

**ASSESSMENT OF GENETIC VARIABILITY AND DIVERGENCE IN
ADVANCED BREEDING LINES OF RICE (*Oryza sativa* L.) IN LOWLANDS OF
HILL ZONE**

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DEPARTMENT OF GENETICS AND PLANT BREEDING

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UNIVERSITY OF AGRICULTURAL AND HORTICULTURAL SCIENCES

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**DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE, SHIVAMOGGA
KELADI SHIVAPPA NAYAKA
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CERTIFICATE

This is to certify that the thesis entitled '**ASSESSMENT OF GENETIC VARIABILITY AND DIVERGENCE IN ADVANCED BREEDING LINES OF RICE (*Oryza sativa* L.) IN LOWLANDS OF HILL ZONE**' submitted in partial fulfillment of the requirements for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **GENETICS AND PLANT BREEDING** to the College of Agriculture, Shivamogga, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga is a bonafide record of research work carried out by **HONNESH, H. R., ID. No. MA1TAI0344** (honneshhr23@gmail.com) during the period of study in this university under my guidance and supervision and no part of this thesis has previously formed the basis for the award of any other degree, diploma, associateship, fellowship or any other similar titles.

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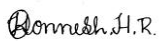
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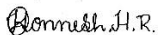
Assessment of Genetic Variability and Divergence in Advanced Breeding Lines of Rice (*Oryza sativa* L.) in Lowlands of Hill Zone


(HONNESH, H. R.)

ABSTRACT

The present study was undertaken to evaluate thirty-nine advanced breeding lines of rice in Randomized Complete Block Design with two replications during *Kharif* 2020 at ZAHRS, Mudigere for variability, diversity, correlation and path analysis for thirteen yield and yield attributing characters. The same lines were screened for blast reaction at AHRS, Ponnampet. Analysis of Variance revealed significant differences among the advanced breeding lines for all the characters studied. Moderate PCV, GCV coupled with high heritability and high GAM were recorded for traits *viz.*, plant height, total number of grains per panicle, test weight, grain L/B ratio, straw yield, grain yield and harvest index. Number of tillers per plant, number of productive tillers per plant, panicle length, panicle fertility, straw yield and harvest index exhibited positive and significant phenotypic association with grain yield. Harvest index had the highest positive direct effect on grain yield whereas highest positive indirect effect of grain yield with trait harvest index *via* panicle fertility was recorded. Using Mahalanobis' D^2 statistics advanced breeding lines were grouped into six clusters, the cluster I consists of maximum number of advanced breeding lines (18) followed by cluster III (11) and cluster II (7). Based on cluster distance, the highest intra cluster distance was shown by cluster III and cluster IV while cluster V showed highest inter cluster distance. Among all the characters, the maximum per cent contribution towards divergence was made by test weight followed by plant height. Rice lines screened for blast disease showed that 16 lines were moderately blast resistant. The line KPR-2 \times IS-1-4-1-2 was found to be the best performing line for lowland situation of hill zone.

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ಗುಡ್ಡಗಾಡು ವಲಯದ ತಗ್ಗು ಪ್ರದೇಶದಲ್ಲಿ ಭತ್ತದ ಸುಧಾರಿತ ಪ್ರಜನನ ಸಾಲುಗಳಲ್ಲಿ ಅನುವಂಶಿಕ ವ್ಯತ್ಯಾಸ ಮತ್ತು
ವೈವಿಧ್ಯತೆಯ ಮೌಲ್ಯಮಾಪನ

(ಹೊನ್ನೇಶ್, ಹೆಚ್. ಆರ್.)

ಸಾರಾಂಶ

ಪ್ರಸ್ತುತ ಅಧ್ಯಯನವನ್ನು ವಲಯ ಕೃಷಿ ಮತ್ತು ತೋಟಗಾರಿಕಾ ಸಂಶೋಧನಾ ಕೇಂದ್ರ, ಮೂಡಿಗೆರೆಯಲ್ಲಿ ೨೦೨೦ ರ ಮುಂಗಾರಿನಲ್ಲಿ ಹದಿಮೂರು ಇಳುವರಿ ಮತ್ತು ಅವುಗಳ ಗುಣಲಕ್ಷಣಗಳ ಅನುವಂಶಿಕ ವ್ಯತ್ಯಾಸ, ಗುಣಲಕ್ಷಣಗಳ ಸಂಯೋಜನೆ, ಮಾರ್ಗ ಮತ್ತು ವೈವಿಧ್ಯತೆಯ ವಿಶ್ಲೇಷಣೆಯ ಸ್ವರೂಪ ಮತ್ತು ಪರಿಮಾಣವನ್ನು ನಿರ್ಧರಿಸುವ ಉದ್ದೇಶದಿಂದ ೩೯ ಸುಧಾರಿತ ಪ್ರಜನನ ಸಾಲುಗಳನ್ನು ಎರಡು ಪ್ರತಿಗಳಲ್ಲಿ ಯಾದೃಚ್ಛಿಕ ಸಂಪೂರ್ಣ ಬ್ಲಾಕ್ ವಿನ್ಯಾಸದಲ್ಲಿ ಹಾಕಲಾಗಿತ್ತು. ಅದೇ ಸಾಲುಗಳನ್ನು ಕೃಷಿ ಮತ್ತು ತೋಟಗಾರಿಕಾ ಕೇಂದ್ರ ಪೊನ್ನಂಪೇಟೆಯಲ್ಲಿ ಭತ್ತದ ಬೆಂಕಿರೋಗ ನಿರೋಧಕ ಶಕ್ತಿಯನ್ನು ತಿಳಿಯಲು ಪರಿಶೀಲಿಸಲಾಯಿತು. ಅನೋವ ಪರೀಕ್ಷೆಯ ಮೂಲಕ ಸುಧಾರಿತ ಪ್ರಜನನ ಸಾಲುಗಳ ಎಲ್ಲಾ ಗುಣಲಕ್ಷಣಗಳಲ್ಲೂ ಗಮನಾರ್ಹ ವ್ಯತ್ಯಾಸವನ್ನು ಹೊಂದಿರುವುದು ಕಂಡುಬಂದಿದೆ. ಸಸ್ಯದ ಎತ್ತರ, ಪ್ರತಿ ತೆನೆಯಲ್ಲಿ ಕಾಳಿನ ಸಂಖ್ಯೆ, ಕಾಳುಗಳ ಪರೀಕ್ಷಾ ತೂಕ (೧೦೦೦), ಕಾಳಿನ ಉದ್ದ/ಅಗಲ ಅನುಪಾತ, ಒಣ ಹುಲ್ಲಿನ ಇಳುವರಿ, ಕಾಳಿನ ಇಳುವರಿ ಮತ್ತು ಸುಗ್ಗಿಯ ಸೂಚ್ಯಂಕಗಳಿಗೆ ಮಧ್ಯಮ ಪಿ.ಸಿ.ವಿ. ಮತ್ತು ಜಿ.ಸಿ.ವಿ. ಯ ಜೊತೆ ಅಧಿಕ ವಂಶಾನುಗತೆ ಹಾಗೂ ಅನುವಂಶೀಯ ಮುಂಚಿತತೆ ದಾಖಲಾಗಿದೆ. ಕಾಳಿನ ಇಳುವರಿಯು ತೆಂಡೆಗಳ ಸಂಖ್ಯೆ (ಪ್ರತಿ ಸಸ್ಯಕ್ಕೆ), ಫಲದಾಯಕ ತೆಂಡೆಗಳ ಸಂಖ್ಯೆ (ಪ್ರತಿ ಸಸ್ಯಕ್ಕೆ), ತೆನೆಯ ಉದ್ದ, ತೆನೆಯ ಫಲವತ್ತತೆ, ಒಣ ಹುಲ್ಲಿನ ಇಳುವರಿ ಮತ್ತು ಸುಗ್ಗಿಯ ಸೂಚ್ಯಂಕದೊಂದಿಗೆ ಗಮನಾರ್ಹ ಧನಾತ್ಮಕ ಸಂಬಂಧವನ್ನು ಹೊಂದಿರುವುದು ಸದರಿ ಅಧ್ಯಯನದಿಂದ ದೃಢಪಟ್ಟಿದೆ. ಸುಗ್ಗಿಯ ಸೂಚ್ಯಂಕ ಧಾನ್ಯದ ಇಳುವರಿ ಜೊತೆ ಅತಿ ಹೆಚ್ಚಿನ ನೇರ ಧನಾತ್ಮಕ ಪರಿಣಾಮವನ್ನು ಹೊಂದಿರುತ್ತವೆ. ಸುಗ್ಗಿಯ ಸೂಚ್ಯಂಕ ತೆನೆಯ ಫಲವತ್ತತೆಯ ಮುಖಾಂತರ ಕಾಳಿನ ಇಳುವರಿಯೊಂದಿಗೆ ಅತಿ ಹೆಚ್ಚಿನ ಪರೋಕ್ಷ ಧನಾತ್ಮಕ ಪರಿಣಾಮವನ್ನು ಹೊಂದಿರುತ್ತದೆ. ಮಹಾಲಾನೋಬಿಸ್ ಡಿ^೨ ಸಂಖ್ಯಾಶಾಸ್ತ್ರವು ಸುಧಾರಿತ ಪ್ರಜನನ ಸಾಲುಗಳನ್ನು ಆರು ಗುಂಪುಗಳನ್ನಾಗಿ ವಿಂಗಡಿಸಲಾಗಿದೆ, ಇವುಗಳಲ್ಲಿ ಮೊದಲನೆಯ ಗುಂಪು ಅತ್ಯಧಿಕ ವಂಶವಾಹಿ ಬಗೆಗಳನ್ನು (೧೮) ಹೊಂದಿದೆ ನಂತರದಲ್ಲಿ ಮೂರನೆಯ ಗುಂಪು (೧೧) ಹಾಗೂ ಎರಡನೆಯ ಗುಂಪು (೭) ವಂಶವಾಹಿ ಬಗೆಗಳನ್ನು ಹೊಂದಿವೆ. ಗುಂಪಿನ ದೂರವನ್ನು ಆಧರಿಸಿ ೩ ನೇ ಗುಂಪು ಅತಿ ಹೆಚ್ಚಿನ ಆಂತರಿಕ ದೂರವನ್ನು ಹೊಂದಿದೆ ಮತ್ತು ಅತಿ ಹೆಚ್ಚು ಊಳುದೂರವು ೪ ಮತ್ತು ೫ ನೇ ಗುಂಪುಗಳ ನಡುವೆ ಕಂಡುಬಂದಿದೆ. ಕಾಳುಗಳ ಪರೀಕ್ಷಾ ತೂಕ (೧೦೦೦) ಹಾಗೂ ಸಸ್ಯದ ಎತ್ತರ ಒಟ್ಟು ಅನುವಂಶಿಕ ವ್ಯತ್ಯಾಸಕ್ಕೆ ಹೆಚ್ಚಿನ ಕೊಡುಗೆ ನೀಡಿದೆ. ಭತ್ತದ ಪ್ರಜನನ ಸಾಲುಗಳನ್ನು ಬೆಂಕಿರೋಗ ನಿರೋಧಕ ಶಕ್ತಿಗಾಗಿ ಪರೀಕ್ಷಿಸಿದಾಗ ೧೬ ಭತ್ತದ ಸಾಲುಗಳು ಮಧ್ಯಮ ಬೆಂಕಿರೋಗ ನಿರೋಧಕ ಶಕ್ತಿ ತೋರಿಸಿರುವುದು ಕಂಡುಬಂದಿದೆ. ಕೆ.ಪಿ.ಆರ್. - ೨ × ಐ.ಎಸ್-೧-೪-೧-೨ ಗುಡ್ಡಗಾಡು ತಗ್ಗು ಪ್ರದೇಶದ ಪರಿಸ್ಥಿತಿಗಳಿಗೆ ಅತ್ಯುತ್ತಮವಾದ ಕಾರ್ಯಕ್ಷಮತೆಯ ಭತ್ತದ ಸಾಲಾಗಿ ಗುರುತಿಸಲಾಗಿದೆ.

