 4.2. Mean performance of Thirty two rice genotypes and various yield attributing characters

Sr. No.	Genotypes	Days to appearance of first flower	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of tillers per plant	Panicle length (cm)	Number of filled spikelets / panicle	Number of unfilled spikelets / panicle	Total number spikelets /panicle
1	**BARCKKV – 13**	95	98	129	100	17.30	23.20	121	27	149
2	**Sai**	97	100	129	84	15.10	22.90	110	18	128
3	**Sairam NR – 9**	95	99	127	98	13.60	21.60	141	43	185
4	**Ratnagiri – 6**	96	99	130	105	8.50	25.90	141	23	165
5	**Palghar – 1**	98	100	130	108	16.85	24.90	138	20	159
6	**Wada Kolam**	101	104	134	122	9.40	24.40	156	30	186
7	**NR – 212**	98	100	128	85	8.85	18.95	106	31	137
8	**NR – 81**	97	100	129	77	6.90	21.70	176	27	203
9	**Komal – 101**	98	101	131	104	6.55	24.10	154	51	206
10	**Pusa 170-2-10-2-19**	96	99	129	78	7.35	21.75	131	36	167
11	**WGL – 14**	98	100	130	98	5.20	21.30	133	23	156
12	**RP 6334-111-5-2-1**	97	100	131	104	8.45	28.50	222	32	254
13	**CR 4069-111-1-1-4-5-7**	98	102	132	99	7.50	22.30	138	23	161
14	**RP-6329-100-3-21-1**	95	97	129	112	5.45	25.90	134	41	175
15	**CRAC-3998-41-2**	97	100	129	102	5.50	23.20	177	19	197
16	**RP-6354-10-21-06**	94	99	129	92	6.60	24.30	154	71	226
17	**NWGR -13052**	92	94	123	101	5.90	21.60	118	42	160
18	**BPT – 5204**	105	107	139	113	4.80	24.50	97	22	119
19	**RNR – 28362**	97	100	129	120	7.60	23.35	124	13	137

Sr. No.	Genotypes	Days to appearance of first flower	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of tillers per plant	Panicle length (cm)	Number of filled spikelets / panicle	Number of unfilled spikelets / panicle	Total number spikelets /panicle
20	**SKL-07-11-177-50-65-60-14**	92	95	124	113	7.60	24.20	132	44	176
21	**NWGR – 15022**	94	97	127	105	7.80	21.25	116	34	150
22	**BPT – 2845**	98	100	129	103	4.75	22.50	134	41	175
23	**AD – 16163**	96	98	128	98	5.70	22.40	88	39	127
24	**RP-6366 JBC 154-1-14**	97	99	126	107	8.10	24.20	124	29	153
25	**MTU – 1520**	99	101	129	98	6.40	25.50	131	33	165
26	**GNV – 1904**	94	97	128	85	5.70	20.40	112	31	143
27	**Ankur Rupali**	96	98	126	75	11.60	23.40	139	38	178
28	**Pusa 1702-10-289**	99	101	131	101	7.40	25.60	112	33	146
29	**Karjat - 8 (ch)**	102	105	135	92	9.20	23.15	163	27	191
30	**Ratnagiri - 5 (ch)**	87	90	119	81	10.50	17.20	130	37	167
31	**Karjat Shatabdi (ch)**	92	95	124	102	8.50	22.45	134	17	151
32	**Karjat - 4 (ch)**	87	89	119	83	10.10	17.30	124	28	152
	Grand mean	96	98	128	98	8.46	22.93	135	32	167
	Range lowest	**87**	**89**	**119**	**75**	**4.75**	**17.20**	**88**	**13**	**119**
	Highest	**105**	**107**	**139**	**122**	**17.30**	**28.50**	**222**	**71**	**254**
	SE (±)	1.18	1.07	1.19	1.51	0.65	0.94	6.19	2.48	6.71
	CD 5 %	3.40	3.10	3.43	4.38	1.88	2.72	17.87	7.16	19.37
	CV	1.74	1.54	1.31	2.17	10.93	5.83	6.48	10.84	5.67

4. Plant height (cm)

The range for plant height ranged from 75 cm (Ankur rupali) to 122 cm (Wada kolam) with the average of 98 cm. Among the thirty two rice genotypes fourteen genotypes observed less plant height than the average whereas eighteen genotypes gives more plant height than the average.

5. Number of tillers per plant

Tillers per plant varied in number from 4.80 (BPT-2845) to 17.30 (BARCKKV-13), with an average of 8.46. Twelve genotypes recorded more tillers than the average value of the mean, whereas the other twenty genotypes recorded fewer tillers per plant than the overall mean.

6. Panicle length (cm)

The panicle length was found highest for the genotype RP-6334-111-5-2-1 (28.50 cm) and lowest for Ratnagiri- 5 (17.20 cm) while its general mean 22.93 cm among thirty two rice genotypes fifteen genotypes exhibited lowest panicle length than general mean, while seventeen genotypes had highest in panicle length than the general mean.

7. Number of filled spikelet's per panicle

The number of filled spikelets per panicle was found to be vary from 88 (AD- 16163) to 222 (RP-6334-111-5-2-1) with a population mean of 135. From thirty two rice genotypes twenty genotypes were observed less number of filled spikelets per panicle, twelve genotypes were observed more number of filled spikelets per panicle than the population mean.

8. Number of unfilled spikelet's per panicle

Average number of unfilled spikelets per panicle was 32 which was ranged from 13 (RNR- 28362) to 71 (RP- 6354-10-21-06). The eighteen genotypes were recorded least number unfilled spikelets than the average mean, whereas fourteen genotypes were recorded more number unfilled spikelets than the average mean.

9. Total number spikelet's per panicle

The general mean recorded for total number spikelets per panicle was 167 with a range of 119 (BPT- 5204) to 254.40 (RP-6334-111-5-2-1). The twenty genotypes were recorded least number total spikelets per panicle than the general mean, while twelve genotypes recorded highest number spikelets per panicle than the general mean.

10. Spikelet fertility (%)

Spikelet fertility was 80.65 per cent on average. The range for the per cent spikelet fertility among the 32 rice genotypes evaluated was between 68.30 per cent (RP-6354-10-21-06) to 90.36 per cent (RNR- 28362). Sixteen genotypes had the highest spikelet fertility percentage, while sixteen genotypes had the lowest percentage compared to the average.

11. Test weight (g)

The character test weight was found to be highest for the genotype RNR- 28362 (20.63), while Karjat-4 (10.38) recorded lowest test weight among all the thirty two rice genotypes with the general mean of 15.03. From thirty two rice genotypes nineteen genotypes gives lowest test weight and thirteen genotypes gives highest test weight over the general mean.

12. Grain yield per plant (g)

The mean values for the grain yield per plant ranged from 8.50 g (GNV-1904) to 21.30 g (Palghar -1) with a general mean of 12.71 g. Among thirty two genotypes, sixteen genotypes showed significantly lower yield per plant than the general mean value, however sixteen genotypes recorded highest grain yield per plant than the general mean.

13. Straw yield per plant (g)

The straw yield per plant was found highest for the genotype Palghar -1 (32.80 g) and lowest for NR- 212 (12.10 g) while its general mean 17.94 g among thirty two rice genotypes twenty genotypes exhibited lowest straw yield per plant than general mean, while twelve genotypes had significantly highest in straw yield per plant than the general mean.

14. Grain length (mm)

The range of grain length was 4.54 (Karjat Shatabdi) to 6.26 (Pusa 1702-10-289) with a mean of 5.53 overall. Of the thirty-two rice genotypes, fifteen had grain lengths that were substantially shorter than the average, whereas seventeen had grain lengths that were significantly longer than the average.

15. Grain breadth (mm)

Grain breadth ranged from 1.51 (Sairam NR-9) to 2.73 (BPT-2845) while its general mean was 1.88. Amongst thirty two rice genotypes seventeen genotypes had significantly lower grain breadth than the general mean, whereas fifteen genotypes had higher grain breadth than the general mean.

16. Length / breadth ratio

Length / breadth ratio ranged from 1.88 (Karjat Shatabdi) to 3.62 (Ratnagiri-5) while its general mean was 2.98. Sixteen of the thirty-two rice genotypes had grain length/breadth ratios that were substantially lower than the average, whereas sixteen of them had grain length/breadth ratios that were greater than the average.

17. Harvest index (%)

Harvest index was measured as having a general mean of 41.91 for thirty two different rice genotypes, with mean values ranging from 33.29 to 51.98 per cent. The genotype Ratnagiri-5 (51.98%) recorded the greatest harvest index, whereas genotype RNR-28362 (33.29%) recorded the lowest. Seventeen of the thirty-two rice genotypes showed lower harvest index than the general mean, but fifteen genotypes outperformed the general mean in terms of harvest index.

18. Amylose (%)

For thirty two distinct rice genotypes, the per cent amylose was assessed, with values ranging from 20.38 to 24.84 per cent and a mean value of 23.44 as a whole. The genotypes RP 6334-111-5-2-1 achieved the highest per cent amylose, whereas the genotypes RP-6366 JBC 154-1-14 recorded the lowest. In terms of per cent amylose, ten of the thirty-two rice genotypes scored worse than the average, but twenty two genotypes scored greatly above the average.

19. Protein (%)

With a general mean of 5.55 %, the mean values for the per cent protein varied from 3.60% (AD -16163) to 8.36% (BARCKKV – 13). Of the thirty-two genotypes, nineteen genotypes had scored lower than the average value, while thirteen genotypes that were higher than the average.

20. Zinc (ppm)

The mean values for the grain zinc content ranged from 6.46 ppm (WGL-14) to 18.32 ppm (Pusa 1702-10-289) with a general mean of 12.20 ppm. Among thirty two genotypes, fourteen genotypes showed significantly lower zinc content than the general mean value, however eighteen genotypes recorded highest grain zinc content than the general mean.

21. Iron (ppm)

The mean values for the grain iron content ranged from 8.51 ppm (RP-6354-10-21-06) to 20.68 ppm (Pusa 170-2-10-2-19) with a general mean of 14.91 ppm. Among thirty two genotypes, sixteen genotypes showed significantly lower zinc content than the general mean value, however sixteen genotypes recorded highest grain zinc content than the general mean.