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INTRODUCTION

I INTRODUCTION

Rice (*Oryza sativa* L.) is an annual cereal crop with diploid chromosomes ($2n = 24$) classified under the genus *Oryzae* and the family *Poaceae*. Asian rice (*Oryza sativa*) and African rice (*Oryza glaberrima*) are the two distinct cultivated rice types. Asian cultivated rice is economically important than African rice. It was the first sequenced crop genome with an estimated genome size of 430 Mb (Jackson, 2016). It is the major staple food crop for over half of the world's population (Khush, 2005) and provides food security in many developing countries. More than 90 per cent of rice is grown and consumed in Asia, where about 60 *per cent* of the world's population lives, reflecting the value of rice in daily human life. The year 2004 was announced as International Year of Rice by the United Nations Food and Agriculture Organization considering its importance.

Among rice ecosystems, lowland rice ecosystem is found mainly in tropical climate areas, river deltas, flood plain and inland swamps. Bunds are built around lowland fields to capture and conserve rainfall for growth and development of rice plants. In rainfed lowlands, rainfall is the principle source of water for rice cultivation, but in some places water may come from diverted small water courses. Rice fields are undulated with a layer of standing water up to 50 cm during half of growing season. However, variability in rainfall and its distribution normally cause either flood or drought stresses in rainfed lowland rice production (Anon., 2021).

Rice is the world's most important food crop and a staple food for more than half of the global population. It is being grown in more than hundred countries of the world. Globally, rice is cultivated now in 160 million hectares with annual production of around 650 million tonnes of rough rice and average productivity of 4.18 t/ha of rough rice. In India rice is cultivated in an area of 43.95 m. ha. and producing about 116.42 million tonnes with an average productivity of 2.65 t/ha. of milled rice or 3.52 t/ha. of rough rice. In Karnataka, it covers an area of 1.42 m. ha. with a production of 3.57 million tonnes and productivity of 2,464 kg/ha (Anon., 2019).

With an alarming growth in the population throughout the world, the demand for rice will continue to increase in the years to come. Although rice production has increased substantially, it falls short of growing demand due to population increase, rising at a rate of 2 *per cent* annually (Manjunath *et al.*, 2018). In order to meet the food requirements of the growing population, the development of high yielding superior varieties is of prime importance. To achieve the expected targets, development of varieties with higher yield potential by breaking the existing yield plateau by utilizing more diversified parents in the rice breeding programmes is need of the day.

Advanced breeding lines are the pre-released lines that include mostly homozygous lines and few heterozygous lines derived from crossing diverse parents and contain valuable gene combinations, allowing breeders to select the best line. They constitute an important source of genetic variation for utilization in the breeding of high yielding rice varieties and hybrids. Yield enhancement is the major breeding objective in rice breeding programmes and knowledge on the nature and magnitude of the genetic variation governing the inheritance of quantitative characters like yield and its components is essential for successful genetic improvement (Kishore *et al.*, 2015). Hence, the studies on variability and diversity among advanced breeding lines would help in better utilization of the lines for improvement of yield and yield-related traits.

The information about the extent of several genetic parameters, such as Phenotypic Co-efficient of Variation (PCV) and Genotypic Co-efficient of Variation (GCV), broad-sense heritability, genetic gain on which the breeding methods are formulated is pre-requisite for breeding high yielding varieties. Heritability indicates the transmissibility of a character to future generations (Satheeshkumar and Saravanan, 2012). High heritability coupled with high genetic advance is more helpful in forecasting genetic gain (Johnson *et al.*, 1955).

Knowledge about the genetic diversity of germplasm collections and genetic relationships among the breeding materials could be an invaluable aid in crop improvement programmes. Genetic diversity determines the inherent potential of a cross for heterosis and frequency of desirable recombinants in advanced generations. It also permits to select the genetically divergent parents, which can produce new recombinants with desirable traits when they are crossed together. A hybridization programme involving genetically diverse parents belonging to different clusters would provide an opportunity for bringing together gene constellations of diverse nature (Chanbeni *et al.*, 2012). Hence, the assessment of genetic diversity for yield and its components among genotypes is important for planning the future hybridization programme.

For planning a yield improvement programme, knowledge of the relationship between yield and yield contributing characters is important. The study of correlation coefficient among the characters has importance in selection programme because it helps in the construction of selection indices and also permits the prediction of correlated responses (Madhaviatha *et al.*, 2005). The correlation between grain yield and its components may sometimes be misleading due to the complex interrelation between the component characters. It does not provide a clear picture of the influence of one character on another. Splitting of total correlation into direct and indirect effects, therefore, would provide a more meaningful interpretation of such association (Nagaraju *et al.*, 2013). Thus, correlations in combination with path coefficient

analysis are important tools to find out the association and magnitude of direct and indirect influences of one character upon another and aid in the identification of effective selection criteria for yield improvement.

Rice blast is one of the severe damaging diseases affecting lowland rice production, is caused by the non-obligate filamentous ascomycete *Magnaporthe oryzae* (Anamorph = *Pyricularia grisea*) (Qudsia *et al.*, 2017). The blast occurrence in India was recorded for the first time in the Tanjavur delta of Tamil Nadu in 1918. The disease has occurred from time to time in the country, causing severe damage to rice production.

Though blast is common in all three rice ecosystems, (irrigated and rainfed uplands and lowlands) but more severe in lowland ecosystem in Hill Zone of Karnataka. Thus there is a need to identify durable resistance sources in rice for use in the breeding program. The research in this area is continuous as the blast pathogen is dynamic, and the existing resistant genes in the host may become non-functional when new blast races evolve in the field. Therefore, strategies for reducing the losses caused by blast disease which is environmentally sustainable and economically viable need to be developed and implemented urgently.

With this background, the present investigation entitled “Assessment of Genetic Variability and Divergence in Advanced Breeding lines of Rice (*Oryza sativa* L.) in Lowlands of Hill Zone” was carried out with the following objectives:

1. To study the genetic variability in advanced breeding lines of rice
2. To study correlation and path coefficient on yield and its attributing traits
3. To assess the genetic diversity in advanced breeding lines of rice
4. Screening of advanced breeding lines of rice for blast disease

REVIEW OF LITERATURE

II REVIEW OF LITERATURE

Rice (*Oryza sativa* L.) is the important staple food crop among cereals. To meet out the food requirement of the growing population, the development of high yielding varieties through crop improvement is essential. It is consumed by more than half of the world's population (Lopez and Joseph, 2008). Crop improvement depends on the available genetic variability and the extent to which the traits are heritable. An extensive survey of genetic variability and a thorough understanding of the genetic makeup of the crop with the help of biometrical tools are indispensable for initiating an effective breeding programme.

The literature related to the objectives of the present study has been comprehensively reviewed and is presented in this chapter under the following sub-headings.

- 2.1 To study the genetic variability in advanced breeding lines of rice
- 2.2 Studies on correlation and path analysis among yield and its contributing traits
- 2.3 Genetic divergence among the rice advanced breeding lines
- 2.4 Screening of rice advanced breeding lines for blast reaction

2.1 To study the genetic variability in advanced breeding lines of rice

Genetic variability is the prerequisite for any crop improvement programme. Improvement in any trait solely depends on the amount of variability present in the base material of that trait. The variability observed in any population could be due to genetic and environmental factors and also due to the interaction between these factors. The genetic and environmental components of variation were discussed by Johanssen (1909), who attributed the variation in a segregating population to heritable and non-heritable factors. The heritable variance was otherwise called genetic variance.

Akinwale *et al.* (2011) studied the germplasm pool having sufficient genetic variability. They reported high to moderate heritability, genetic advance, significantly lower GCV than PCV, indicating the considerable influence of the environment for traits *viz.*, the total number of grains per panicle, grain yield and panicle weight.

Khriedinuo *et al.* (2011) reported higher heritability estimates for all the traits studied. High GCV was reported for plant height, number of tillers per plant, number of productive tillers per plant, total number of grains per panicle, panicle weight, straw yield and grain yield.

Manoj *et al.* (2011) reported that the mean sum of square for all the 12 characters was significant. High estimates of heritability coupled with high genetic advance as *per cent* of mean were observed for harvest index followed by the total number of grains per panicle, respectively. High estimates of heritability coupled with moderate genetic advance as *per cent* of mean were observed for panicle length.

Sangam *et al.* (2011) evaluated 81 rice genotypes for thirteen quantitative traits to examine the nature and magnitude of variability, heritability and genetic advance. Among all traits, the total number of grains per panicle exhibited high estimates of GCV and PCV followed by harvest index, grain yield. Broad sense heritability was highest for straw yield. The maximum genetic advance as *per cent* of mean was recorded for the number of panicle length with a high heritability value.

Ghosh and Sharma (2012) reported the narrow difference between PCV and GCV for days to fifty *per cent* flowering, sterile spikelet per panicle, fertile spikelet per panicle, panicle length, grain yield per plant, test weight and head rice recovery, indicating less environmental influence. All the characters reportedly exhibited high broad-sense heritability. High heritability and higher genetic advance as *per cent* of the mean for grain yield per plant, sterile spikelet per panicle, fertile spikelet per panicle and 1000 seed weight were also reported.

Khalid *et al.* (2012) reported a high genotypic coefficient of variation and estimated genetic advance for plant height, the number of tillers per plant and 1000 grain weight; high heritability with low genetic advance for days to fifty *per cent* flowering and days to maturity.

Osman *et al.* (2012) evaluated 13 genotypes of upland rice. They recorded the highest genotypic coefficient of variation with high genetic advance for the number of tillers per plant and plant height. High heritability (> 85 %) was recorded for plant height, the number of tillers per plant and 1000 grain weight, whereas days to 50 *per cent* flowering and days to maturity recorded high heritability with low genetic advance.

Pandey *et al.* (2012) evaluated 52 rice genotypes to know the genetic relationship of various polygenetic traits on yield. The magnitude of PCV and GCV were high for straw yield, moderate for grain yield and total number of grains per panicle. However, days to fifty *per cent* flowering, days to maturity, plant height, panicle length, panicle fertility and harvest index had low estimates. They reported high heritability combined with a high genetic advance in *per cent* mean for straw yield, grain yield and total number of grains per panicle.

Ravindra Babu *et al.* (2012) reported high PCV and GCV for the total number of grains per panicle. He presented high heritability coupled with high genetic advance for the number of filled grains per panicle and water uptake.

Aditya and Bhartiya (2013) studied genetic parameters in 18 rice genotypes under a rainfed ecosystem for 15 quantitative traits. The analysis of variance revealed that there were highly significant differences for all the characters among the genotypes. The GCV and PCV estimate was highest for grain yield, followed by panicle fertility and total number of grains per panicle.

Shivaprasad *et al.* (2013) studied genetic variability, genotypic and phenotypic coefficients of variation, heritability and genetic advance in 150 genotypes of rice for eleven yield and its related traits. The estimates of genotypic and phenotypic coefficients of variation (GCV and PCV) were high for all the characters except for days to fifty *per cent* flowering and panicle length. Heritability and genetic advance were high for all the traits except for grain yield and fertile panicle fertility, which had a moderate magnitude of genetic advance, along with high heritability indicating the involvement of additive type of gene action in controlling these characters.

Vanisree *et al.* (2013) reported high estimates of GCV for number of productive tillers per plant and total number of grains per panicle. In contrast, low estimates of GCV were noticed for panicle length and days to fifty *per cent* flowering. Number of productive tillers per plant and filled grain per panicle exhibited high heritability and genetic advance.

Chakraborty *et al.* (2014) recorded the highest PCV and GCV for grain yield, 1000 grain weight and number of productive tillers per plant in 30 local upland rice genotypes indicating the presence of much variation. High heritability and genetic advance were obtained for plant height at maturity, number of productive tillers per plant, 1000-grain weight, panicle fertility and grain yield, indicating that the selection of these traits is likely to accumulate more additive genes leading the better performance of the genotypes.

Hasan Shahriar *et al.* (2014) reported the objective of the study was to know variability in yield, yield contributing characters of rice genotypes at F₉ generation. The genotypes differed significantly for plant height (cm), panicle length, the total number of tillers per plant, productive tillers number per plant, total number of grains per panicle, days to fifty *per cent* flowering, days to maturity, 1000 grains weight and grain yield. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the traits studied, indicating that the measured traits interacted with the environment to some extent.

Ogunbayo *et al.* (2014) laid an experiment in a randomized complete block design (RCBD) to evaluate genetic variation, the heritability of yield and yield-related traits in 48 rice genotypes with three replications. Genotypes varied significantly for all the traits studied, which implies that the genotypes contain adequate genetic variability. Phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV) in all the characters observed. High heritability estimates were obtained for days to flowering (91.37), days to maturity (86.86), plant height at maturity, the number of tillers per plant and panicle length (72.21), indicating that the traits are primarily under genetic control.

Paikhomba *et al.* (2014) evaluated 30 rice hybrids along with a complete set of thirteen parents and checks for variability, heritability and genetic advance in different yield and yield components. The estimates of GCV were lower than the respective PCV, indicating the influence of environmental factors on the expression of the traits studied. Characters like grain yield, harvest index and the total number of grains per panicle showed high heritability coupled with moderate genetic advance as *per cent* of mean.

Sharma *et al.* (2014) evaluated 120 rice genotypes for variability. Analysis of variance revealed a maximum amount of variability in the genotypes for all the characters under study because mean sums of squares due to genotypes were highly significant. High genetic advance and heritability were observed for plant height, the total number of grains per panicle, plant weight, straw yield, grain yield, test weight, the total number of tillers per plant and total number of productive tillers per plant indicating that heritability is due to additive gene action. The direct selection of this trait may be highly effective.

Ekka *et al.* (2015) estimated variability, heritability, genetic advance, correlation and path analysis for 19 characters in 96 accessions of rice germplasm. The highest genotypic coefficient of variation and phenotypic coefficient of variation was recorded for the number of productive tillers per plant and grain yield. Estimates of heritability and genetic advance were high for the number of productive tillers per plant, the total number of grains per panicle and grain yield in genotypes indicating the predominance of additive gene action for these traits and direct selection of these may be highly effective.

Anis *et al.* (2016) analyzed the performance of promising lines in rice for agronomic and genetic performance under Egyptian conditions. ANOVA revealed significant differences among all the genotypes for all traits. The high genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) were recorded for the total number of grains per panicle depicting the existence of a wide spectrum of variability for this trait. The phenotypic variance was higher than the

corresponding genotypic variance for traits. Heritability estimates ranged from 49.16 *per cent* to 99.52 *per cent* for the total number of grains per panicles.

Bhatt *et al.* (2016) conducted an experiment to study variability in rice genotypes. The study revealed that the phenotypic coefficient of variation was highest for grains yield. The number of grains per panicle, length breadth ratio and test weight exhibited a moderate-high phenotypic coefficient. High heritability values were also recorded for test weight and plant height. The estimate of genetic advance was highest for the number of grains per panicle, followed by plant height. However, genetic advance as *per cent* of mean was highest for number of grains per panicle followed by grain yield.

Sameera *et al.* (2016) evaluated 25 rice genotypes and results revealed that high variability, heritability and genetic advance as *per cent* of the mean obtained for productive tillers per plant, number of tillers per plant and total number of grains per panicle. At the same time, days to maturity was recorded with high heritability coupled with low genetic advance as *per cent* of mean.

Edukondalu *et al.* (2017) investigated 40 rice genotypes to study the heritability, 15 characters in rice during *Kharif* 2016. Total number of grains per panicle showed high PCV and GCV whereas, number of grains per panicle, number of tillers per plant, 1000 grain weight, L/B ratio, plant height, grain yield and days to flowering was shown to have high heritability coupled with high genetic advance.

Gour *et al.* (2017) collected data on 83 rice genotypes for their study. Analysis of variance exhibited significant differences among the varieties for different morphological characters. High GCV and PCV were observed for grain yield, straw yield, filled grains per plant, test weight, harvest index and the number of tillers per plant whereas, moderate GCV and PCV were observed for plant height. The filled grains per plant, harvest index, straw yield showed high genetic advance that helped in effective and reliable selection through these characters for crop improvement.

Khaire *et al.* (2017) experimented with 24 rice genotypes in randomize block design during *Kharif* 2015-16. The range of GCV and PCV was 5.76 *per cent* to 24.79 *per cent* and 2.62 *per cent* to 24.34 *per cent*, respectively. The number of filled grains per panicle showed high PCV and GCV. GCV, PCV and broad-sense heritability was 5.76 *per cent* to 24.79 *per cent* and 2.62 *per cent* to 24.34 *per cent* and 20.37 *per cent* to 97.78 *per cent*, respectively. Mean for genetic advance and genetic advance as *per cent* of mean ranged from one *per cent* to 71.22 *per cent* and 2.18 *per cent* to 68.60 *per cent*, respectively.

Nusrat *et al.* (2017) studied 14 traits among 35 rice genotypes to assess genetic variability under temperate conditions of Kashmir valley. The higher values of PCV over GCV indicate the influence of environment on character expression. Harvest index showed the lowest values for 1000 grain weight (6.66) and (7.08) and the highest values of GCV (33.26) and PCV (33.59).

Rashid *et al.* (2017) studied ten rice genotypes to estimate genetic variability using RCBD. Genetic analysis showed a higher PCV than GCV for all the traits, which showed that the traits were influenced by the environment. For the number of filled grains per panicle and plant height, higher PCV and GCV were observed indicates, the possibility of genetic improvement through direct selection. Lower PCV and GCV values for days to fifty *per cent* flowering, days to maturity, panicle length, number of productive tillers plant, fertility (%) and 1000 seed weight indicating the need for the creation of variability by hybridization or mutation followed by selection.

Srujana *et al.* (2017) studied genetic variability, heritability and genetic advance in 29 rice genotypes for 13 quantitative characters. Analysis of variance revealed considerable variability existed among the genotypes. The differences between PCV and GCV were small, indicating little environmental influence on the expression of the characters studied. High to moderate estimates of GCV and PCV were recorded for grain yield per hill, harvest index, total number of grains per panicle and tillers per plant. A high heritability estimate was observed for grains per panicle, days to maturity, straw yield, grain yield, panicles per plant and tillers per plant. High estimates of heritability along with moderate to low estimates of genetic advance were observed for grains per panicle, grain yield, tillers per plant, panicles per plant and straw yield.

Yadav *et al.* (2017) evaluated 35 diverse rice varieties with two checks for 12 quantitative characters under sodic soil. High PCV and GCV were observed in the case of straw yield. In case of plant height, grain yield and productive tillers per plant moderate PCV and GCV were observed. Lower PCV and GCV were observed for spikelet per panicle followed by 1000 grain weight, days to fifty *per cent* flowering, harvest index, days to maturity, panicle length and spikelet fertility. Panicle fertility and harvest index showed moderate heritability. In contrast, high broad-sense heritability was noted for plant height followed by days to fifty *per cent* flowering, straw yield, days to maturity, grain yield, 1000 grain weight and grains per panicle. Among all traits under study, low heritability was recorded for panicle length and productive tillers per plant.

Acharya *et al.* (2018) evaluated eight rice genotypes in RCBD with three replications. The analysis of variance revealed statistically significant differences for all the traits under study, which showed the existence of genetic variability among the varieties except in productive tillers. The higher value of GCV and PCV was recorded

for grains per panicle, harvest index and grain yield. The PCV value observed was higher than the GCV value, which indicated the influence of the environment on the expression of the traits.

Behera *et al.* (2018) conducted an experiment to study genetic variability in 49 elite slender grain rice genotypes for thirteen component characters, including grain yield. Both PCV and GCV were high for grain yield and number of grains per panicle. PCV and GCV were moderate for characters like harvest index, panicle fertility and days to fifty *per cent* flowering, indicating a considerable amount of environmental effect on such characters. High heritability estimates were associated with moderate to high genetic advance as *per cent* mean (GAM) for days to fifty *per cent* flowering, plant height, panicle length, panicle fertility test weight and grain yield.

Manjunath *et al.* (2018) evaluated 23 advanced breeding lines of rice (F_6 generation) to study genetic variability, heritability and genetic advance for grain yield and four associated traits. The analysis of variance revealed statistically significant differences among all the genotypes for all the traits studied. Significant differences were observed for grain yield ranging from 4093.00 to 7177.00 kg ha⁻¹. Higher PCV and GCV values were exhibited by grain yield. High heritability coupled with high genetic advances as *per cent* of mean were recorded for grain yield, plant height and days to fifty *per cent* flowering.

Ranjith *et al.* (2018) studied the variability in 30 rice genotypes. The results revealed that high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for fertile grains, followed by tillers per plant. High heritability coupled with high genetic advance was recorded for plant height.

Tiwari *et al.* (2019) evaluated seven varieties, including Hardinath-1, as standard check-in four different locations in the RCBD with three replications. All the varieties and locations showed significant variations for all the traits studied. GCV was lower than PCV for all traits studied. The magnitudes of GCV were relatively higher for grain yield, 1000 grain weight and days to maturity. The highest broad-sense heritability of 94 *per cent* was recorded in days to maturity and the lowest heritability of 16 *per cent* was observed in plant height.