Table 4.2. Mean performance of Thirty two rice genotypes and various yield attributing characters

Sr. No.	Genotypes	Spikelet fertility (%)	Test weight (g)	Grain yield per plant (g)	Straw yield per plant (g)	Grain length (mm)	Grain Breadth (mm)	Length / Breadth ratio	Harvest Index (%)
1	**BARCKKV – 13**	81.61	12.30	16.80	23.50	5.33	1.56	3.42	41.71
2	**Sai**	85.70	12.32	9.90	16.50	5.74	1.68	3.43	37.60
3	**Sairam NR - 9**	76.48	11.05	14.20	17.80	5.32	1.51	3.52	44.37
4	**Ratnagiri – 6**	85.70	16.23	14.80	18.10	5.34	1.92	2.78	45.09
5	**Palghar – 1**	87.22	16.61	21.30	32.80	5.51	1.89	2.91	39.34
6	**Wada Kolam**	83.73	13.22	12.30	21.30	5.57	1.69	3.31	36.53
7	**NR – 212**	77.47	12.50	9.00	12.10	5.36	1.65	3.25	42.86
8	**NR – 81**	86.68	14.24	11.30	12.20	5.50	1.62	3.40	48.03
9	**Komal – 101**	74.96	12.70	10.10	16.50	5.44	1.84	2.97	38.04
10	**Pusa 170-2-10-2-19**	78.26	16.55	9.60	14.80	5.62	1.92	2.94	39.37
11	**WGL – 14**	85.19	14.40	11.20	17.60	5.52	1.84	3.00	38.93
12	**RP 6334-111-5-2-1**	87.43	16.39	15.80	26.10	5.62	1.81	3.12	37.79
13	**CR 4069-111-1-1-4-5-7**	85.36	18.61	16.20	19.70	5.84	2.22	2.63	45.16
14	**RP-6329-100-3-21-1**	76.36	14.56	13.60	16.00	5.73	2.03	2.83	46.04
15	**CRAC-3998-41-2**	89.90	19.48	11.50	14.50	5.77	2.05	2.82	44.31
16	**RP-6354-10-21-06**	68.30	14.48	12.90	16.60	5.74	1.82	3.16	43.74
17	**NWGR -13052**	73.60	14.73	11.90	13.80	5.24	1.74	3.02	46.35
18	**BPT – 5204**	81.50	17.61	12.60	19.20	5.74	1.94	2.96	39.65

Sr. No.	Genotypes	Spikelet fertility (%)	Test weight (g)	Grain yield per plant (g)	Straw yield per plant (g)	Grain length (mm)	Grain Breadth (mm)	Length / Breadth ratio	Harvest Index (%)
19	**RNR – 28362**	90.36	20.63	13.50	27.10	5.82	2.09	2.79	33.29
20	**SKL-07-11-177-50-65-60-14**	75.05	18.38	14.40	23.80	5.69	1.95	2.92	37.69
21	**NWGR – 15022**	77.10	15.40	11.90	19.70	5.94	2.18	2.74	37.71
22	**BPT – 2845**	76.53	14.50	13.00	21.90	5.68	2.73	2.08	37.23
23	**AD – 16163**	69.41	14.72	9.10	12.70	5.42	1.84	2.95	41.89
24	**RP-6366 JBC 154-1-14**	81.13	14.59	9.60	17.40	5.63	1.75	3.22	35.57
25	**MTU – 1520**	79.46	14.46	12.90	16.40	5.24	2.14	2.46	44.02
26	**GNV – 1904**	78.04	16.54	8.50	12.20	5.43	1.96	2.78	41.26
27	**Ankur Rupali**	78.35	12.70	12.90	15.50	5.74	1.81	3.17	45.45
28	**Pusa 1702-10-289**	76.76	17.54	11.10	13.30	6.26	2.03	3.09	45.46
29	**Karjat - 8 (ch)**	85.70	14.37	13.60	14.20	5.46	1.68	3.25	49.17
30	**Ratnagiri - 5 (ch)**	77.77	12.34	14.00	13.10	5.58	1.54	3.62	51.98
31	**Karjat Shatabdi (ch)**	88.52	16.51	17.10	25.40	4.54	2.41	1.88	40.25
32	**Karjat - 4 (ch)**	81.34	10.38	10.40	12.50	4.78	1.55	3.09	45.32
	Grand mean	80.65	15.03	12.71	17.94	5.53	1.88	2.98	41.91
	Range lowest	**68.30**	**10.38**	**8.50**	**12.10**	**4.54**	**1.51**	**1.88**	**33.29**
	Highest	**90.36**	**20.63**	**21.30**	**32.80**	**6.26**	**2.73**	**3.62**	**51.98**
	SE (±)	1.41	0.18	0.88	1.39	0.04	0.01	0.03	2.93
	CD 5 %	4.06	0.54	2.54	4.01	0.13	0.04	0.10	8.46
	CV	2.47	1.77	9.81	10.97	1.22	1.22	1.73	9.90

Table 4.2. Mean performance of Thirty two rice genotypes and various yield attributing characters

Sr. No.	Genotypes	Amylose (%)	Protein (%)	Zinc (ppm)	Iron (ppm)
1	**BARCKKV – 13**	24.58	8.36	9.38	15.51
2	**Sai**	23.52	7.67	12.58	15.65
3	**Sairam NR – 9**	24.68	4.91	7.05	12.56
4	**Ratnagiri – 6**	24.51	7.60	11.51	18.43
5	**Palghar – 1**	24.40	6.35	11.93	18.42
6	**Wada Kolam**	24.72	6.11	9.66	17.49
7	**NR – 212**	24.52	4.75	8.37	13.70
8	**NR – 81**	20.44	4.60	9.38	12.58
9	**Komal – 101**	23.56	4.65	10.08	18.46
10	**Pusa 170-2-10-2-19**	24.23	6.10	12.51	20.68
11	**WGL – 14**	20.39	4.42	6.46	13.59
12	**RP 6334-111-5-2-1**	24.84	4.49	14.46	12.47
13	**CR 4069-111-1-1-4-5-7**	21.61	5.19	14.34	10.56
14	**RP-6329-100-3-21-1**	24.25	5.85	13.31	11.57
15	**CRAC-3998-41-2**	24.47	4.41	11.61	10.66
16	**RP-6354-10-21-06**	24.54	5.26	14.66	8.51
17	**NWGR -13052**	21.40	5.72	14.43	10.43
18	**BPT – 5204**	21.60	4.88	15.53	18.56
19	**RNR – 28362**	21.67	5.37	15.52	15.67

Sr. No.	**Genotypes**	**Amylose (%)**	**Protein (%)**	**Zinc (ppm)**	**Iron (ppm)**
20	**SKL-07-11-177-50-65-60-14**	23.70	5.01	7.48	17.47
21	**NWGR-15022**	24.36	3.90	11.50	15.47
22	**BPT-2845**	24.43	4.86	16.55	11.51
23	**AD -16163**	22.02	3.60	10.37	8.61
24	**RP-6366 JBC 154-1-14**	20.38	5.97	13.43	10.38
25	**MTU – 1520**	23.98	4.59	12.64	17.50
26	**GNV – 1904**	21.50	4.90	12.53	11.59
27	**Ankur Rupali**	24.60	5.44	16.46	14.73
28	**Pusa 1702-10-289**	24.55	5.37	18.32	13.65
29	**Karjat - 8 (ch)**	24.52	7.10	8.40	20.44
30	**Ratnagiri - 5 (ch)**	24.57	7.55	13.47	19.68
31	**Karjat Shatabdi (ch)**	23.36	5.73	14.45	18.62
32	**Karjat - 4 (ch)**	24.55	6.87	12.45	15.75
	Grand mean	23.44	5.55	12.20	14.91
	Range lowest	**20.38**	**3.60**	**6.46**	**8.51**
	Highest	**24.84**	**8.36**	**18.32**	**20.68**
	SE (±)	0.33	0.19	0.29	0.30
	CD 5 %	0.95	0.56	0.86	0.88
	CV	2.00	4.98	3.45	2.91

4.1.3 GENETIC PARAMETERS

For various yield-contributing features, the estimations of components of variation, coefficient of variation, heritability, genetic advance, and genetic advance as a percentage of mean are shown in Tables 4.3 and 4.4 fig. 4.1 shows a graphic representation of genotypic and phenotypic coefficient of variation, heritability and genetic progress as a percentage of the mean.

4.1.3.1 Components of variation

The environment considerably influenced most of the polygenic characters of economic importance. Therefore, available total variation of the population was partitioned into phenotypic, genotypic and environmental variance.

Table 4.3. Estimates of Components of variation for yield and yield attributing characters in rice.

Sr. No.	Characters	Phenotypic variance	Genotypic variance	Environmental variance
1	**Days to appearance of first flower**	14.18	11.39	2.79
2	**Days to 50% flowering**	14.96	12.65	2.31
3	**Days to maturity**	17.39	14.55	2.84
4	**Plant height (cm)**	150.73	146.12	4.61
5	**Number of tillers per plant**	11.20	10.34	0.86
6	**Panicle length (cm)**	6.63	4.84	1.79
7	**Number of filled spikelet’s per panicle**	703.39	626.57	76.82
8	**Number of unfilled spikelet’s per panicle**	137.50	125.17	12.32
9	**Total number spikelet’s per panicle**	884.05	793.84	90.21
10	**Spikelet fertility (%)**	34.53	30.55	3.97
11	**Test weight (g)**	5.97	5.89	0.07
12	**Grain yield per plant (g)**	8.48	6.92	1.56
13	**Straw yield per plant (g)**	27.75	23.88	3.88
14	**Grain length (mm)**	0.10	0.10	0.00
15	**Grain breadth (mm)**	0.07	0.07	0.00
16	**Length / breadth ratio**	0.14	0.14	0.00
17	**Harvest index (%)**	27.58	10.34	17.24
18	**Amylose (%)**	2.34	2.12	0.22
19	**Protein (%)**	1.39	1.32	0.07
20	**Zinc (ppm)**	8.80	8.62	0.18
21	**Iron (ppm)**	14.32	14.14	0.19

For the twenty one characteristics under investigation, the phenotypic variation varied from 0.07 to 884.05, the genotypic variance from 0.07 to 793.84, and the environmental variance from 0.00 to 90.21. All of the traits under examination had wider phenotypic variations than their corresponding genotypic variances. Total number spikelet's per panicle (884.05), number of filled spikelet's per panicle (703.39), plant height (150.73), number of unfilled spikelet's per panicle (137.50), spikelet fertility (34.53), straw yield per plant (27.75), harvest index (27.58) were the traits with the highest phenotypic variance.

The total number spikelet's per panicle (793.84) had the highest genotypic variance, followed by number of filled spikelet's per panicle (626.57), plant height (146.12), number of unfilled spikelet's per panicle (125.17), spikelet fertility (30.55), straw yield per plant (23.88). For each of the twenty one characteristics, the environmental variations were less than the genotypic variances. This showed that environmental factors rather than genotypic factors were more important for the development of these traits.

4.1.3.2 Coefficient of variation

Table 4.4 provides the estimates of PCV and GCV at the phenotypic and genotypic levels, respectively. In general, the size of the corresponding genotypic coefficients of variation was smaller than the phenotypic coefficients of variation. The traits number of tillers per plant (39.55), number of unfilled spikelet's per panicle (36.23), straw yield per plant (29.35), iron (25.37), zinc (24.30), grain yield per plant (22.90), protein (21.30), number of filled spikelet's per panicle (19.63), total number spikelet's per panicle (17.76), gives highest value for phenotypic coefficient of variation. While a significant amount of phenotypic coefficient of variation was reported for the test weight (16.25), grain breadth (14.05), length / breadth ratio (12.61), harvest index (12.53), plant height (12.44) and panicle length (11.23).

A genotypic coefficient of variation is a statistical indicator of how much genetic diversity there is in a population. The number of tillers per plant (38.01) had the highest genotypic coefficient of variation, followed by the number of unfilled spikelets per panicle (34.57), straw yield per plant (27.23), iron (25.20), zinc (24.05), protein (20.71) and grain yield per plant (20.69). Number of filled spikelet's per panicle (18.53), total number spikelet's per panicle (16.83), test weight (16.15), had moderate genotypic coefficients. The genotypic coefficient of variation was small for the grain breadth (14.00), length / breadth ratio (12.49), plant height (12.25).

4.1.3.3 Heritability and Genetic advance

Gross variation must be divided into heritable and non-heritable components. The heritability in the present experiment ranged from 37.50 % for the harvest index to 99.29 % for the grain breadth. With the exception of the harvest index, all the studied traits show significant heritability. In general, heritability ranged from low to high.

The trait total number spikelet's per panicle (55.00) had the maximum level of genetic advance, followed by the number of filled spikelets per panicle (48.67), plant height (24.52) and number of unfilled spikelets per panicle (21.99). In contrast, the spikelet fertility (10.71) and straw yield per plant (9.34), iron (7.69) as well as days to maturity (7.19), days to 50 % flowering (6.73), number of tillers per plant (6.37), days to appearance of first flower (6.23) observed lowest value for the genetic advance. This suggests that the rate of genetic advancement varied from low to high.

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

Sr. No.	Characters	PCV (%)	GCV (%)	ECV (%)	h^2b	GA	GAM
1	**Days to appearance of first flower**	3.92	3.51	1.74	80.30	6.23	6.49
2	**Days to 50% flowering**	3.92	3.60	1.54	84.53	6.73	6.82
3	**Days to maturity**	3.25	2.97	1.31	83.67	7.19	5.50
4	**Plant height (cm)**	12.44	12.25	2.18	96.94	24.52	24.84
5	**Number of tillers per plant**	39.55	38.01	10.93	92.36	6.37	75.24
6	**Panicle length (cm)**	11.23	9.59	5.83	73.02	3.87	16.89
7	**Number of filled spikelet's per panicle**	19.63	18.53	6.49	89.08	48.67	36.03
8	**Number of unfilled spikelet's per panicle**	36.23	34.57	10.85	91.04	21.99	67.95
9	**Total number spikelet's per panicle**	17.76	16.83	5.67	89.80	55.00	32.85
10	**Spikelet fertility (%)**	7.29	6.85	2.47	88.49	10.71	13.28
11	**Test weight (g)**	16.25	16.15	1.78	98.80	4.97	33.07
12	**Grain yield per plant (g)**	22.90	20.69	9.82	81.61	4.90	38.50
13	**Straw yield per plant (g)**	29.35	27.23	10.97	86.03	9.34	52.02
14	**Grain length (mm)**	5.82	5.69	1.23	95.56	0.63	11.46
15	**Grain breadth (mm)**	14.05	14.00	1.22	99.29	0.54	28.75
16	**Length / breadth ratio**	12.61	12.49	1.71	98.16	0.76	25.49
17	**Harvest index (%)**	12.53	7.67	9.91	37.50	4.06	9.68
18	**Amylose (%)**	6.53	6.21	2.00	90.60	2.86	12.18
19	**Protein (%)**	21.30	20.71	4.99	94.51	2.30	41.48
20	**Zinc (ppm)**	24.30	24.05	3.45	97.98	5.99	49.04
21	**Iron (ppm)**	25.37	25.20	2.91	98.68	7.69	51.58

Low to high genetic advance as a percentage of mean was shown for the several features under research, ranging from 5.50 per cent for days to maturity to 75.24 per cent for the number of tillers per plant. The number of tillers per plant had the highest figure of genetic advance as a percentage of the mean (75.24%), followed by the number of unfilled spikelets per panicle (67.95%), straw yield per plant (52.02%), iron (51.58%), zinc (49.04%), protein (41.48%) and grain yield per plant (38.50%), number of filled spikelets per panicle (36.03%), test weight (33.07%), total number spikelet's per panicle (32.85%) and grain breadth (28.75) had moderate estimates of genetic advance as a percentage of the mean. Low estimations of genetic advancement as a percentage of mean were recorded by the remaining characters .

4.2 Correlation

The link between the yield and the yield-attributing features must be studied since the grain yield or seed yield is a complicated character that depends on several independent characters. The correlation coefficient was computed for each feasible combination of the traits in order to understand the relationship between the characters at the phenotypic and genotypic levels. The mutual link between yield and its component features may be seen *via* correlation analysis. An efficient method of anticipating selection response and locating suitable individuals in breeding populations is to evaluate phenotypic and genotypic correlation. Tables 4.5 and 4.6 show, respectively, the phenotypic and genotypic connections between the twenty one traits examined in the current investigation.

4.2.1.Phenotypic correlation coefficient

Grain yield per plant had highly significant and positive correlation with plant height (0.339), number of tillers per plant (0.357), panicle length (0.360), spikelet fertility (0.347), straw yield per plant (0.686) and significant correlation with number of filled spikelets per panicle (0.280), test weight (0.268) and iron (0.295) Conversely there was no significant association (positive or negative) between grain yield and other features.

The character days to appearance of first flower indicated highly significant and positive correlation with days to 50 per cent flowering (0.959), days to maturity (0.895), panicle length (0.465), grain length (0.373), While significant negative correlation with protein (-0.363) and plant height (0.311), test weight (0.249) had significant correlation with days to appearance of first flower.

The character days 50 per cent flowering exhibited highly significant and positive correlation with days to maturity (0.909), panicle length (0.472), grain length (0.393), whereas protein (-0.320) had significant negative correlation with days 50 per cent flowering and plant height (0.303), test weight (0.267) had significant correlation with days 50 per cent flowering. However remaining characters had either positive or negative but non-significant correlation with days 50 per cent flowering.

Days to maturity showed highly significant and positive correlation with panicle length (0.503), grain length (0.377), plant height (0.350) and test weight (0.302) had significant positive correlation days to maturity, while significant negative correlation with protein (-0.267). Moreover leftover characters had either positive or negative but non-significant correlation with days maturity.

The trait plant height has highly significant and positive correlation with panicle length (0.552), test weight (0.447), straw yield per plant (0.580), grain breadth (0.347), grain yield per plant (0.339) but negative correlation with harvest index (-0.423) and significant negative correlation with length/ breadth ratio(-0.309). Although there was no significant association (positive or negative) between plant height and other traits.

Number of tillers per plant had highly significant and positive correlation with straw yield per plant (0.332), length / breadth ratio (0.435), amylose (0.363), protein (0.483), grain yield per plant (0.357) but negative correlation with test weight (-0.391), grain breadth (-0.457) and significant positive correlation with iron (0.263) However remaining traits had either positive or negative but non-significant correlation number of tillers per plant.

For panicle length highly significant and positive correlation found with number of filled spikelet's per panicle (0.417), total number spikelet's per panicle (0.390), test weight (0.373), straw yield per plant (0.390) and grain yield per plant (0.360). But significant positive correlation with grain length (0.305).

The number of filled spikelet's per panicle showed highly significant and positive correlation found with total number spikelet's per panicle (0.919), spikelet fertility (0.403) and significant positive correlation with grain yield per plant (0.280). Although there was no significant association (positive or negative) between plant height and other traits.

The number of unfilled spikelet's per panicle showed highly significant and positive correlation with total number spikelet's per panicle (0.456), but negative correlation with spikelet fertility (-0.861) and test weight (-0.324) and significant negative correlation with straw yield per plant (-0.272), iron (-0.275). Although there was no significant association (positive or negative) between plant height and other traits.

The character total number spikelet's per panicle exhibited significant and positive correlation with amylose (0.303), whereas there was no significant association (positive or negative) between total number spikelet's per panicle and other characters.

Spikelet fertility showed highly significant and positive correlation with test weight (0.332) straw yield per plant (0.403), grain yield per plant (0.347) and significant positive correlation with iron (0.287) while other traits had non-significant positive or negative correlation with the spikelet fertility.

Test weight reported highly significant and positive correlation with straw yield per plant (0.361), grain length (0.389), grain breadth (0.565) but negative correlation with length / breadth ratio (-0.481), protein (-0.350) and significant negative correlation with amylose (-0.264) while positive with grain yield per plant (0.268).

The straw yield per plant exhibited highly significant and positive correlation with grain breadth (0.327), grain yield per plant (0.686) but negative highly significant correlation with harvest index (-0.576). The trait length/breadth (-0.313) ratio showed significant and negative correlation with straw yield per plant. It having non-significant positive correlation with amylose (0.116), zinc (0.015) and iron (0.225). The character straw yield per plant showed non-significant negative correlation with grain length (-0.002).

Grain length was negatively and highly significant correlated with protein (-0.404). It had non-significant positive correlation with zinc (0.138), grain breadth (0.15), length / breadth ratio (0.217), amylose (0.001) and grain yield per plant (0.008).

Grain breadth revealed positive and highly significant association with zinc (0.371) but negative highly significant correlation with length / breadth ratio (-0.917), protein (-0.379) and having negative significant correlation with harvest index (-0.264). It had positive non-significant association with grain yield per plant (0.214).

The length / breadth ratio exhibited negative and significant correlation with zinc (-0.314) and having non-significant positive correlation with harvest index (0.228), amylose (0.069), protein (0.225), iron (0.003). The character length/breadth ratio showed non-significant negative correlation with grain yield per plant (-0.181).

The trait harvest index non-significantly and positively associated with amylose (0.162), protein (0.173), zinc (0.013), and grain yield per plant (0.109).

For trait amylose positive significant correlation observed with iron (0.318) and it having non-significant positive correlation with protein (0.242), zinc (0.038), grain yield per plant (0.236).

Protein (%) exhibited non-significant positive correlation with zinc (0.188), iron (0.166) but negatively associated with the grain yield per plant (-0.123).

Zinc (ppm) content in grain recorded negative and non-significant correlation with grain yield per plant (-0.126) and iron (-0.208).

Iron (ppm) content in grain recorded positive and significant correlation with grain yield per plant (0.295).

Table 4.5. Phenotypic correlation for yield and yield contributing traits

Character	DFF	D50F	DTM	PLHT	NTPP	PL	NFSPP	NUSPP	NTSPP	SF	TW	SYPP	GL	GB	LB	HI	Amylose	Protein	Zinc	Iron	GYPP
DFF	1**																				
D50F	0.959**	1**																			
DTM	0.895**	0.909**	1**																		
PLHT	0.311*	0.303*	0.350**	1**																	
NTPP	-0.12	-0.123	-0.122	-0.157	1**																
PL	0.465**	0.472**	0.503**	0.552**	-0.044	1**															
NFSPP	0.083	0.141	0.134	0.04	-0.007	0.417**	1**														
NUSPP	-0.233	-0.176	-0.171	-0.12	-0.22	0.046	0.069	1**													
NTSPP	-0.018	0.056	0.052	-0.012	-0.093	0.390**	0.919**	0.456**	1**												
SF	0.239	0.233	0.222	0.146	0.234	0.156	0.403**	-0.861**	0.02	1**											
TW	0.249*	0.267*	0.302*	0.447**	-0.391**	0.373**	0.072	-0.324**	-0.064	0.332**	1**										
SYPP	0.113	0.121	0.147	0.580**	0.332**	0.390**	0.205	-0.272*	0.075	0.403**	0.361**	1**									
GL	0.373**	0.393**	0.377**	0.169	-0.159	0.305*	0.009	0.119	0.055	-0.109	0.389**	-0.002	1**								
GB	0.163	0.154	0.158	0.347**	-0.457**	0.237	-0.065	-0.089	-0.093	0.07	0.565**	0.327**	0.15	1**							
LB	-0.043	-0.023	-0.044	-0.309*	0.435**	-0.166	0.077	0.144	0.126	-0.113	-0.481**	-0.313*	0.217	-0.917**	1**						
HI	-0.168	-0.154	-0.139	-0.423**	0.029	-0.189	0.073	0.099	0.104	-0.085	-0.23	-0.576**	-0.123	-0.264*	0.228	1**					
Amylose	-0.13	-0.106	-0.075	-0.05	0.363**	0.112	0.235	0.238	0.303*	-0.098	-0.264*	0.116	0.001	-0.031	0.069	0.162	1**				
Protein	-0.363**	-0.320**	-0.267*	-0.183	0.483**	-0.243	-0.082	-0.122	-0.121	0.101	-0.350**	-0.052	-0.404**	-0.379**	0.225	0.173	0.242	1**			
Zinc	-0.113	-0.128	-0.092	-0.022	-0.136	0.107	-0.105	0	-0.093	-0.027	0.213	0.015	0.138	0.371**	-0.314*	0.013	0.038	0.188	1**		
Iron	0.06	0.036	0.056	-0.005	0.263*	-0.038	-0.008	-0.275*	-0.116	0.287*	-0.04	0.225	-0.182	-0.071	0.003	-0.016	0.318*	0.166	-0.208	1**	
GYPP	0.1	0.128	0.154	0.339**	0.357**	0.360**	0.280*	-0.188	0.176	0.347**	0.268*	0.686**	0.008	0.214	-0.181	0.109	0.236	-0.123	-0.126	0.295*	1**

DFF- Days to appearance of first Flower	**D50F- Days to 50% flowering**	**DTM- Days to maturity**	**PLHT- Plant Height (cm)**	**NTPP- Number of tillers plant^{-1}**	**PL- Panicle Length (cm)**
NFSPP- Number of filled spikelets panicle^{-1}	**NUSPP- Number of unfilled spikelets panicle^{-1}**	**NTSPP- Total number of spikelets panicle^{-1}**	**SF – Spikelets Fertility (%)**	**TW- Test weight (g)**	**SYPP- Straw yield plant^{-1}**
GL- Grain length (mm)	**GB- Grain Breadth (mm)**	**L/B- Length/breadth Ratio**	**HI- Harvest index (%)**	**Amylose %**	**Protein %**
Zinc (ppm)	**Iron (ppm)**	**GYPP- Grain yield plant^{1}**			

4.2.2 Genotypic correlation coefficient

The results of the genotypic correlation coefficient in the current study (Table 4.6) showed a positive and highly significant association between grain yield per plant and straw yield per plant (0.876) followed by panicle length (0.548), number of tillers per plant (0.479), plant height (0.436), number of filled spikelets per panicle (0.356), spikelet fertility (0.330) and test weight (0.325). It showed a positive significant correlation with the total number of spikelet per panicle (0.267). Conversely there was no significant association (positive or negative) between grain yield and other characters.