Longkho *et al.* (2020) carried out an investigation on rice genotypes. From the coefficient of variation (CV) values, the variability was highest in grain yield, followed by the number of productive tillers, grain yield and 100 grain weight. Grain yield per plant showed high estimates of GCV and PCV. In contrast, moderate estimates of GCV and PCV were observed in plant height, number of grains and 100-grain weight. Low estimates of GCV and PCV were found in panicle length and spikelet fertility. The

estimates of GCV and PCV values for 100-grain weight and panicle length showed a wide difference, which indicated the more significant role of environmental factors influencing the expression of these characters.

Sarker, U. *et al.* (2020) developed seven advanced breeding lines through a hybridization breeding program. A popular cultivar was used to study variability and heritability in rice for grain yield and its related agronomic traits. High genetic variability was observed for the number of filled grains per panicle, plant height, grain yield, 1000-grain weight, duration of flowering and maturity, number of tillers and panicle length.

Sudeepthi *et al.* (2020) studied 107 elite rice genotypes to study the variability, heritability and genetic advance as *per cent* of mean for yield and yield component traits. High PCV and GCV were recorded for productive tillers per plant, while high heritability was recorded for all the traits studied. Further, the high genetic advance as *per cent* of mean was recorded for plant height, the number of productive tillers per plant, the total number of grains per panicle, test weight and grain yield. Among these, productive tillers per plant had recorded a high variability, heritability and genetic advance as *per cent* of mean indicating its effectiveness as an important selection criterion for the yield improvement.

Vanisri *et al.* (2020) evaluated 38 cold-tolerant rice genotypes for genetic variability, correlation and path analysis for yield and yield attributing traits. Genetic analysis revealed high GCV and PCV for tillers per plant, panicle length and grain yield. High heritability coupled with high genetic advance as *per cent* of the mean was observed for plant height, tillers per plant and grain yield.

Bhargavi *et al.* (2021) evaluated 52 rice genotypes in randomized block design for twelve metric traits to estimate the extent of genetic variability, heritability (broad sense) and genetic advance as *per cent* of mean. Among the 12 characters studied, high phenotypic and genotypic coefficients of variation were recorded for the traits *viz.*, panicle number per plant, test weight and grain yield per plant indicating that a large amount of variation is present among the genotypes. High heritability coupled with high genetic advance as *per cent* of mean was recorded for the total number of panicle, test weight and grain yield.

Donkor *et al.* (2021) conducted an experiment to estimate the genetic variability for yield and yield-related traits of 45 newly released rice genotypes. The Genotypic Coefficient of Variation (GCV) was lower than the Phenotypic Coefficient of Variation (PCV) for all the traits, indicating the influence of environment on the traits. Panicle length recorded moderate heritability and moderate genetic advance, which suggests that they can be improved through direct selection due to predominant additive variation and indicating that a moderate level of genetic variability is present in these characters.

Gupta *et al.* (2021) investigated 46 exotic rice germplasm along with four checks and estimated the genetic variability parameters in yield and yield contributing characters. Analysis of variance indicated significant genotypic differences among the genotypes for the yield, its components for all the characters. High GCV and PCV values were observed for characters *viz.*, straw yield, harvest index, grain yield, productive tillers per plant and 1000 seed weight. High heritability coupled with high genetic advance as *per cent* of mean was observed for straw yield followed by harvest index, grain yield, productive tillers per plant, days to fifty *per cent* flowering and number of filled grains per panicle which indicated that the additive type of gene action controlled these traits.

2.2 Studies on correlation and path analysis among yield and its contributing traits

Genetic correlation among yield and yield attributing traits determine the extent and direction of association of plant traits. Path analysis furnishes information on the influence of each contributing trait to yield directly and indirectly and enables the breeders to rank the genetic attributes according to their contribution. Correlation coefficient analysis can be used to determine the nature and degree of the relationship between characters. Correlation between important characters is helpful in the selection of suitable plant type. The details of findings related to this study are reviewed below.

Akhtar *et al.* (2011) studied for variances, heritability, correlation (genotypic and phenotypic) and path coefficient analysis. The number of grains per panicle, days to maturity and 1000-grain weight showed a strong correlation with yield.

Bagheri *et al.* (2011) studied twenty-six rice genotypes to determine the relationship between grain yield and yield components. Significant correlation with grain yield was observed in panicle length ($r = 0.818$), the total number of grains per panicle ($r = 0.617$), the number of filled grains per panicle ($r = 0.790$) and the panicle number per plant ($r = 0.498$). Path coefficient analysis results revealed that the highest positive direct effect (0.510) on grain yield was shown to be possessed by panicle length. Grain yield linearly correlated with panicle length, the number of panicle per plant and the number of filled grains per panicle.

Elizabeth *et al.* (2011) reported grain yield had a significant positive correlation with days to fifty *per cent* flowering, plant height, panicle length, number of filled grains per panicle and 100 seed weight. A positive and significant correlation was observed with days to fifty *per cent* flowering, number of filled grains per panicle and spikelet fertility (%). Path coefficient analysis revealed that direct selection for days to fifty *per cent* flowering, 100 seed weight and panicle length would likely increase grain yield.

Fiyaz *et al.* (2011) reported that the number of productive tillers, total spikelet per panicle, days to fifty *per cent* flowering and plant height exhibited a significant positive association with grain yield. The direct effect of these traits on grain yield through harvest index was very high.

Hasan *et al.* (2011) reported a significant positive association of grain yield with the number of productive tillers per plant, number of panicles, panicle fertility and 1000 grain weight at both genotypic and phenotypic levels.

Mina *et al.* (2011) reported that path analysis for grain yield indicated that the number of grains per panicle had positive direct effects and days to maturity, plant height had negative direct effects on grain yield under optimum irrigation conditions. While number of filled grains per panicle had positive direct effects, days to fifty *per cent* flowering had a negative direct effect.

Padmaja *et al.* (2011) conducted an experiment on correlation and path analysis in rice germplasm. The study revealed that plant yield showed maximum significant correlation with 100 seed weight and productive tillers per plant followed by panicle fertility, total tillers per plant, grains per panicle and panicle length.

Selvaraj *et al.* (2011) reported that in path coefficient analysis, test weight exhibited a maximum positive direct effect on grain yield per plant followed by the number of filled grains per panicle, plant height, panicle length, number of tillers per plant and days to fifty *per cent* flowering and they primarily contributed to yield and could be relied upon to select genotypes to improve the genetic yield potential of rice.

Babu *et al.* (2012) carried out an investigation to study the correlation and path analysis in twenty-one popular hybrids of rice. The results revealed a significant positive association of grain yield per plant with the number of productive tillers. Path coefficient analysis revealed that the positive direct effect on yield was exhibited by panicle length and the number of productive tillers per plant. The number of productive tillers per plant possessed both positive association and high direct effect among the characters studied. Hence, this trait could be used in selection for this character would yield a better result.

MuhammadAshfaq *et al.* (2012) conducted a study on yield-related traits in rice for panicle length ($r = 0.265^{**}$), seeds per panicle ($r = 0.266^{**}$) and seed weight per panicle ($r = 0.339^{**}$) showed a significant positive correlation with grain yield.

Ramya *et al.* (2012) reported a significant positive association of grain yield per plant with the total number of tillers per plant and the number of productive tillers per plant. Path coefficient analysis also confirmed that the total number of tillers per plant was an important yield determinant, as evident from their magnitude of direct contribution to grain yield.

Sravan *et al.* (2012) reported grain yield per plant had a significant positive correlation with straw yield per plant, harvest index, panicles per plant, plant height, number of grains per panicle, panicle length, test weight and panicle fertility. Path analysis revealed that the straw yield was the major contributor of grain yield, followed by harvest index and number of grains per panicle.

Aukaoma *et al.* (2013) evaluated 15 rice breeding lines to determine the relationship between yield and other traits. Correlation coefficient analysis revealed that the number of grains per plant had the highest and significant correlation with grain yield ($r = 0.7643$). Days to maturity and days to fifty *per cent* flowering had a negative but high correlation. The study showed that the number of grains per plant could be used as the most reliable selection index for yield improvement in rice since it is the most contributing attribute to yield.

Gulzar *et al.* (2013) reported grain yield is positively and significantly correlated with the number of tiller per plant and number of grain per panicle at both genotypic and phenotypic levels. The results of a genotypic path analysis revealed that panicle fertility had the highest positive direct effect followed by plant height and days to fifty *per cent* flowering.

Amit *et al.* (2014) studied 40 rice accessions and reported that grain yield has a strong positive significant association with tillers per plant, panicles per plant, panicle length, straw yield, harvest Index, number of grains per panicle and test weight.

Nikhil *et al.* (2014) conducted an experiment to study the correlation and path analysis in 40 rice genotypes. Character association of the yield attributing traits revealed a significantly positive association of grain yield with straw yield and the number of panicles per plant. Hence, selection for these traits can improve yield. Path coefficient analysis revealed that straw yield and harvest index exhibited a positive direct effect on yield. Among these characters, straw yield possessed both positive association and high direct effects. Hence, selection for this character could bring improvement in yield and yield components in rice.

Singh *et al.* (2014) evaluated 38 rice germplasm accessions for 12 traits to assess the character association for grain yield with yield attributing traits. The genotypic correlation coefficient was higher than the phenotypic correlation coefficient, indicating a strong inherent association for grain yield and other traits. Days to fifty *per cent* flowering, days to maturity, the total number of tillers per plant, total grains per panicle, panicle fertility and straw yield showed strong positive and significant association with grain yield.

Venkatalakshmi *et al.* (2014) evaluated 70 rice genotypes to study the nature and extent of correlation among yield and yield attributing characters. The results revealed that grain yield to be positively and significantly associated with days to maturity, number of productive tillers per plant and plant height indicating the importance of these traits as selection criteria in yield improvement programmes.

Allam *et al.* (2015) studied the correlation and path analysis in 23 genotypes of basmati rice for grain yield, its component traits and grain quality traits. High significant positive genotypic and phenotypic correlation for grain yield was observed in days to maturity, effective panicles and number of grains per panicle. Effective panicles per plant imparted the highest positive direct effects on yield followed by test weight, number of grains per panicle and panicle fertility when assessed for path coefficient analysis.

Gayathri and Padmalatha (2015) studied the correlation and path analysis in twenty-five medium duration rice varieties. Character association of the yield attributing traits revealed a significant positive association of grain yield with plant height, 1000 seed weight and panicle length. Path coefficient analysis revealed that 1000 seed weight recorded maximum positive direct effect on yield followed by panicle length. Among these characters, 1000 seed weight and panicle length possessed both positive association and high direct effects.

Mahendra Bhati *et al.* (2015) studied genetic variability, correlation and path coefficient analysis on 30 elite rice genotypes. Correlation studies revealed that the correlation between grain yield was positively significant with harvest index, straw yield, test weight and plant height at genotypic and phenotypic levels. Path coefficients revealed that the harvest index, straw yield, number of grains per panicle, number of tillers per hill and plant height had a high positive direct effect on grain yield at genotypic and phenotypic levels.