The character days to appearance of first flower indicated highly significant and positive correlation with days to 50 per cent flowering (0.98), days to maturity (0.995), plant height (0.354) panicle length (0.650) and grain length (0.417) but highly significant and negative correlation with harvest index (-0.489), protein (-0.464). And spikelet fertility (0.306), test weight (0.299) had significant positive correlation with days to appearance of first flower, while number of unfilled spikelet's per panicle (-0.282) negative significant association with days to appearance of first flower.

The character days to 50% flowering showed highly significant and positive correlation with days to maturity (0.97), panicle length (0.641), grain length (0.432), plant height (0.339), but highly significant and negative correlation with harvest index (-0.454), protein (-0.478). The spikelet fertility (0.266) and test weight (0.301) showed significant positive correlation with days to 50% flowering.

Days to maturity showed highly positive significant correlation with plant height (0.387), panicle length (0.655), test weight (0.324), grain length (0.441) but it had negative highly significant correlation with harvest index (-0.420) and protein (-0.390). The trait spikelet fertility (0.262) had significant positive correlation with days to maturity.

The trait plant height has highly significant and positive correlation with straw yield per plant (0.651) followed by panicle length (0.563), test weight (0.456), grain breadth (0.356), grain yield per plant (0.436) but negative correlation with harvest index (-0.742). It showed significant negative correlation with length/breadth ratio (-0.319) and protein (-0.250). Although there was no significant association (positive or negative) between plant height and other traits.

Number of tillers per plant had highly significant and positive correlation with straw yield per plant (0.385) followed by length / breadth ratio (0.471), amylose (0.430), protein (0.618), iron (0.355) and grain yield per plant (0.479) but negative correlation with test weight (-0.419), grain breadth (-0.479).

For panicle length highly significant and positive correlation found with number of filled spikelet’s per panicle (0.355), total number of spikelet’s per panicle (0.327) test weight (0.430), grain length (0.372), grain yield per plant (0.548) and straw yield per plant (0.543). The harvest index (-0.534) and protein (-0.394) formed highly significant but negative correlation with panicle length.

The number of filled spikelet’s per panicle showed highly significant and positive correlation found with total number spikelet’s per panicle (0.918), spikelet fertility (0.399) and grain yield per plant (0.356). Amylose (0.265) recorded significant positive correlation with number of filled spikelet’s per panicle.

The number of unfilled spikelet’s per panicle showed highly significant and positive correlation with total number spikelet’s per panicle (0.464), but negative and highly significantly correlation with spikelet fertility (-0.861), test weight (-0.335), straw yield per plant (-0.288). It having significant positive association with harvest index (0.316), amylose (0.296) and negatively correlated with iron (-0.315). Whereas, it had non-significant association (positive or negative) between number of unfilled spikelet’s per panicle and other characters.

The character total of number spikelet’s per panicle exhibited non-significant and positive correlation with spikelet fertility (0.013), straw yield per plant (0.087), grain length (0.069), length/ breadth (0.135), harvest index (0.227), while significant and positively correlated with amylose (0.353). The grain yield per plant (0.267) noted significant positive correlation with total number spikelet’s per panicle. Rest of the characters had non-significant negative correlation with total number spikelet’s per panicle.

Spikelet fertility showed highly significant and positive correlation with straw yield per plant (0.434) followed by test weight (0.349), iron (0.336) and grain yield per plant (0.330). It having negative significant correlation with harvest index (-0.287). While other traits had non-significant either positive or negative correlation with the spikelet fertility.

Test weight reported highly significant and positive correlation with straw yield per plant (0.384), grain length (0.406) grain breadth (0.570) and grain yield per plant (0.325) but highly negative association with length / breadth ratio (-0.485), harvest index (-0.383), protein (-0.515) whereas significant negative association with amylose (-0.270).

Grain length had non-significant positive correlation with grain breadth (0.152), length / breadth ratio (0.205), zinc (0.177) and negatively non-significantly correlated with harvest index (-0.189) amylose (-0.005), iron (-0.241), grain yield per plant (-0.005). The per cent protein (-0.563) recorded highly significant and negative correlation with grain length.

Table 4.6. Genotypic correlation for yield and yield contributing traits

Character	DFF	D50F	DTM	PLHT	NTPP	PL	NFSPP	NUSPP	NTSPP	SF	TW	SYPP	GL	GB	LB	HI	Amylose	Protein	Zinc	Iron	GYPP
DFF	**1****																				
D50F	0.98**	**1****																			
DTM	0.995**	0.97**	**1****																		
PLHT	0.354**	0.339**	0.387**	**1****																	
NTPP	-0.133	-0.131	-0.174	-0.167	**1****																
PL	0.650**	0.641**	0.655**	0.563**	-0.075	**1****															
NFSPP	0.117	0.183	0.175	-0.002	-0.012	0.355**	**1****														
NUSPP	-0.282*	-0.186	-0.183	-0.137	-0.218	0.029	0.075	**1****													
NTSPP	-0.008	0.089	0.083	-0.056	-0.097	0.327**	0.918**	0.464**	**1****												
SF	0.306*	0.266*	0.262*	0.145	0.236	0.144	0.399**	-0.861**	0.013	**1****											
TW	0.299*	0.301*	0.324**	0.456**	-0.419**	0.430**	0.077	-0.335**	-0.065	0.349**	**1****										
SYPP	0.211	0.212	0.233	0.651**	0.385**	0.543**	0.226	-0.288*	0.087	0.434**	0.384**	**1****									
GL	0.417**	0.432**	0.441**	0.176	-0.148	0.372**	0.025	0.119	0.069	-0.1	0.406**	-0.001	**1****								
GB	0.177	0.164	0.173	0.356**	-0.479**	0.284*	-0.066	-0.09	-0.094	0.074	0.570**	0.352**	0.152	**1****							
LB	-0.045	-0.023	-0.04	-0.319*	0.471**	-0.199	0.087	0.145	0.135	-0.111	-0.485**	-0.338**	0.205	-0.921**	**1****						
HI	-0.489**	-0.454**	-0.420**	-0.742**	-0.004	-0.534**	0.114	0.316*	0.227	-0.287*	-0.383**	-0.638**	-0.189	-0.443**	0.389**	**1****					
Amylose	-0.118	-0.088	-0.083	-0.055	0.430**	0.144	0.265*	0.296*	0.353**	-0.143	-0.270*	0.122	-0.005	-0.034	0.072	0.213	**1****				
Protein	-0.464**	-0.478**	-0.390**	-0.250*	0.618**	-0.394**	-0.105	-0.21	-0.176	0.202	-0.515**	-0.093	-0.563**	-0.540**	0.337**	0.730**	0.447**	**1****			
Zinc	-0.176	-0.187	-0.151	-0.038	-0.196	0.101	-0.128	-0.016	-0.12	-0.017	0.229	0.038	0.177	0.416**	-0.342**	0.055	0.09	0.055	**1****		
Iron	0.089	0.071	0.105	0.002	0.355**	-0.008	-0.006	-0.315*	-0.131	0.336**	-0.036	0.255*	-0.241	-0.092	-0.001	-0.068	0.337**	0.536**	-0.039	**1****	
GYPP	0.149	0.178	0.221	0.436**	0.479**	0.548**	0.356**	-0.124	0.267*	0.330**	0.325**	0.876**	-0.005	0.246	-0.216	-0.194	0.228	0.163	0.063	0.136	**1****

DFF- Days to appearance of first Flower	**D50F- Days to 50% flowering**	**DTM- Days to maturity**	**PLHT- Plant Height (cm)**	**NTPP- Number of tillers plant-1**	**PL- Panicle Length (cm)**
NFSPP- Number of filled spikelets panicle-1	**NUSPP- Number of unfilled spikelets panicle-1**	**NTSPP- Total number of spikelets panicle-1**	**SF – Spikelets Fertility (%)**	**TW- Test weight (g)**	**SYPP- Straw yield plant-1**
GL- Grain length (mm)	**GB- Grain Breadth (mm)**	**L/B- Length/breadth Ratio**	**HI- Harvest index (%)**	**Amylose %**	**Protein %**
Zinc (ppm)	**Iron (ppm)**	**GYPP- Grain yield plant1**			

Grain breadth revealed positive and highly significant association with zinc (0.416) but negative and highly significant correlation with length / breadth ratio (-0.921), harvest index (-0.443), protein (-0.540).

The length / breadth ratio exhibited highly positive significant correlation with harvest index (0.389), protein (0.337) but highly negative significant with zinc (-0.342). While other traits had non-significant either positive or negative correlation with the length / breadth ratio.

The trait harvest index highly significant and positively correlated with protein (0.730), where as it found non-significant positive correlation with amylose (0.213), zinc (0.055) and negative non-significant with iron (-0.068), grain yield per plant (-0.194).

For trait amylose highly positive significant correlation observed with protein (0.447), iron (0.337), grain yield per plant (0.228) and zinc (0.09) noted non-significant positive correlation with amylose.

Protein (%) exhibited highly significant positive correlation with iron (0.536). As the trait per cent protein having positive but non-significant correlation with the zinc (0.055) and grain yield per plant (0.163).

Zinc (ppm) content in grain recorded positive and non-significant correlation with grain yield per plant (0.063), while non-significant negative correlation with iron (-0.039).

Iron (ppm) content in grain recorded positive and non-significant correlation with grain yield per plant (0.136).

DISCUSSION

Genetic variability studies offer fundamental knowledge about the genetic traits of the population, on which breeding strategies are developed for further crop development. Additionally, these investigations are useful for understanding the type and degree of variability that can be linked to a variety of factors, including crop sensitivity to the environment, hereditary traits, and genetic advancement. For the purpose of creating an effective breeding strategy for the development of high-yielding varieties, the identification of significant yield components and their associations with yield and with one another is particularly helpful. The correlation coefficient, which measures the degree of symmetrical link between two variables or characteristics, aids in our knowledge of the nature and scope of the relationship between yield and the features that make up its components.

In context of the above, the current study was conducted to quantify the different genetic variability parameters, explore the relationships between characteristics, and evaluate the correlation in thirty two genotypes of rice (*Oryza sativa* L.).

4.3 General performance of genotypes

4.3.1 Genetic variability

The main requirement for a crop breeding programme is genetic variation. As a result, plant breeders are always looking for new strategies to explore and recombinate genetic material to gather or create variety. Before using diverse techniques, plant breeders should have a thorough understanding of the nature, expression, and extent of variability present in the population of crops. Therefore, assessing population variability becomes a pre-requisite for each breeding effort.

The analysis of variance in the current experiment showed that genotypes reported a large range of variation and that genotype differences were significant for each of the twenty-one features under examination. Nevertheless, the level of variation varied depend greatly on the characters in concern. Highly significant variations in treatment (genotypes) suggested that all of the features under examination had a considerable level of variability. The methods of selection to be used in each situation would rely on how well we understood the type and degree of variability. These findings were in conformity to those of Rukmini devi *et al.* (2016), Rashmi *et al.* (2017), Pratap *et al.* (2018) and Bandi *et al.* (2018).

The wide range of variation were observed for the characters days to appearance of first flower (87 to 105 days), days to 50 per cent flowering (89 to 107 days), plant height (75 to 122 cm), number of filled spikelet per panicle (88 to 222), number of unfilled spikelet per panicle (13 to 71), total number spikelet per panicle (119 to 254). Mustafa and Elsheikh (2007), Khaire *et al*. (2017), Pratap *et al.* (2018), Bhargavi *et al*. (2021) and Chavan *et al.* (2022) noted a similar range of variation in these traits.

The characters days to maturity (119 to 139 days), number of tillers per plant (4.75 to 17.30), panicle length (17.20 to 28.50 cm), spikelet fertility (68.30 to 90.36 %), test weight (10.38 to 20.63 g), grain yield per plant (8.50 to 21.30 g), straw yield per plant (12.10 to 32.80 g), harvest index (33.29 to 51.98 %), zinc (6.46 to 18.32 ppm) and iron (8.51 to 20.68 ppm). These results are in agreement with the findings of Parimala *et al.* (2020), Abebe *et al.* (2017), Gamphala *et al*. (2015) and Girma *et al.* (2018).

Narrow range of variation were recorded for the traits like grain length (4.54 to 6.26 mm), grain breadth (1.51 to 2.73 mm), l/b ratio (1.88 to 3.62) amylose (20.38 to 24.84 %) and protein (3.93 to 10.65 %). Similar, results were reported by Jayasudha *et al.* (2010) and Kurmanchali *et al.* (2019).

Rice grain yield has complicated characteristics and is significant commercially. Studies are therefore primarily concerned with assessing the yield potential of various genotypes. In the present investigation grain yield per plant recorded wide range of variation for thirty two different genotypes ranged from 8.50 g in GNV-1904 to 21.30 g in Palghar-1. The genotypes *viz.*, Palghar-1 (21.30 g), Karjat Shatabdi (17.10 g), BARCKKV-13 (16.80 g), CR-4069-111-1-1-4-5-7 (16.20 g), RP-6334-111-5-2-1 (15.80 g), Ratnagiri -5 (14.00 g), SKL-07-11-177-50-65-60-14 (14.40 g). These genotypes were found to be best for its gain yield per plant Similar, results observed by Pratap *et al*. (2018).

Grain types such as long slender, short slender, medium slender, long bold, and short bold are distinguished by their quality traits, which include grain length, grain breadth, and length/breadth ratio. Grain length varied from 4.54 mm to 6.26 mm with the general mean of 5.53 mm. The longest grain length were recorded in Pusa 1702-10-289 (6.26 mm) followed by NWGR-15022 (5.94 mm), CR-4069-111-1-1-4-5-7 (5.84 mm), RNR-28362 (5.82 mm), CRAC-3998-41-2 (5.77 mm), RP-6354-10-21-06 (5.74 mm), and short length in Karjat Shatabdi (4.54 mm), Karjat-4 (4.78 mm), NWGR-13052 (5.24 mm), MTU-1520 (5.24 mm).

As character grain breadth also gives highest value ranged from 1.51 mm to 2.73 mm with the mean of 1.88 mm. The maximum breadth were recorded in BPT-2845 (2.73 mm), CR-4069-111-1-1-4-5-7 (2.22 mm), NWGR-15022 (2.18 mm), MTU-1520 (2.14 mm), Karjat Shatabdi (2.41 mm) and minimum grain breadth were recorded in Sairam NR-9 (1.51 mm), Ratnagiri-5 (1.54 mm), Karjat-4 (1.55 mm) and BARCKKV-13 (1.56 mm).

Based on Ramaiah's (1969) systematic categorization of rice, thirty two distinct rice genotypes were divided into different grain types for the current study. The all genotypes are classified into long slender (LS), short slender (SS), medium slender (MS), long bold (LB) and short bold (SB) (Table 4.7). Out of thirty two genotypes, one genotypes had long slender (LS) type grain, fifteen genotypes had short slender (SS), fifteen genotypes were having medium slender (MS) type grain and one genotypes had short bold (SB) grain type. The medium slender grain type is most preferred grain type and higher yield than other types.

4.3.2 Components of variation

Each character's overall variability may be broken down into three categories: phenotypic, genotypic, and environmental. This makes it easier to distinguish between the study's heritable and non-heritable features. In general, for various traits, phenotypic variations were larger than matching genotypic variances.

The phenotypic variance was higher for the total number spikelet’s per panicle (884.05), number of filled spikelet’s per panicle (703.39), plant height (150.7), number of unfilled spikelet’s per panicle (137.50), spikelet fertility (34.53), straw yield per plant (27.75), harvest index (27.58), days to maturity (17.39), days to 50% flowering (14.96), days to appearance of first flower (14.18), number of tillers per plant (11.20), zinc (8.80), grain yield per plant (8.48), panicle length (6.63), test weight (5.97), amylose content (2.34), protein content (1.39), length / breadth ratio (0.14), grain length (0.10) and grain breadth (0.07).

The genotypic variance was higher for the total number spikelet’s per panicle (793.84) had the highest genotypic variance, followed by number of filled spikelet’s per panicle (626.57), plant height (146.12), number of unfilled spikelet’s per panicle (125.17), spikelet fertility (30.55), straw yield per plant (23.88), days to maturity (14.55), iron (14.14), days to 50 per cent flowering (12.65), days to appearance of first flower (11.39), number of tillers per plant (10.34), harvest index (10.34), zinc (8.62), grain yield per plant (6.92), test weight (5.89), panicle length (4.84), amylose (2.12), protein (1.32), length / breadth ratio (0.14), grain length (0.10), and grain breadth (0.07).

The computed genetic parameters showed that there was a considerable degree variation found between the phenotypic and genotypic variances. Among all the thirty two genotypes the characters total number spikelet’s per panicle, number of filled spikelet’s per panicle, plant height, number of unfilled spikelet’s per panicle, spikelet fertility, straw yield per plant gives highest value for phenotypic variance than the corresponding genotypic variances. Similar findings were observed by Sameera *et al*. (2015), Khaire *et al*. (2017).

4.3.3 Coefficient of variation

The amount of variation present in the population for a particular characteristic is measured by the genotypic and phenotypic coefficients of variation. For many individual features, it was discovered that genotypic coefficients of variance were often less than matching phenotypic coefficients of variation. But for many characters, the variations between GCV and PCV were less, showing that such characters were less affected by their environment. This was in agreement with the findings of Veerabadhiran *et al.* (2009), Dhurai *et al.* (2014).

Higher PCV and GCV estimations were noted for the characters, number of tillers per plant (39.55, 38.01), number of unfilled spikelet's per panicle (36.23, 34.57), straw yield per plant (29.35, 27.33), iron (25.37, 25.20), zinc (24.30, 24.05), grain yield per plant (22.90, 20.69) and protein (21.30, 20.71). This suggests that the genotypes used for study have a diverse genetic background, and selection for these traits might aid in the genetic development of crops. These findings matched those of studies conducted by Meena *et al.* (2018), Mourya *et al.* (2018), Saha *et al.* (2019)

For characters like number of filled spikelet's per panicle (19.63, 18.53), total number spikelet's per panicle (17.76, 16.83), test weight (16.25, 16.15), grain breadth (14.05, 14.00), length / breadth ratio (12.61, 12.49), plant height (12.44, 12.25), harvest index (12.53, 7.67), moderate estimations of PCV and GCV were found. These findings are consistent with those of Gokulkrishnan *et al.* (2014), Gour *et al.* (2017).

The characters like panicle length (11.23, 9.59), spikelet fertility (7.29, 6.85), amylose (6.53, 6.21), grain length (5.82, 5.69), days to appearance of first flower (3.92, 3.51), days to 50 per cent flowering (3.92, 3.60), days to maturity (3.25, 2.97). These results are in conformity with the findings of Rashid *et al.* (2017), Ram *et al.* (2017) and Veerabadhiran *et al.* (2009).

4.3.4 Heritability and genetic advance

An excellent measure of how traits are passed down from one set of parents to their offspring is heritability, which is the heritable component of phenotypic variation (Falconer, 1960). According to Robinson's (1949) categorization, the heritability estimates in the current study were high for each feature. Genetic progress expressed as a percentage of the mean depends on the measurement and is thus used to compare characteristics. For various yield and yield-attributing characteristics, the heritability values ranged from 37.5% to 99.29%.

For each of the characteristics analyzed, heritability estimates were high. The figures for grain breadth, test weight, iron, length/breadth ratio, zinc, and plant height were particularly high. High heritability shows that the traits are amenable to selection. The genetic advance values in the current study varied from 0.54 to 55.00. The greatest genetic advance was documented for total spikelets per panicle (55.00). The genetic advance values as a percentage of the mean varied from 5.50 to 75.24.

Table 4.7. Classification of thirty two rice genotypes into different grain types

Sr. No.	Genotype	Grain length (mm)	L/B Ratio	Grain Type
1	BARCKKV – 13	5.33	3.42	Short Slender
2	Sai	5.74	3.43	Short Slender
3	Sairam NR – 9	5.32	3.52	Short Slender
4	Ratnagiri – 6	5.34	2.78	Medium Slender
5	Palghar – 1	5.51	2.91	Medium Slender
6	Wada Kolam	5.57	3.31	Short Slender
7	NR – 212	5.36	3.25	Short Slender
8	NR – 81	5.50	3.40	Short Slender
9	Komal – 101	5.44	2.96	Medium Slender
10	Pusa 170-2-10-2-19	5.62	2.93	Medium Slender
11	WGL – 14	5.52	3.00	Short Slender
12	RP 6334-111-5-2-1	5.62	3.11	Short Slender
13	CR 4069-111-1-1-4-5-7	5.84	2.63	Medium Slender
14	RP-6329-100-3-21-1	5.73	2.83	Medium Slender
15	CRAC-3998-41-2	5.77	2.82	Medium Slender
16	RP-6354-10-21-06	5.74	3.15	Short Slender
17	NWGR -13052	5.24	3.02	Short Slender
18	BPT – 5204	5.74	2.96	Medium Slender
19	RNR – 28362	5.82	2.78	Medium Slender
20	SKL-07-11-177-50-65-60-14	5.69	2.92	Medium Slender
21	NWGR-15022	5.94	2.73	Medium Slender
22	BPT-2845	5.68	2.08	Medium Slender
23	AD -16163	5.42	2.95	Medium Slender
24	RP-6366 JBC 154-1-14	5.63	3.22	Short Slender
25	MTU – 1520	5.24	2.45	Medium Slender
26	GNV – 1904	5.43	2.78	Medium Slender
27	Ankur Rupali	5.74	3.17	Short Slender
28	Pusa 1702-10-289	6.26	3.08	Long Slender
29	Karjat - 8 (ch)	5.46	3.25	Short Slender
30	Ratnagiri - 5 (ch)	5.58	3.62	Short Slender
31	Karjat Shatabdi (ch)	4.54	1.88	Short Bold
32	Karjat - 4 (ch)	4.78	3.09	Short Slender

High estimates of broad sense heritability observed for grain breadth (99.29%), test weight (98.80%), iron (98.68%), l/b ratio (98.16%), zinc (97.98%), plant height (96.94%), grain length (95.56%), protein (94.51%), number of tillers per plant (92.36%), number of unfilled spikelet's per panicle (91.04%), amylose (90.60%), total number spikelet's per panicle (89.80%), number of filled spikelet's per panicle (89.08%), spikelet fertility (88.49%), straw yield per plant (86.03%), days to 50% flowering (84.53%), days to maturity (83.67%), grain yield per plant (81.61%), days to appearance of first flower (80.30%), panicle length (73.02%). Low heritability estimate was observed in harvest index (37.50%). These results are according with the findings of Kurmanchali *et al.* (2019), Meena *et al.* (2018), Gokulkrishnan *et al.* (2014), Islam *et al.* (2015).