Sarwar *et al.* (2015) carried an experiment to estimate the correlation and path coefficient analysis among 42 Aman rice genotypes. From the analysis, it was estimated that yield was significantly and positively correlated with days to maturity, productive tillers per plant and total tillers per plant as well as these traits engaged positive direct effect on yield per plant and this indicated that the selection for days to maturity, number of tillers per plant and productive tillers per plant would likely the best parameter for improvement in yield per plant.

Dhurai *et al.* (2016) conducted an experiment using 32 rice genotypes to estimate correlation coefficients and path analysis for grain yield and yield contributing traits in rice. The experiments were laid down in a randomized complete block design with three replications. Highly significant variation was obtained for almost all the

characters studied. Character association analysis revealed a significant positive association of grain yield with harvest index, days to maturity and number of grains per panicle. Correlations among yield components were positive, encouraging rapid improvement of yield. Path analysis revealed that harvest index and days to maturity had shown high positive effects on grain yield.

Muthuramu and Sakthivel (2016) studied correlation and path analysis for eight yield-related traits in 23 rice genotypes under the upland rice ecosystem. Productive tillers per plant and harvest index expressed a positive and significant correlation with grain yield. The trait, straw yield positively and significantly correlated with days to fifty *per cent* flowering, productive tillers per plant and the number of filled grains per panicle. The traits straw yield and harvest index expressed a high direct effect, and productive tillers per plant had a moderate direct effect on grain yield. The traits productive tillers per plant, straw yield and harvest index should be given more importance for enhancing grain yield under the upland rice ecosystem.

Kumar *et al.* (2017) reported both at the genotypic and phenotypic level, grain yield had a significant positive association with plant height, panicle length, number of filled grains per panicle and number of grains per panicle. But it had a significant negative association with the number of tillers per plant and test weight. The number of grains per panicle had a direct and positive effect on grain yield followed by days to maturity, plant height, panicle fertility and test weight.

Lakshmi *et al.* (2017) studied the F₇ generation of aromatic rice. Correlation studies revealed a positive significant correlation of grain yield with panicle length, filled grains per panicle, 1000-grain weight and L/B ratio at both phenotypic and genotypic levels and the number of productive tillers at a phenotypic level indicating these characters were important for yield improvement. Path coefficient analysis revealed that panicle length exerted the highest direct effect on grain yield followed by the number of filled grains per panicle, 1000-grain weight, number of productive tillers per hill and plant height, indicating the selection for these characters is likely to bring about an overall improvement in plant yield directly.

Priya *et al.* (2017) investigated the character association and the magnitude of direct and indirect effects of yield component traits of rice for 11 characters. Character association studies revealed that traits like productive tillers per plant, grains per panicle, test weight, panicle length, days to maturity, plant height and days to fifty *per cent* flowering had a significant positive association with grain yield at the phenotypic level.

Ramya *et al.* (2017) studied the correlation and path analysis in 56 genotypes of rice. Character association studies revealed that the grain yield per plant showed a significant positive association with the number of productive tillers per plant, panicle length and the number of filled grains per panicle. Path coefficient analysis revealed that the traits *viz.*, 1000-grain weight, numbers of filled grains per panicle, number of productive tillers per plant, days to fifty *per cent* flowering and plant height were directly influencing the grain yield per plant.

Bhujel *et al.* (2018) studied correlation and path coefficients analysis among seven morphological characters in 24 rice genotypes. Grain yield had a significant negative correlation with days to fifty *per cent* flowering while a positive correlation with 1000 grain weight, panicle fertility and panicle length. The path coefficient analysis showed the highest positive direct effect of 1000 grain weight on grain yield, followed by panicle length and panicle fertility.

Iqbal *et al.* (2018) used a randomized complete block design to evaluate 14 elite rice genotypes with three replications. Correlation analysis showed grain yield is positively correlated with days to maturity ($r = 0.46^{**}$) and negative correlation with 1000 grain weight ($r = -0.30^*$).

Kumar and Sonali (2018), in their study, indicated that straw yield, harvest index, spikelet fertility, 1000 grain weight, length and breadth ratio, plant height and panicle length showed a positive and significant correlation with grain yield per plant to emerge as most important associates of grain yield in rice. Path analysis identified straw yield followed by harvest index as most important direct yield contributing character and straw yield per plant followed by 1000 grain weight and panicle length exhibited high order of positive indirect effect.

Rachana *et al.* (2018) examined correlation and path analysis in 46 rice genotypes for yield and its components. Correlation studies revealed a highly significant and positive association of grain yield with days to fifty *per cent* flowering, tillers per plant, productive tillers per plant and straw yield. Path coefficient analysis showed that productive tillers per plant exerted the highest positive direct effect followed by panicle length, the number of grains per panicle, test weight, panicle weight, harvest index and straw yield indicating that selection for these characters is likely to bring about an overall improvement in grain yield directly.

Shrestha *et al.* (2018) conducted an experiment to study the association of yield attributing characters with grain yield and path analysis in 12 rice genotypes. The correlation coefficient analysis revealed the positive and significant association of 1000 grain weight, while plant height showed a negative and non-significant correlation with yield. Path analysis showed 1000 grain weight had a positive and high direct effect on grain yield.

Singh *et al.* (2018) studied the correlation and path analysis in 84 rice (*Oryza sativa* L.) varieties. Straw yield, harvest index, 1000-grain weight, productive tillers and panicle length showed positive and significant correlation with grain yield to emerge as the most important associates of grain yield in rice. Path analysis identified straw yield followed by harvest index as most important direct as well as indirect yield.

Kamana *et al.* (2019) worked on 11 rice genotypes to decipher association among them using correlation and path studies. The study showed that grain yield was significantly positively correlated with panicle length while positively and non-significantly correlated with days to fifty *per cent* flowering and straw yield except for plant height, panicle fertility, test weight and productive tillers. Panicle length had a maximum positive direct effect on grain yield followed by test weight and productive tillers, which was useful for selection and further improvement of rice genotypes.

Mutturaj *et al.* (2019) studied the degree of association between grain yield and yield attributing characters and their direct, indirect effects on grain yield in twenty-seven advanced breeding lines of rice (F₆ generation). The result revealed that straw yield and harvest index showed a significant positive correlation with grain yield per hectare. Therefore, the improvement of these traits through selection will automatically result in increased grain yield. Straw yield, days to maturity, harvest index, panicle length, days to fifty *per cent* flowering, number of productive tillers per plant, number of filled grains per panicle and test weight exhibited a positive direct effect on grain yield.

Sarker *et al.* (2020) observed significant and desirable correlations for the number of filled grains per panicle, panicle fertility (%), days to fifty *per cent* flowering both at the genotypic and phenotypic level. Considering genetic parameters, correlation and path coefficient analysis, direct selection based on the number of filled grains per panicle and panicle fertility would significantly increase rice grain yield.

Vanisri *et al.* (2020) evaluated 38 cold-tolerant rice genotypes for genetic variability, correlation and path analysis for yield and yield attributing traits. Grain yield had a positive significant correlation with plant height, tillers per plant, panicle length, panicle fertility and filled grains per panicle at the phenotypic level. Path coefficient analysis determined plant height, panicle length and filled grains per panicle, exhibiting a direct positive effect on yield. Selection for these traits helps in improving seed yield.

Fentie *et al.* (2021) studied 30 lowland rice genotypes to determine the magnitude of association of yield and yield attributed traits. Grain yield ha⁻¹ had positive and highly significant phenotypic and genotypic correlations with filled grains panicle⁻¹, panicle weight, straw yield and harvest index, but it had negative genotypic

and phenotypic correlation with test weight. Straw yield, harvest index, number of filled grains panicle⁻¹ and panicle plant⁻¹ exerted the highest positive direct effect on grain yield while days to flowering exerted a negative direct effect on grain yield at both genotypic and phenotypic levels.

Islam *et al.* (2021) studied ten popular upland rice genotypes to determine the nature of the relationship between grain yield with other yield contributing traits. The experiment was designed as a completely randomized block design with three replications. The result showed that plant height, productive tillers, panicle length, harvest index and total number of grains per panicle were positively significant correlated with grain yield per genotypes. Path analysis indicated that plant height, productive tillers, panicle length and filled grain exhibited a positive direct effect on grain yield. Among these traits, total number of grains per panicle, panicle fertility and productive tillers possessed high positive direct effects.

2.3 Genetic divergence among the rice advanced breeding lines

Knowledge on the nature and magnitude of genetic variability present in the crop species is helpful in formulating a successful breeding programme. It has been known that greater will be the chances of obtaining the desirable gene combinations. Mahalanobis' D^2 statistics is an effective tool in quantifying the degree of genetic divergence at the genotypic level and provides a measure of association between geographic distribution and genetic diversity based on generalized distance (Mahalanobis', 1936).

Garg *et al.* (2011) carried out an investigation with the 48 genotypes of rice to study the nature and magnitude of genetic divergence using D^2 statistics. Seventeen yield and quality traits were recorded on the genotypes raised in the design with three replications. The forty-eight genotypes were grouped into five clusters based on Euclidean cluster analysis, with cluster-I containing the maximum of 18 genotypes.

Chakma *et al.* (2012) conducted an experiment to determine the genetic diversity among 39 rice genotypes. The genotypes were grouped into six clusters based on Mahalanobis' D^2 statistics. Cluster I consisted of the highest number of (11) genotypes, whereas cluster-IV consisted of the lowest number of (3) genotypes. Cluster-III showed maximum mean yield. The maximum inter-cluster distance was recorded between clusters II and III. Cluster-III had the highest mean values for grain yield, harvest index, 1000-grain weight and the number of productive tillers per plant. The test weight and grain yield showed maximum contribution towards genetic divergence.

Lal and Chauhan (2012) grouped 48 rice genotypes into seven clusters based on Mahalanobis' D^2 multivariate analysis and observed maximum number of genotypes in cluster I, followed by Cluster V. Cluster II and IV comprised only three genotypes in each cluster. Maximum cluster distance was recorded between Cluster-II and VI, whereas the minimum distance between Clusters-I and III. The maximum intracluster distance was observed in clusters VII and minimum in cluster VI.

Thomas and Gabriael (2012) evaluated 69 genotypes of rice (*Oryza sativa* L.) based on D^2 values, and the genotypes were grouped into nine clusters. Cluster I, V and VIII were the largest containing 12 genotypes, followed by cluster III with nine genotypes. The highest inter-cluster distance was observed between clusters II and VII.

Ramanjaneyulu *et al.* (2014) studied the ten popular low land rice genotypes under the aerobic condition on alfisols. Based on morphological traits, they were grouped into four clusters indicated the existence of a significant amount of variability. The maximum intra-cluster distance was observed in cluster III. The yield trait 1000-grain weight exhibited the maximum contribution to total genetic divergence (57.78 %) followed by grain yield (15.56 %), number of grains per spikelet (11.11 %), straw yield (6.67 %) and spikelet length (4.44 %).