Genetic advance signifies genetic improvement under selection. The efficiency of selection in enhancing attributes can be better understood by expressing genetic advance as a percentage of the mean. The value of genetic advance ranged from 0.54 (grain breadth) to 55.00 (total number spikelet's per panicle). High estimates of genetic advance were observed for the characters like total number spikelets per panicle (55.00%), number of filled spikelets per panicle (48.67), plant height (24.52), number of unfilled spikelets per panicle (21.99%), spikelet fertility (10.71%) and straw yield per plant (9.34%). Whereas low for iron (7.69%), days to maturity (7.19%), days to 50% flowering (6.73%), number of tillers per plant (6.37%), days to appearance of first flower (6.23%), zinc (5.99%), test weight (4.97%), grain yield per plant (4.90%), harvest index (4.06%), panicle length (3.87%), amylose (2.89), protein (2.30), l/b ratio (0.76%), grain length (0.63%) and grain breadth (0.54%). Anjaneyulu *et al.* (2010), Krishna *et al.* (2010), Aditya *et al.* (2013), Kurmanchali *et al. (*2019) also recorded similar kind of results in rice.

Genetic advance as per cent of mean varied from 5.50 per cent for days to maturity to 75.24 per cent for number of tillers per plant. Highest values for genetic advance per cent of mean noted by number of tillers per plant (75.24%) followed by number of unfilled spikelet's per panicle (67.95%), straw yield per plant (52.02)%, iron (51.58%), zinc (49.04%), protein (41.48%), grain yield per plant (38.50%), number of filled spikelet's per panicle (36.03%), test weight (33.07%), total number spikelet's per panicle (32.85%), grain breadth (28.75%), length / breadth (25.49%), plant height (24.84%), panicle length (16.89%), spikelet fertility (13.28%), amylose (12.18%), grain length (11.46%), harvest index (9.68%), days to 50% flowering (6.82%), days to appearance of first flower (6.49%), days to maturity (5.50%). The results were in accordance with Sameera *et al.* (2016), Gokulkrishnan *et al.* (2014), Yadav *et al.* (2017).

The most important selection criteria are heritability and genetic advance. In general, genetic advance and heritability estimates work better together than just heritability estimates to increase the genetic gain under selection. High heritability estimates and high genetic advance estimates as a percentage of the mean were documented for number of tillers per plant (92.36%, 75.24%), number of unfilled spikelet's per panicle (91.04%, 67.95%), straw yield per plant (86.03%, 52.02%), grain breadth (99.29%, 28.75%), test weight (98.8%, 33.07%), l/b ratio (98.16%, 25.49%), zinc (97.98%, 49.04%), iron (98.68%, 51.58%), protein (94.51%, 41.48 %), plant height (96.94%, 24.84%), grain length (95.56%, 11.46%), amylose (90.60%, 12.18%) total number spikelet's per panicle (89.80%, 32.85%), number of filled spikelet's per panicle (89.08%, 36.03), spikelet fertility (88.49%, 13.28%), grain yield per plant (81.61%, 38.50%), panicle length (73.02%, 16.89%), days to 50% flowering (84.53%, 6.82%), Similar kind of results were recorded by the Gokulkrishnan *et al.* (2014), Yadav *et al.* (2017), Gour *et al.* (2017), Sameera *et al.* (2016).

High genetic advance as a percentage of the mean and heritability indicated additive gene action and less environmental influence in the development of specific traits. Therefore, crop improvement programmes would be more successful if they improved these traits that have high heritability together with strong genetic advancement as a percentage mean.

High heritability estimates and low genetic advance as percent mean was detected in days to appearance of first flower (80.30%, 6.49%), days to maturity (83.67%, 5.50%), Low heritability estimates and low genetic advance as percent mean was recorded in harvest index (37.50%, 9.68%). These traits are affected by non-additive gene activity, so choosing them would not be beneficial for future crop development programmes. Similar findings were recorded by Sammera *et al*. (2016), Ajmera *et al.* (2017), Rashmi *et al*. (2017).

4.4 Correlation studies

To determine how the numerous traits explored in the current experiment interacted with one another, correlation analyses were conducted. It is a significant statistical constant that indicates the strength and direction of the correlation between the yield and its constituent phenotypic and genotypic traits. A few more component qualities combine to form the polygenic trait known as yield. Because of this, plant breeders require knowledge of the relationships between yield and the qualities that contribute to yield in order to successfully complete a breeding programme. Selection that just considers phenotypic association is ineffective because it provides a false genetic representation of how different characteristics interact. Therefore, it is crucial to understand both phenotypic and genotypic coefficients in order to determine the proportional genotypic correlation contribution of each of the component features on yield and to give desired genotypes precedence during selection programmes.

The genotypic and phenotypic correlation coefficients between characteristics in all genotypes were examined in the current experiment. The genotypic correlation coefficient is often greater than the phenotypic correlation coefficient. Grain yield per plant can be increased by choosing germplasms with the best performances for these traits, as shown by the genotypic and phenotypic correlation of grain yield per plant with plant height, straw yield per plant, number of tillers per plant, panicle length and spikelet fertility which were highly significant and positive. The findings demonstrated that number of tillers per plant, plant height was all positively and substantially linked with grain production per plant also observed by Thippani *et al.* (2017), Bhati *et al*. (2015), Dhavaleshwar *et al*. (2019).

The character days to appearance of first flower indicated highly significant and positive correlation with days to 50 per cent flowering, days to maturity, panicle length and grain length but highly significant and negative correlation with protein. While test weight had significant correlation with days to appearance of first flower both at genotypic and phenotypic level.

The character days to 50 per cent flowering showed highly significant and positive correlation with days to maturity, panicle length, grain length but highly significant and negative correlation with protein. While significant positive correlation with test weight however remaining characters had either positive or negative but non-significant correlation with days 50 per cent flowering. Immanual *et al.* (2011), Venkata Lakshmi *et al.* (2014), Ishwarya Lakshmi *et al*. (2020) revealed similar results for days to 50 per cent flowering.

Days to maturity showed highly significant and positive correlation with panicle length, grain length, plant height and test weight and had significant correlation with days to maturity but it had negative significant correlation with protein. Basavaraja *et al.* (2011) also reported that days to maturity had highly significant and positive correlation with the plant height.

The trait plant height has highly significant and positive correlation with panicle length, test weight, straw yield per plant, grain breadth, grain yield per plant but negative correlation with harvest index both at genotypic and phenotypic level. Although significant negative correlation with length/ breadth ratio. Bhati *et al.* (2015) and Thippani *et al*. (2017), Immanual *et al*. (2011) reported that plant height were positively and substantially linked with grain production per plant.

Number of tillers per plant had highly significant and positive correlation with straw yield per plant, length / breadth ratio, amylose, protein, grain yield per plant but negative correlation with grain breadth, test weight. Prasad *et al*. (2017), Basavaraja *et al.* (2011), Immanual *et al*. (2011) observed similar results for number of tillers per plant.

For the trait panicle length highly significant and positive correlation found with straw yield per plant, number of filled spikelet’s per panicle, total number spikelet’s per panicle, test weight, grain yield per plant but it had negative correlation with harvest index. These findings are in agreement with the work on correlation studies by Basavaraja *et al*. (2011). Immanual *et al*. (2011)

The number of filled spikelet's per panicle showed highly significant and positive correlation found with total number spikelet's per panicle, spikelet fertility and significant positive correlation with grain yield per plant. Although there was no significant association (positive or negative) between plant height and other traits. Tulasi *et al.* (2016), Thorat *et al.* (2019), Zeleke and Worede (2021) Immanual *et al.* (2011) Kalyan *et al.* (2017), reported that grain yield had significant and positive correlated with number of filled spikelet per panicle.

The number of unfilled spikelet's per panicle showed highly significant and positive correlation with total number spikelet's per panicle but highly significant and negative correlation with spikelet fertility, straw yield per plant and test weight.

The character total number spikelet's per panicle exhibited non-significant and positive correlation with spikelet fertility, straw yield per plant, grain length, length/ breadth ratio and harvest index, while significant and positively correlated with amylose and grain yield per plant at genotypic level. Rest of the characters had non-significant negative correlation with total number spikelet's per panicle. The findings showed that total number spikelet's per panicle significant and positively correlated with grain yield per plant were earlier observed by Basavaraja *et al.* (2011), Thorat *et al.* (2019), Ishwarya Lakshmi *et al.* (2020).

Spikelet fertility showed highly significant and positive correlation with test weight, straw yield per plant, grain yield per plant but showed significant and positive correlation with iron. While other traits had non-significant either positive or negative correlation with the spikelet fertility. Thorat *et al.* (2019) examines the same type and degree of correlation between yield and the characteristics that contribute to yield.

Test weight reported highly significant and positive correlation with grain breadth, straw yield per plant, grain length, but highly significant negatively associated with length / breadth ratio, protein whereas significant positive association with grain yield per plant and significant negative association with amylose. Grain yield was significantly positively correlated with trait test weight also reported by Basavaraja *et al.* (2011), Bhati *et al.* (2015), Immanual *et al.* (2011)

The straw yield per plant exhibited highly significant positive correlation with grain breadth, grain yield per plant but negative significant correlation with harvest index and having non-significant positive correlation with amylose and zinc. It showed non-significant negative correlation with grain length, protein. Similar observations were confirmed by Dhavaleshwar *et al.* (2019), Thorat *et al.* (2019), Zeleke and Worede (2021)

Grain length had negatively and highly significant correlation with protein and but having non-significant positive with grain breadth, length / breadth ratio and zinc. It is negative non-significantly correlated with harvest index. Sabesan *et al.* (2009), Vijaykumar (2015) reported similar kind of results.

Grain breadth revealed positive and highly significant association with zinc and it having negative highly significant correlation with length / breadth ratio, protein. But with grain yield per plant the character grain breadth formed non-significant positive association. The results were in accordance with Sabesan *et al.* (2009), Vijaykumar (2015).

The length/breadth ratio exhibited negative and significant correlation with zinc. The character length/breadth ratio showed non-significant negative correlation with grain yield per plant.

The trait harvest index exhibited non-significant positive correlation with amylose, zinc, and grain yield per plant but negative non-significant with iron. These were in consonance with the result of Bhati *et al*. (2015), Tulasi *et al*. (2016), Dhavaleshwar *et al*. (2019), Zeleke and Worede (2021).

For trait amylose positive significant correlation observed with iron and it having non-significant positive correlation with zinc and grain yield per plant. Both at the genotypic and phenotypic level. The correlation analysis showed that grain yield was significantly associated with amylose Similar, results also observed by Basavaraja *et al.* (2011)

Protein exhibited highly significant positive correlation with iron. As the trait per cent protein having positive but non-significant correlation with the zinc and grain yield per plant. Jiang *et al.* (2007) reported similar kind of results.

Zinc content in grain recorded positive and non-significant correlation with grain yield per plant, while non-significant negative correlation with iron. While iron content in grain recorded positive and non-significant correlation with grain yield per plant. Anandan *et al*. (2011) also reported that grain yield had positively associated with zinc and iron content.

CHAPTERV : SUMMARY AND CONCLUSIONS

The present study titled "**Assessment of genetic variability for grain yield and its components in fine Rice (*0ryza sativa* L.)**" was carried out with thirty two rice genotypes for its twenty one yield and yield attributing characters. The present experiment was conducted at Education and Research farm, Department of Agriculture Botany, Dapoli in a Randomized Block Design with two replications to assess the experimental material during *Kharif,* 2021. This study examined the kind and degree of genetic variability as well as the degree of relationship between grain yield and its constituent traits.

Five randomly chosen plants from each genotype per replication were used as the basis for the observations. Twenty one characters studied in this experiment were days to appearance of first flower, days to 50 per cent flowering ,days to maturity, plant height (cm), number of tillers per plant, panicle length (cm), number of filled spikelet's per panicle, number of unfilled spikelet's per panicle, total number spikelet's per panicle, spikelet fertility (%), test weight (g), grain yield per plant (g), straw yield per plant (g), grain length (mm), grain breadth (mm), length / breadth ratio, harvest index (%), amylose (%), protein (%), zinc (ppm), iron (ppm).

For each character, highly substantial variance was found throughout the whole genotype population. This demonstrated the existence of significant variance and provided an adequate opportunity for choosing viable genotypes from the current range of genotypes for yield enhancement. The characteristics with the largest range of variation were total number spikelet's per panicle, number of filled spikelet's per panicle, plant height, number of unfilled spikelet's per panicle, whereas grain breadth, length/breadth and protein showed less variation.

The genotypes NWGR-13052, SKL-07-11-177-50-65-60-14, Ratnagiri-5, Karjat-4 were found early for days to appearance of first flower indicating that these genotypes could act as donors in a programme of hybridization to develop early maturity rice varieties, while most late flowered genotype was BPT-5204.

The genotypes Wada kolam followed by RNR-28362, BPT-5204, SKL-07-11-177-50-65-60-14 and RP-6329-100-3-21-1 were tallest among all thirty two rice genotypes. The maximum number of tillers per plant were observed for the genotypes BRCKKV-13 followed by Palghar-1, Sai and Sairam NR-9. The highest panicle length was for the genotypes RP 6334-111-5-2-1, Ratnagiri-6, RP 6329-100-3-21-1, Pusa 1702-10-289, MTU-1520 and Palghar-1.

The highest number of filled spikelets per panicle were recordedfor the genotypes RP 6334-111-5-2-1 followed by CRAC-3998-41-2, NR-81, and Karjat-8. The genotypes RNR-28362 followed by Karjat Shatabdi, Sai, CRAC-3998-41-2 recorded lowest number of unfilled spikelets per panicle. The total number of spikelets per panicle were maximum for the genotypes RP 6334-111-5-2-1 followed by RP 6354-10-21-06, Komal-101, NR-81. Spikelet fertility noted highest for the gentypes RNR 28362, CRAC-3998-41-2, Karjat Shatadi, RP 6334-111-5-2-1 and Palghar-1.

The highest test weight were recorded for the genotypes RNR-28362, CRAC-3998-41-2, CR 4069-111-1-1-4-5-7 and SKL-07-11-177-50-65-60-14. The highest grain yield per plant were observed for the genotypes Palghar-1 followed by Karjat Shatabdi, BRCKKV-13, CR 4069-111-1-1-4-5-7. The genotypes Palghar-1, RNR-28362, RP 6334-111-5-2-1, RP 6334-111-5-2-1 and SKL-07-11-177-50-65-60-14 estimated highest straw yield per plant. The genotypes Ratnagiri-5 (51.98 per cent), Karjat-8 (49.17 per cent), NR-81 (48.03 per cent), NWGR-13052 (46.35 per cent) had highest harvest index.

The highest grain length, grain breadth and length/breadth ratio were recorded by Pusa 1702-10-289 (6.26 mm), BPT-2845 (2.73 mm) and Ratnagiri-5 (3.62), respectively.

The variance analyses conducted for this study showed that for all features, phenotypic variation was larger in size than genotypic variance. For most features, the phenotypic and genotypic variation were closer to one another in terms of size, indicating a lesser influence of the environment upon how these traits appeared.

In general, the size of the corresponding genotypic coefficients of variation was smaller than the phenotypic coefficients of variation (PCV) (GCV). The number of tillers per plant, number of unfilled spikelet’s per panicle, straw yield per plant (g), iron (ppm), zinc (ppm) and grain yield per plant (g) all showed high genotypic and phenotypic coefficients of variation.

Significant heritability values were recorded for all the characters. All the characters under study showed high heritability except harvest index. The characters total number of spikelets per panicle, number of filled spikelets per panicle and plant height showed comparatively higher estimates of genetic advance. Genetic advance as per cent of mean were high for number of tillers per plant, number of unfilled spikelets per panicle, straw ield per plant, iron, zinc, protein and grain yield per plant.

According to characters association studies, most characters had genotypic correlation coefficients that were significantly greater than their phenotypic correlation coefficients. At both the phenotypic and genotypic levels, the plant height, number of tillers per plant, panicle length, spikelet fertility and straw yield per plant all showed highly significant positive correlations with the grain yield per plant, whereas the number of unfilled spikelet’s per panicle and the length/breadth ratio showed non- significant negative correlation coefficients.

Conclusion

Based on the results of the current investigation, it is observed that the genotypes showed significant genetic variability for all the characters under study linked to the yield, most of the characteristics showed high estimates of heritability and genetic advance, demonstrating the dominance of additive gene action. This suggests that there is plenty of scope for choosing promising genotypes to increase productivity. Using the right breeding methods and programmes, this variability might be successfully managed to create better kinds. The simultaneous selection of plant height, number of tillers per plant, number of unfilled spikelet's per panicle, total number spikelet's per panicle, number of filled spikelet's per panicle, straw yield per plant and grain length could aid in the genetic improvement of yield in the rice genotypes under study, according to correlation for yield.

- The genotypes Palghar-1, BARCKKV-13, RP 6334-111-5-2-1 and CR 4069-111-1-1-4-5-7 were identified as the best for yield and yield attributing charactersagainst check Karjat Shatabdi.
- The genotypes Ratnagiri - 6, SKL-07-11-177-50-65-60-14, and Sairam NR-9 were identified as the best for yield and yield attributing characters against check Ratnagiri-5.
- In order to create a newhigh yielding, good quality fine rice variety the above genotypes may be effectively used as parents in subsequent breeding programmes.

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Weather data (*Kharif*-2021)

Date	Metero-logical Week	Rainfall (m.m.)	No. of Rainy days	Temperature (^{0}C.)		Humidity (%)	
				Max	Min	Mor.	Even.
14/05/21 to 20/05/21	20	205.6	5	33.2	23.6	84	66
21/05/21 to 27/05/21	21	0.0	0	32.6	23.7	84	65
28/05/21 to 03/06/21	22	92.6	2	32.9	23.9	89	70
04/06/21 to 10/06/21	23	279.8	5	30.8	22.4	95	80
11/06/21 to 17/06/21	24	581.6	7	28.3	22.3	96	88
18/06/21 to 24/06/21	25	332.6	7	29.7	22.6	93	86
25/06/21 to 01/07/21	26	197.0	7	29.1	22.6	96	86
02/07/21 to 08/07/21	27	57.4	3	30.9	24.0	92	81
09/07/21 to 15/07/21	28	695.0	7	27.6	22.5	98	96
16/07/21 to 22/07/21	29	970.2	7	27.1	22.4	98	97
23/07/21 to 29/07/21	30	164.8	7	28.4	23.4	93	89
30/07/21 to 05/08/21	31	89.8	7	28.3	23.2	94	86
06/08/21 to 12/08/21	32	73.3	5	29.5	22.8	96	82
13/08/21 to 19/08/21	33	178.8	7	28.4	21.7	95	86
20/08/21 to 26/08/21	34	109.8	3	29.1	21.8	96	79
27/08/21 to 02/09/21	35	74.2	6	28.8	21.9	96	83
03/09/21 to 09/09/21	36	598.2	7	28.5	22.1	98	89
10/09/21 to 16/09/21	37	238.4	6	28.5	23.0	96	86
17/09/21 to 23/09/21	38	224.9	6	28.8	22.3	96	88
24/09/21 to 30/09/21	39	120.6	6	29.1	22.0	96	83
01/10/21 to 07/10/21	40	14.4	2	31.7	22.4	94	74
08/10/21 to 14/10/21	41	13.0	2	31.6	22.0	93	76
15/10/21 to 21/10/21	42	0.0	0	31.7	20.1	92	70
22/10/21 to 28/10/21	43	0.0	0	32.4	17.5	89	62
29/10/21 to 04/11/21	44	0.0	0	33.0	18.6	85	63
05/11/21 to 11/11/21	45	10.2	1	32.5	17.9	90	62
12/11/21 to 18/11/21	46	25.0	2	33.4	19.2	93	60
19/11/21 to 25/11/21	47	4.4	0	31.9	21.6	94	65
26/11/21 to 02/12/21	48	33.0	1	31.1	18.1	92	62
03/12/21 to 09/12/21	49	20.0	2	29.8	17.1	94	67
10/12/21 to 16/12/21	50	0.0	0	32.5	16.2	94	52
17/12/21 to 23/12/21	51	0.0	0	31.2	13.5	95	54
24/12/21 to 31/12/21	52	0.0	0	30.4	13.2	95	62
		5404.6	**120.0**				

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This letter confirms that manuscript titled **"Assessment of genetic variability for grain yield and its components in fine rice (*Oryza sativa* L.)"** authored by **SA Chendake, RL Kunkerkar, SS Desai, Dr. SS Chavan, RV Dhopavkar and KS Sarak** has been accepted for publication.

Yours Sincerely,

Akhil Gupta

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THESIS ABSTRACT

a)	Title of the thesis	: ASSESSMENT OF GENETIC VARIABILITY FOR GRAIN YIELD AND ITS COMPONENTS IN FINE RICE (*Oryza sativa* L.)
b)	Full name of the student	: Chendake Shubham Annaso
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	: 2022
f)	Major subject	: Genetics and Plant Breeding
g)	Total number of pages in the thesis	: 76
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j)	Signature, Name and address of forwarding authority	:

Field experiment was conducted during *Kharif*, 2021 at Education and Research farm, Department of Agricultural Botany, College of Agriculture, Dapoli, Ratnagiri. The current study was conducted with objectives to estimate the genetic variability for yield and yield attributing characters and to estimate the genotypic and phenotypic correlation coefficient of different characters in thirty-two genotypes of rice (*Oryza sativa* L.). Based on the results of the current investigation, it is observed that the genotypes showed significant genetic variability for all the characters under study linked to the yield, most of the characteristics showed high estimates of heritability and genetic advance, demonstrating the dominance of additive gene action. The genotypes Palghar-1, BARCKKV-13, RP 6334-111-5-2-1, CR 4069-111-1-1-4-5-7, Ratnagiri-6 and SKL-07-11-177-50-65-60-14 were identified as the best for yield and yield attributing characters. In order to create a new high yielding, good quality fine rice variety these genotypes may be effectively used as parents in subsequent breeding programmes.