Neeraj *et al.* (2015) studied genetic diversity in rice genotypes. Out of all genotypes, five clusters were formed. Among five clusters, cluster-I was the largest (9 genotypes), followed by cluster V (7 genotypes) and cluster II and III with three genotypes, respectively. The cluster mean for plant height, the number of grains per panicle, straw yield and grain yield grain were exhibited minimum in cluster V and the maximum in cluster II, whereas days to fifty *per cent* flowering and days to maturity exhibited minimum in cluster-IV and maximum in cluster-I.

Praveen *et al.* (2015) investigated 51 genotypes of rice to study the nature and magnitude of genetic divergence using D^2 statistics. Thirteen yield traits were recorded on the genotypes for diversity analysis. The genotypes were grouped into eight clusters based on Euclidean cluster analysis, with clusters IV, VII, VIII containing a maximum of nine genotypes. The maximum intra-cluster distance was observed in cluster II indicating more significant genetic divergence among the genotypes of this cluster. Test weight and plant height contributed 52.94 *per cent* of total divergence. Maximum inter cluster distance was recorded between clusters V and VIII, followed by clusters IV and VIII, indicating wide genetic diversity and it may be used in the rice hybridization programme for improving grain yield.

Chandramohan *et al.* (2016) studied genetic diversity in 44 genotypes of rice. Based on D^2 analysis, the genotypes were grouped into 11 clusters. Based on inter-cluster distance, genotypes from clusters IV and V followed by V and IX could be used

as parents for future hybridization programmes. Cluster mean analysis revealed that genotypes JGL 21820 and JGL 21849 could be used in the breeding programme for obtaining high yielding super fine grain segregants. The traits like days to fifty *per cent* flowering and 1000 grain weight manifested the highest contribution towards total divergence. Therefore, these traits could be given due importance for further crop improvement.

Tejaswini *et al.* (2016) grouped rice genotypes into 12 clusters and reported that cluster V constituted the maximum number of genotypes. The genotypes falling in cluster-XII had the maximum divergence, which was closely followed by cluster-IX and the maximum inter cluster Euclidean values was observed between cluster-II and XII followed by cluster-IX and XII, suggesting that the genotypes constituted in these clusters may be used as parents for future hybridization programmes.

Babu and Sreelakshmi (2017) assessed 50 rice genotypes to study the nature and magnitude of genetic divergence using D^2 statistics. Fifty genotypes were grouped into six clusters based on the genetic distance between them. Cluster-I has the maximum number of genotypes (12), followed by cluster II with nine entries. Cluster-VI and Cluster-III showed maximum (746.9) and minimum (327.8) intracluster distances, respectively. Clusters III and VI (827.45) showed maximum inter-cluster distance followed by clusters III and IV, indicating wide genetic diversity.

Bhinda and Karnwal (2017) evaluated 42 genotypes of rice to study diversity for yield contributing and quality traits in advanced breeding lines of rice, including three check varieties. Nature and magnitude of genetic divergence was assessed using Mahalanobis' D^2 statistics, through which the 42 genotypes were grouped into seven clusters. Cluster IV having 17 genotypes, was the largest, whereas clusters I and VII were monogenotypic clusters. The maximum inter-cluster distance was found between clusters II and VII (98.237), indicating the suitability of genotypes from these clusters for hybridization.

Guru *et al.* (2017) evaluated 58 rice genotypes for ten yield attributing characters using D^2 analysis to study the diversity pattern among the genotypes. The genotypes were grouped into 13 clusters, of which clusters VII and XII (36.93) followed by clusters II and VI (33.48) and clusters XI and XIII (33.35) recorded maximum inter-cluster distance. The intra-cluster distance was maximum in cluster-VII (9.54) followed by cluster-V (8.91) and cluster-IV (8.28), indicating hybridization involving genotypes within the same clusters may result in good cross combinations. The traits *viz.*, panicle weight, test weight and total grain number per panicle together contributed 94.37 *per cent* towards total divergence.

Rashmi *et al.* (2017) studied the nature and magnitude of genetic divergence in 22 advanced breeding lines of rice for thirteen yield and yield attributing characters. The genotypes were grouped into five clusters. Cluster-I constituted the maximum number of advanced breeding lines (18). Among the five clusters, cluster-I, with a total score of 29 across the thirteen characters, secured the first rank, followed by cluster-III, with 33 score secured the second rank. Cluster-IV, with the highest score of 46, secured the fourth rank. The inter-cluster distance was maximum between clusters III and IV (9.48), followed by clusters III and V (9.19). The maximum intracluster distance was observed for cluster-I (3.48). Traits like the number of spikelets and the number of grains per panicle were the major contributors to the total genetic divergence.

Sarawgi *et al.* (2017) grouped rice germplasm accessions into eight clusters and reported cluster-VIII had the highest mean value for 100 grain weight, and Cluster-II had the highest mean value for panicle length, effective tillers/plant and L/B ratio. Based on mean performance, suggested selecting better genotypes from different clusters for most of the characters.

Amit *et al.* (2018) studied the existing genetic diversity in 36 advanced rice breeding lines through Mahalanobis D^2 statistics for grain yield and quality traits. Based on the D^2 analysis, the genotypes were grouped into six clusters. Cluster-II contained the highest number of genotypes (17), followed by cluster I (12), cluster-III (4) and the clusters IV, V and VI are mono-genotypic. Among the twenty-one traits studied, the maximum contribution was made by Kernel elongation ratio (71.90 %) followed by biological yield per plant (4.76 %), amylase content (4.60 %) and 1000-grain weight (4.13 %). Therefore, these characters may be given importance during the hybridization programme.

Kazipyo *et al.* (2018) evaluated 32 genotypes of rice to assess the genetic divergence for 13 quantitative characters. Based on the relative magnitude of D^2 values, the genotypes were grouped into seven clusters. Cluster-II constituted the maximum number of genotypes with 15 genotypes. The maximum inter-cluster distance was observed between clusters VII and III, followed by clusters VII and IV. Maximum genetic divergence was exhibited by days to maturity (49.19 %) followed by plant height (17.54 %), spikelets per panicle (16.33 %) and biological yield (11.29 %).

Shivani *et al.* (2018) investigated 26 rice genotypes to study the nature and magnitude of genetic divergence using D^2 statistic. Twenty-six genotypes were grouped into six clusters, with cluster-I containing the maximum of 11 genotypes. Cluster II had maximum intracluster distance indicating greater genetic divergence between the genotypes. The maximum inter-cluster distance was recorded between cluster III and IV, followed by cluster I and VI indicating wide genetic diversity. The number of spikelets per panicle had the maximum contribution of individual traits to the divergence among genotypes.

Suwansa *et al.* (2018) studied genetic divergence in 22 upland rice varieties. Based on the D^2 analysis, the varieties are grouped into three clusters. Group-I consisted of nine genotypes, group-II consisted of five genotypes and group-III contained six genotypes. Group-I exhibited the highest mean values for traits, such as plant height, days to fifty *per cent* flowering, flag leaf width and one thousand grains weight. Group-II showed the highest mean values for traits like days to maturity, flag leaf length, panicle length and the number of panicles per plant. Group-III showed the highest mean values for the number of tillers per hill, yield per plant and number of panicles per plant.

Solanki *et al.* (2019) studied genetic diversity among 60 genotypes of rice, which were grouped into 12 clusters. Maximum genetic divergence was observed between cluster V and IX, followed by Cluster V and VII, while closest proximity was noticed between cluster I and IX. The characters viz., grain yield, grain L/B ratio, panicle length and amylose content contributed much to the total genetic divergence. On the basis of cluster mean values, cluster-IX was superior for grain yield, plant height and panicle weight; cluster-XII for days to fifty *per cent* flowering; cluster-XI for effective tillers per plant; cluster-VIII for panicle length; cluster-IV for straw yield and cluster-VII for harvest index.

Dhakal *et al.* (2020) studied genetic divergence with 30 rice landraces using principal component analysis. Landraces were grouped into six clusters, where 12 landraces were grouped into cluster-I. Cluster analysis showed maximum and minimum intracluster distance in cluster-VI ($D^2 = 35.77$) and cluster-I ($D^2 = 18.59$), respectively. The maximum intercluster distance was obtained between clusters V and VI ($D^2 = 40.18$), followed by clusters III and VI ($D^2 = 36.17$) and clusters IV and VI ($D^2 = 35.74$). Cluster III showed the highest mean value for grain width, flag leaf breadth, yield, and the minimum mean value for plant height, while mean values of total grain per panicle, filled grain percentage, and thousand-grain weight were maximum in cluster-IV. Mean values of effective tiller and kernel width were found maximum in clusters V and VI, respectively.

Manjunath *et al.* (2020) estimated the nature and magnitude of genetic divergence in 23 rice genotypes in six environments using Mahalanobis D^2 statistics by considering 13 quantitative characters. D^2 analysis revealed a considerable amount of diversity in the material. The genotypes were grouped into six clusters. Cluster-I constituted the maximum number of genotypes (16). The genotypes falling in cluster-II had the maximum divergence. The inter cluster distance was maximum between cluster I and IV (10.34), followed by cluster III and V (9.82), suggesting that the genotypes constituted in these clusters may be used as parents for future breeding programme. Traits like; days to maturity, plant height (cm), the number of grains per panicle, test weight (g), harvest index (%), days to fifty *per cent* flowering, panicle length (cm) were the major contributors to genetic divergence.

Sinha *et al.* (2020) carried out an experiment with 22 lowland genotypes using RBD and were analyzed for genetic divergence with the help of Mahalanobis' D^2 statistics. Twenty-two genotypes of rice were grouped into six clusters using Tocher's method. Cluster-I consist of the maximum number of genotypes forming the largest cluster, followed by cluster-VI having three genotypes. The highest intracluster distance was observed in cluster-VI, followed by Cluster-I. Maximum inter cluster distance was observed between cluster-III and Cluster-IV followed by cluster-III and cluster-IV. *Per cent* contribution of 15 characters and towards total genetic divergence was found maximum for 1000 grain weight followed by days to flowering, grain length.

Sujitha *et al.* (2020) studied genetic divergence and traits association among 108 rice genotypes, nine morphological traits. Based on their D^2 values, the genotypes were grouped into 14 clusters, and the maximum of 37 genotypes were grouped under cluster-I. The highest intra and inter cluster distance was observed in cluster-X and between cluster XII and XIV, respectively. The trait grain length recorded maximum contribution to the divergence, followed by plant height.

Barhate *et al.* (2021) studied 45 genotypes of Aromatic Rice for genetic divergence. The observations were recorded on thirteen quantitative characters. All the characters showed highly significant differences among the genotypes for all the characters, indicated that an appreciable amount of diversity was present among the genotypes. The 45 genotypes were grouped into 10 clusters, and the clusters I, II, IV, V and VI contained 21, 4, 2, 8 and 5 genotypes, respectively. While the clusters III, VII, VIII, IX and X were monogenotypic. D^2 analysis revealed that there was a wide diversity between the genotypes.

Kumari *et al.* (2021) studied 119 rice breeding lines with two local checks and subjected them to the principle component analysis (PCA) and cluster analysis to estimate the existing genetic diversity for yield contributing characters. Cluster analysis revealed that the rice lines were classified into 12 divergent clusters by both PCA and Tocher's method. Among the 12 clusters, cluster-I had the highest number of breeding lines (18) and cluster-XI had the least number of lines (2) in PCA cluster analysis, whereas, in Tocher's method, the highest number of lines observed in cluster 5 (34) followed by cluster 1(33).

2.4 Screening of rice advanced breeding lines for blast reaction

Rice blast caused by *Pyricularia oryzae* is one of the most damaging and an important disease of rice in many parts of the world. Rice blast occurs erratically in most rainfed lowland environments, being severe in some seasons and low in another

season. This disease accounts for yield loss up to 65 *per cent* in a susceptible cultivar of rice (Vasudevan, 2014). A genotype with resistance to blast disease offered scope in breeding programme to evolve multiple tolerance genotypes.

Odile *et al.* (2011) evaluated 172 national and 47 foreign accessions for leaf blast resistance by inoculating plants with three strains of *Magnaporthe oryzae*, representing the pathogen genetic diversity existing in Italy. Only 15 out of 172 Italian accessions were resistant to all three fungal strains.

Ghaley *et al.* (2012) screened 352 landraces against 32 R gene lines. They reported 19 lines as completely resistant with zero disease score and 163 lines showed partial resistance to early leaf and panicle blast, respectively.

Santosh Kumar *et al.* (2012) showed rice genotypes resistance against blast disease under rainfed lowland ecosystem. Significant differences were observed for resistance to blast disease among genotypes. The screening revealed that only a few entries were highly resistant against blast disease.

Bashir *et al.* (2013) screened 100 germplasm accessions. They found 27 accessions carrying resistance specific. Differential screening results coupled with scoring information classified the genotypes into separate categories. Out of the 100 accessions, 11 were moderately susceptible and in nine other genotypes were susceptible to blast.

Idowu *et al.* (2013) screened 34 varieties plus one local check for resistance to rice blast disease caused by a fungus (*Magnaporthe oryzae*) at Ibadan and Ikenne under natural infection for two years. Results revealed that the 35 varieties responded differently to blast infection, and the two sites were significantly different from each other.

Naveenkumar *et al.* (2013) evaluated 122 genotypes of Basmati and non-basmati Indica rice genotypes against blast disease under induced epiphytotic conditions and reported 13 genotypes as resistant to blast. Nine genotypes carried blast resistance genes but were susceptible under induced epiphytotic conditions. The rice genotype VLD-61 had no resistance genes; however, it expressed strong resistance against blast.

Barnwal *et al.* (2014) screened 193 rice (*Oryza sativa* L.) genotypes for disease resistance against blast caused by *Pyricularia oryzae* Cav. at the blast hot spot of Rice Research Farm, BAU, Ranchi showed differential reactions indicating genetic variation in rice for blast resistance. Nine genotypes *viz.*, RP 4075-345-132-27, CN 1918, CN 1383-5-11, RR 440-167, NDR 9211, OR 1924-4, SJR 5, GP DHAN and CRHR-29 were found highly resistant to leaf blast.

Jayawardana *et al.* (2014) evaluated 34 rice varieties, including Sri Lankan and IRRI recommended rice varieties for blast resistance. Varieties like Tetep, Bg359, Bg304, IR64, Bg352 and Bg357 were found to be highly resistant, 17 were resistant and 17 were susceptible to the fungal infection. Varieties like LD125, Bg94/1, Bw267-3, Bw451, Bw400, H7, Bg34-6, H10 and IRRI119 were highly susceptible to blast.

Vasudevan *et al.* (2014) conducted a large-scale screen for new rice blast resistance sources in 4246 geographically diverse rice accessions originating from 13 major rice-growing countries. The accessions were selected from a total collection of over 120,000 accessions based on their annotated rice blast resistance information in the International Rice Gene bank. They obtained 186 resistant genotypes and 1436 moderately resistant genotypes, and the remaining genotypes are moderately susceptible, susceptible and highly susceptible.

Dar *et al.* (2015) conducted a field trial for disease screening of rice germplasm consisting of nine parents, 27 crosses and one local check under natural epiphytotic conditions and the results revealed that none of the test lines was immune or highly resistant. Four crosses, namely, K-08-60 × IR-68888A, K-08-61 × SKAU-11A, K-08-61 × IR-68888A, PS-5 × SKAU-11A and one parent PS-5 were found to be resistant. Seven hybrids and four parents displayed moderately resistant response. Three crosses and an equal number of parents were found to be moderately susceptible. Rest of the crosses and parents showed susceptibility to highly susceptible responses.

Hossain and Hegde (2016) screened the rice germplasm under natural conditions against rice blast. Results showed that none of the germplasm was immune to blast, 17 genotypes were resistant to leaf blast, but none of them were resistant to neck blast. Eight genotypes were moderately resistant to both leaf blast and neck blast. Eighteen genotypes showed highly susceptible reaction to leaf blast.

Pandey (2016) investigated rates of infection of leaf blast on 12 cultivars of rice in upland agricultural conditions in Rewa, Madhya Pradesh in India during the year 2011 and 2012. The highly susceptible traditional cultivar Gurmata, Dehula and Indrajal showed a high degree of incidence, apparent infection rates and severities. Among the improved cultivars, Basmati shows a high level of susceptibility under congenial weather conditions; however, the other cultivars show slow blasting and conclude that the study helps to identify and characterize the cultivars having slow blasting resistance, despite moderate disease levels which can be used in breeding programs to develop varieties with high levels of resistance.

Sabin *et al.* (2016) conducted an experiment for screening 50 rice genotypes under natural epidemic conditions against seedling blast (*P. grisea*). Based on the result, Taichung-176 and Sankharika showed the highest percentage of incidence and severity of the disease. Sabitri, however, was found to be most resistant among genotypes with the lowest percentage of incidence and severity.

Harish (2016) carried out an experiment to screen 100 rice genotypes for leaf blast disease reaction at Agricultural and Horticultural Research Station (AHRS) Ponnampet (a hot spot for blast disease) during *Kharif* 2015. It is evident that out of 100 genotypes, 12 shows high resistance, 26 genotypes exhibited resistance, 43 genotypes were moderately resistant, 17 genotypes were moderately susceptible, and one genotype each in susceptibility and highly susceptible. At AHRS, Ponnampet, most genotypes exhibited moderate resistance to leaf blast disease compared with the susceptible genotype Intan.

Rijal *et al.* (2017) evaluated a total of 314 and 346 rice genotypes with resistant (Sabitri) and susceptible checks (Sankarika) under epiphytotic conditions during 2016 and 2017 summer seasons at Rampur, respectively. During 2016 disease severity varied from 1 to 9 and only five genotypes, Sabitri, IR 12L 110, WAS 122-IDS14-WASB-FKRI, IR 10F 559 and IR 10F 616, were resistant, 30 moderately resistant, 150 susceptible and 129 highly susceptible against blast disease. Similarly, in 2017 out of 346 genotypes, 23 were resistant, 72 were moderately resistant, 191 were susceptible, and 155 were highly susceptible. Most of the highly susceptible genotypes were knocked down at the time of disease scoring.

Qudsia *et al.* (2017) evaluated a total of fifty-two rice genotypes, including one susceptible check, Basmati C-622, to find out new sources of resistance and assess their diversity based on the reactions against *P. oryzae*. The test genotypes were evaluated against leaf blast after three weeks of inoculation by following the standard evaluation system for rice introduced by the International Rice Research Institute, Philippines. The diversity of the 52 genotypes was also assessed based on blast symptoms. Moderately resistant reactions were observed with genotypes KSK-470, KSK-463, KSK-460, PK 8685-5-1-1-1, KSK-462, KSK-474, PK 3810-30-1, KSK- 471 and KSK-472.

Hosagoudar *et al.* (2018) studied 13 different advanced varietal lines, including existing varieties, as checks at Agricultural and Horticultural Research Station, Ponnampet. Results on field screening of genotypes for leaf blast reaction revealed that out of thirteen entries, none of the genotypes was found to be highly resistant. Three genotypes were found resistant (IET-24471, Tunga (LC), Savitri (ZC)), eight genotypes were found to be moderately resistant (IET-24443, Dhanrasi (NC), 24480, 24474, 23565, 23930, 24450, 24367), two genotypes were found to be moderately susceptible (IET-24451, 23561), none of the genotype was found to be susceptible and highly susceptible.

Sheshaiah *et al.* (2018) carried out an experiment with 35 germplasm lines screened during *Kharif* 2014 for blast resistance under field conditions by the UBN technique at AHRS, Ponnampet. The resistant checks (Tadukan and Tetep), shown

highly resistant response, KPR-1, KPR-2, Kiruwana and IR-64 recorded resistant response whereas Jaya, Intan, Ambemori, Bheemasaali, Chittiga and FR-13A were recorded highly susceptible to the leaf blast along with susceptible checks (CO-39 and HR-12).

Saikiran *et al.* (2019) carried out an experiment with 12 parents, 32 hybrids along with a susceptible check (TN1) to identify the superior hybrids and their parents with blast resistance by adopting Uniform Blast Nursery (UBN) at Rice Research Center, ARI, Rajendranagar during *Rabi*, 2017-18. The results indicate that, among the testers, JMS 13B showed resistant reaction while the other three testers showed susceptible reaction. Among the eight lines, five lines showed moderately susceptible reaction, while lines JGL 18047 and IET 26274 showed a resistant reaction. Four hybrids viz., JMS 13A x JGL 18047, CMS 23A x RNR 11450, JMS 13A x IET 26264 and JMS 13A x IET 26274 were resistant to screening reaction, and 11 hybrids were moderately susceptible to the blast disease.

Krishna *et al.* (2020) conducted an experiment was to evaluate the maintainer lines blast resistance and yield component traits in rice. The present investigation was carried out during *Rabi* 2018-19 with 40 genotypes and TN 1 (susceptible check). The genotypes were screened against leaf blast by adopting Uniform Blast Nursery (UBN) method at Rice Research Centre, Rajendranagar and scored as per Standard Evaluation System (SES) scale (IRRI-2013). Accordingly, based on the disease scoring, the genotypes were categorized as resistant, moderately resistant, moderately susceptible and susceptible types. It was found that 13 lines were resistant to screening reaction, 12 lines were moderately resistant and ten lines were found to be moderately susceptible, and three lines were susceptible.

MATERIAL AND METHODS

III MATERIAL AND METHODS

The details of the material used and methodology followed in the present investigation studies on ‘Assessment of Genetic Variability and Divergence in Advanced Breeding lines of Rice (*Oryza sativa* L.) in Lowlands of Hill Zone’ are presented briefly in this chapter. It also provides the statistical tools employed in drawing inferences on the characters considered in the present investigation.