Key words: Rice, Genotypes, Genetic variability, Yield *etc.*

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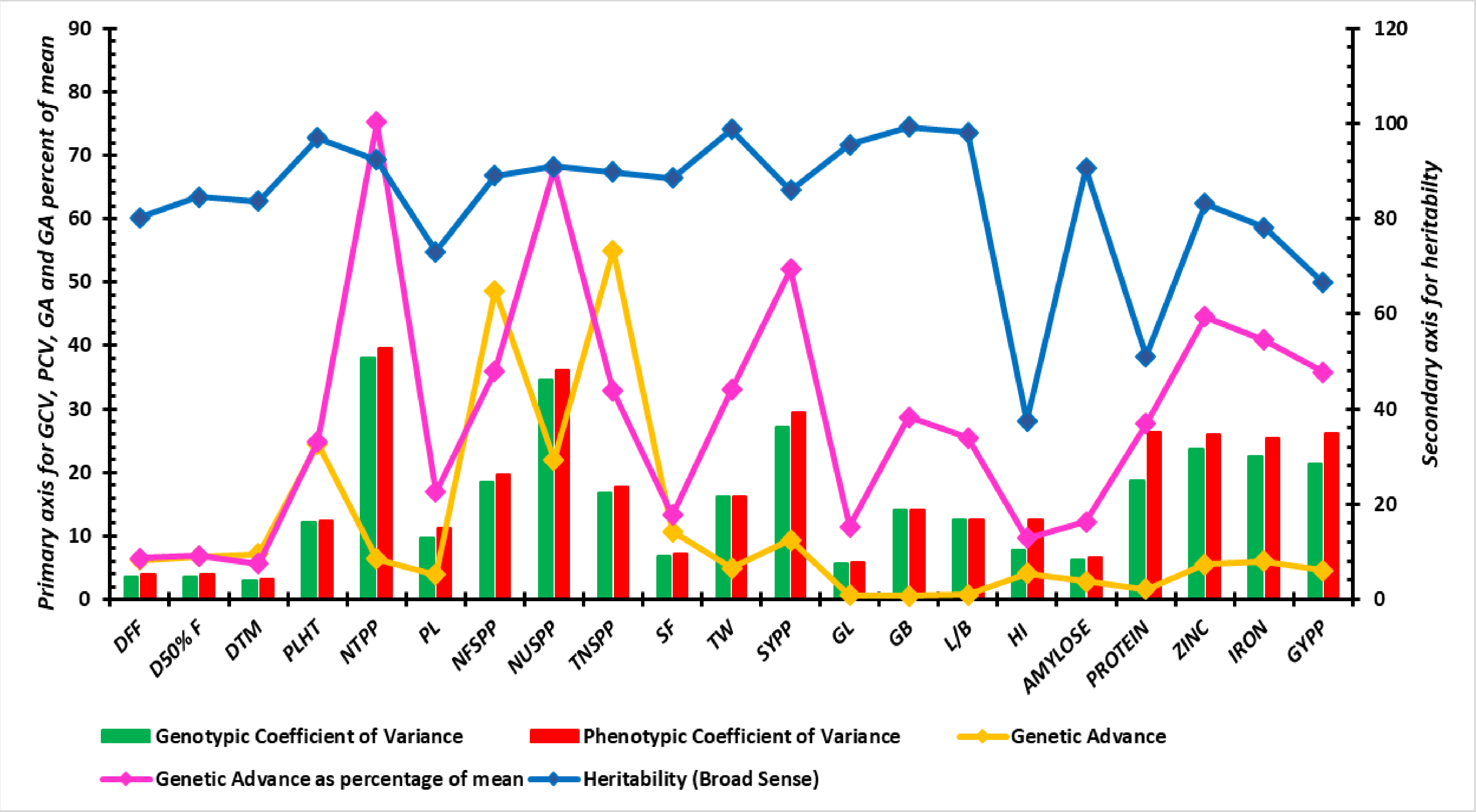

Fig. 4.1. Shows a graphical representation of genotypic and phenotypic coefficient of variation, heritability and genetic advance as a percentage of the mean.

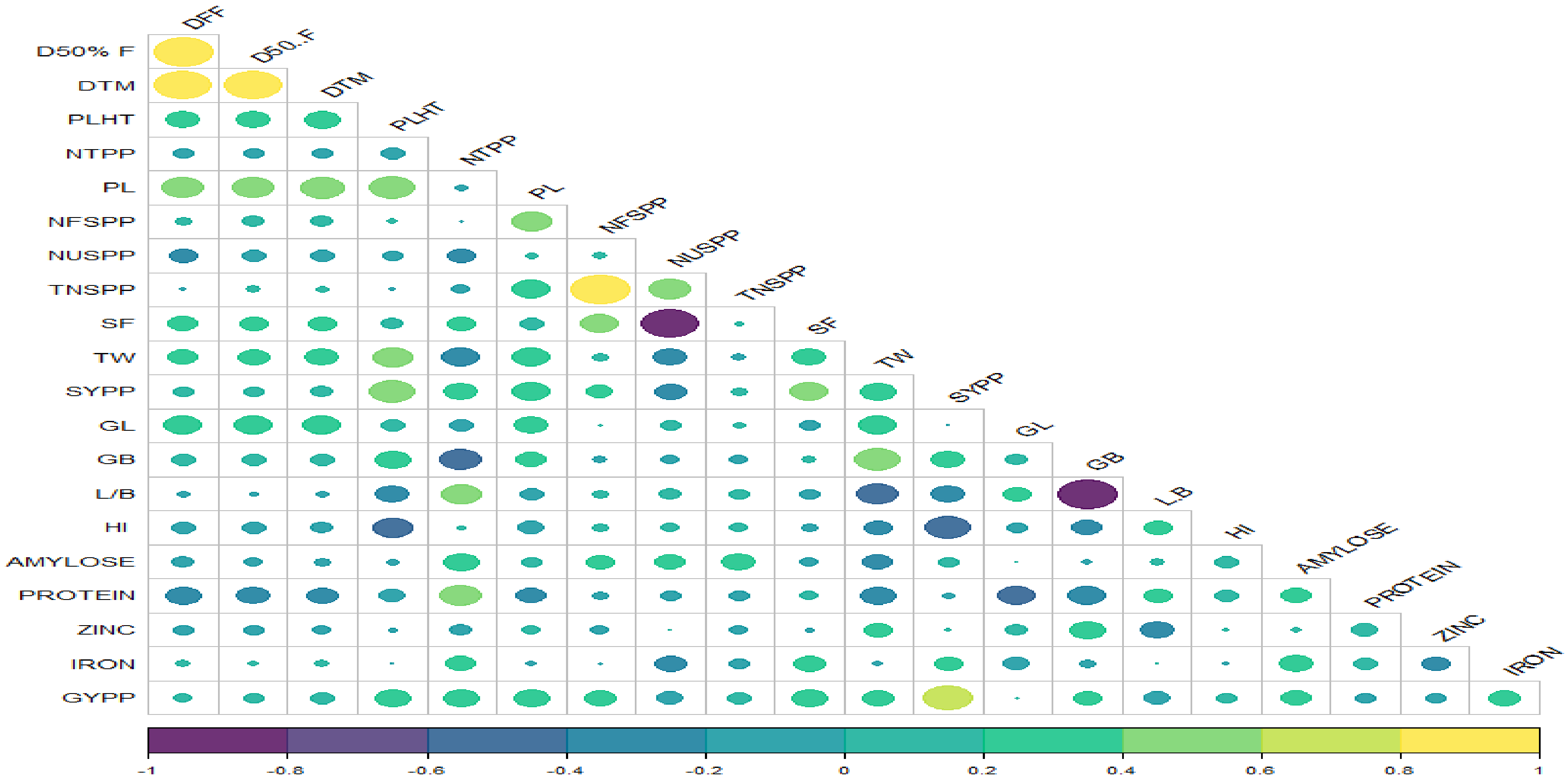

Fig. 4.2. Phenotypic corplot

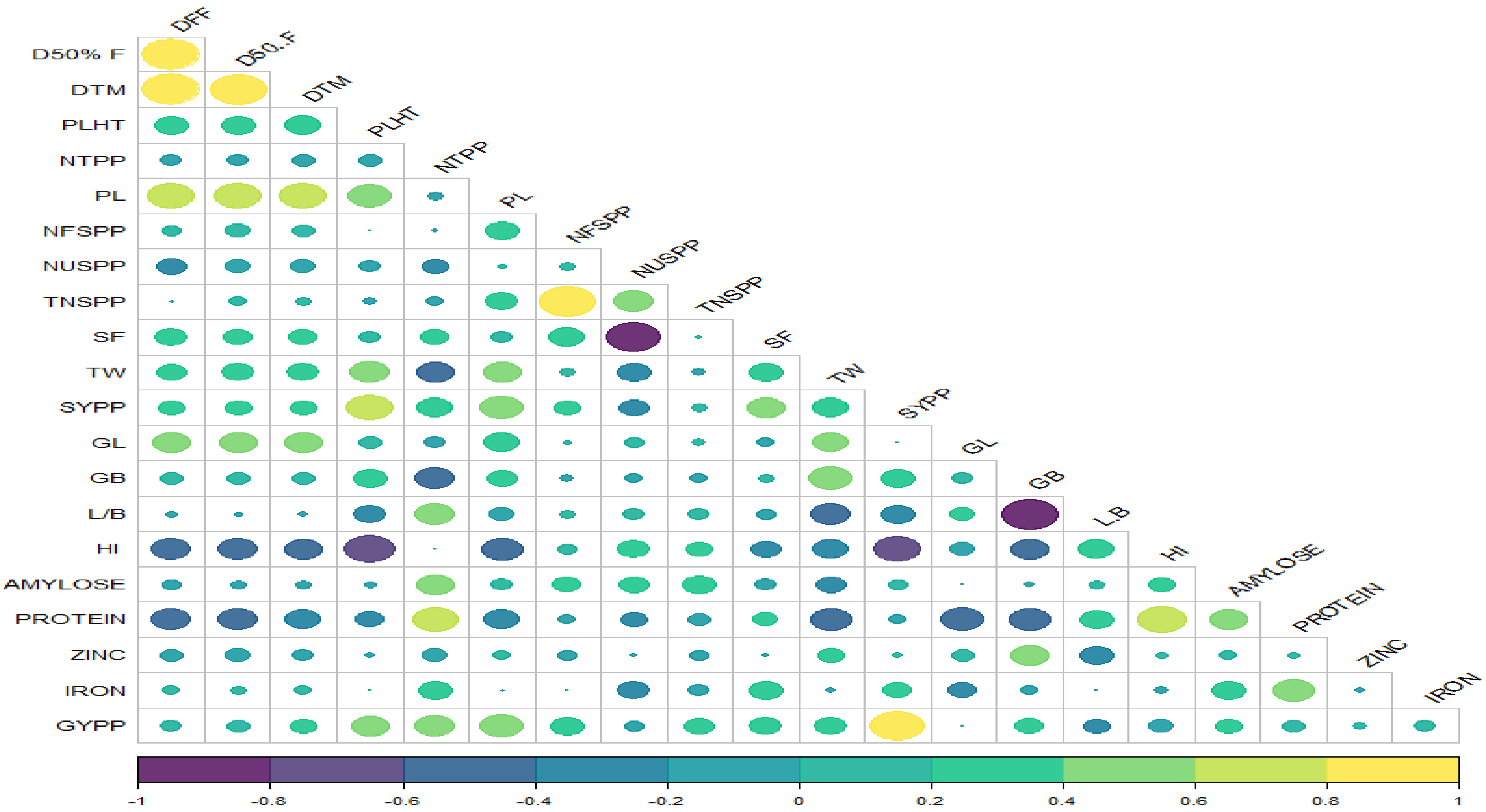

Fig. 4.3. Genotypic corplot

Sr. No.	Name of Genotypes	Sr. No.	Name of Genotypes
1	Karjat-4(ch)	17	RP-6354-10-21-06
2	BARCKKV-13	18	NWGR-13052
3	Sai	19	BPT-5204
4	Sairam NR-9	20	RNR-28362
5	Ratnagiri 6	21	SKL-07-11-177-50-65-60-14
6	Palghar-1	22	NWGR-15022
7	Wada kolam	23	BPT-2845
8	NR-212	24	AD-16163
9	NR-81	25	RP-6366 JBC 154-1-14
10	Komal-101	26	MTU-1520
11	Pusa 170-2-10-2-19	27	GNV-1904
12	WGL-14	28	Ankur Rupali
13	RP 6334-111-5-2-1	29	Pusa-1702-10-289
14	CR 4069-111-1-1-4-5-7	30	Karjat-8(ch)
15	RP-6329-100-3-21-1	31	Ratnagiri-5(ch)
16	CRAC-3998-41-2	32	Karjat Shatabdi (ch)

Plate I: Different genotypes of Rice (Husked)

Plate II: Different genotypes of Rice (De-husked)

INTRODUCTION

REVIEW OF LITERATURE

MATERIALS AND METHODS

RESULTS AND DISCUSSION

SUMMARY AND CONCLUSION

LITERATURE CITED

APPENDICES