3.1 Experimental location

The studies on genetic variability and diversity in advanced breeding lines of rice for yield and yield related characters was studied at Zonal Agricultural and Horticultural Research Station (ZAHRS), Mudigere and screening for blast disease was carried out at Agricultural and Horticultural Research Station (AHRS), Ponnampet during *kharif* 2020. The experimental site ZAHRS, Mudigere falls under Hill Zone of Karnataka (Zone –9) and geographically situated at 13°8'3"N latitude and 75°38'30"E longitude at an altitude of 915 meters above the mean sea level and AHRS, Ponnampet too falls in Hill Zone of Karnataka but geographically situated at 12.14907°N latitude and 75.94052°E longitude with an altitude of 851 meters above the mean sea level.

3.2 Description of the experimental material

The experimental materials for the present study comprised of 35 advanced breeding lines of F₆ generation with four checks *viz.*, KHP-10, KHP-11, KHP-13 and Tunga collected from Department of Genetics and Plant Breeding, College of Agriculture, Shivamogga. The advanced breeding lines are derived from the crosses *viz.*, JGL-1798 × KPR-2, KPR-2 × IS, KPR-2 × Jyothi, KPR-2 × Basu, Jyothi × Tunga and Gandhsali × HYD.

The advanced breeding lines of rice evaluated in the present investigation are enlisted in Table 1.

3.3 Experimental methods

3.3.1 Experimental layout

The experiment was laid out in puddled field by following Randomized Complete Block Design (RCBD) with two replications.

Table 1: List of advanced breeding lines evaluated under present investigation including checks

Sl. No.	Genotype names	Sl No.	Genotype names
1	JGL-1798 × KPR-2-7-2-3-1-1-1	21	KPR-2 × Basu-2-1-6-2
2	JGL-1798 × KPR-2-2-6-3-1	22	KPR-2 × Basu-1-5-1-4
3	JGL-1798 × KPR-2-3-7-3-1-2	23	KPR-2 × IS × Gandhsali-2-4-4-3
4	JGL-1798 × KPR-2-2-6-3-2	24	Jyothi × Tunga-4-3
5	JGL-1798 × KPR-2-3-7-4-1	25	Jyothi × Tunga-4-6
6	JGL-1798 × KPR-2-7-2-2-7-2	26	Jyothi × Tunga-2-6-1
7	JGL-1798 × KPR-2-2-4-1-1	27	Jyothi × Tunga-4-5
8	JGL-1798 × KPR-2-2-6-5-2	28	Jyothi × Tunga-2-4
9	KPR-2 × IS-9-2-2-2	29	Jyothi × Tunga-2-6-2
10	KPR-2 × IS-1-4-1-2	30	Gandhsali × HYD-5-2-2-4-2-2
11	KPR-2 × IS-9-2-2-1	31	Gandhsali × HYD-5-3-4-1-3-4
12	KPR-2 × IS-1-4-2-1	32	Gandhsali × HYD-5-1-4-1-4
13	KPR-2 × Jyothi-2-1-4-1	33	IS × HYD-3-2-1-2-2
14	KPR-2 × Jyothi-2-1-8-5-3	34	IS × HYD-3
15	KPR-2 × Jyothi-2-5-6-1	35	KPR-1 × Jyothi-1-6-2-1-1-2
16	KPR-2 × Basu-1-6-1-1	36	KHP-10(Check)
17	KPR-2 × Basu-1-4-2-1	37	KHP-11(Check)
18	KPR-2 × Basu-1-4-3-1	38	KHP-13(Check)
19	KPR-2 × Basu-1-2-2-1	39	Tunga(Check)
20	KPR-2 × Basu-1-4-1-1		

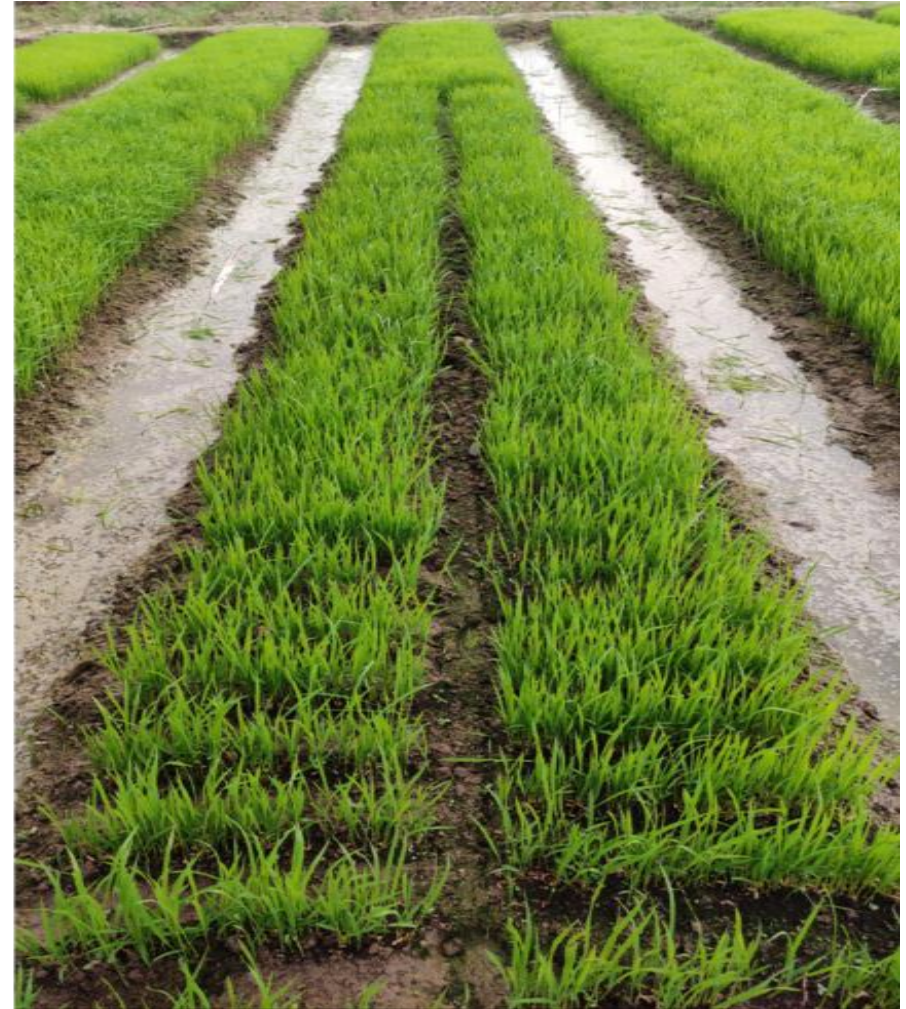


Plate 1: Nursery operations at ZAHRS, Mudigere



Plate 2: Overview of an experimental paddy field at ZAHRS, Mudigere



Plate 3: Overview of an experimental paddy field at AHRS, Ponnampet

3.3.2 Sowing and planting

Seeds of all the advanced breeding lines were sown in raised beds of one sq.m. on 25th June 2020 at ZAHRS, Mudigere as per nursery package. Later, 21 days old seedlings were transplanted to the main field at the rate of one seedling per hill with a spacing of 20 cm between rows and 15 cm between the plants within a row. Recommended package of practices was followed to ensure uniform and healthy crop stand.

3.3.3 Method of sampling and recording observations

Five plants from each advanced breeding line were selected and labeled leaving one meter distance from border for recording biometric observations. The average value of observations recorded on these five plants was considered for statistical analysis. Similarly, plant morphological and grain characters of each genotype were recorded by selecting single or group of plants depending on all characters at different stages of crop growth. The characters on which the observations recorded are described below.

3.3.3.1 Days to fifty per cent flowering

The number of days taken by each advanced breeding lines from sowing to the opening of the first flower in fifty *per cent* of the plants was observed and recorded as days to fifty *per cent* flowering.

3.3.3.2 Days to maturity

The total number of days taken by each advanced breeding line from sowing to physiological maturity was recorded.

3.3.3.3 Plant height (cm)

Plant height was measured in centimeters from the base of the plant to the tip of the panicle excluding awns at maturity using scale.

3.3.3.4 Panicle length (cm)

Length of the panicle was measured from flag leaf node to the tip of panicle using scale and expressed in centimeters.

3.3.3.5 Number of tillers per plant

Number of tillers per plant was recorded by counting both the productive and unproductive tillers in each hill.

3.3.3.6 Number of productive tillers per plant

The number of tillers bearing panicles per plant was recorded by excluding the tillers which do not bear panicles.

3.3.3.7 Total number of grains per panicle

Number of filled grains was counted in randomly selected five panicles and was taken as grain per panicle as the average of five plants.

3.3.3.8 Panicle fertility (%)

The *per cent* panicle fertility was calculated by using the formula given below and expressed in percentage.

$$\text{Panicle fertility(\%)} = \frac{\text{Number of filled grains per panicle}}{\text{Total number of grains per panicle}} \times 100$$

3.3.3.9 Test weight (g)

Weight of 1000 randomly selected filled grains was measured using electronic balance and expressed in grams.

3.3.3.10 L/B ratio

The length and breadth of grain was measured by using a digital rice grain analyzer. The ratio of length to breadth was determined by dividing the length of a single grain with corresponding breadth.

3.3.3.11 Grain yield (kg/ha)

Grain yield obtained from the net plot was cleaned, dried, weighed and expressed as kg/ha.

3.3.3.12 Straw yield (kg/ha)

After sun drying the straw to a constant weight the straw weight of net plot was calculated and estimated for ha in kgs.

3.3.3.13 Harvest index

The harvest index of each genotype was calculated by taking the ratio of grain yield per plant to straw yield per plant and expressed in *per cent*.

3.3.3.14 Visual scoring of the blast on percentage disease incidence

Visual scoring was done on the percentage of disease incidence by considering the entire row of each genotype, by a random viewing of lesions for types (LT %) and visual disease leaf area (DLA {v}) using 0-9 scale.

Scoring for leaf blast was done at nursery stage by using scale given by IRRI, Philippines (1996) as below

Rating scale	Disease severity	Host response
0	No lesion observed	Highly Resistant
1	Small brown specks of pin point size	Resistant
2	Small roundish to slightly elongated, necrotic grey spots, about 1 to 2 mm in diameter with a distinct brown margin. Lesions are mostly found on the lower leaves	Moderately Resistant
3	Lesion type same as in 2, but significant number of lesions on the upper leaves	Moderately Resistant
4	Typical susceptible blast lesions, 3 mm or longer infecting less than 4 % of leaf area	Moderately Susceptible
5	Typical susceptible blast lesions of 3 mm or longer infecting 4 to 10 % of the leaf area	Moderately Susceptible
6	Typical susceptible blast lesions of 3 mm or longer infecting 11 to 25 % of the leaf area	Moderately Susceptible
7	Typical susceptible blast lesions of 3 mm or longer infecting 26 to 50 % of the leaf area	Susceptible
8	Typical susceptible blast lesions of 3 mm or longer infecting 51 to 75 % of the leaf area many leaves are dead	Highly Susceptible
9	Typical susceptible blast lesions of 3 mm or longer infecting more than 75 % leaf area affected	Highly Susceptible

3.4 Statistical analysis

3.4.1 Analysis of variance (ANOVA)

The data of mean value for all the characters were analyzed for their variance following Randomized Complete Block Design outlined by Cochran and Cox (1957). Analysis was done using software WINDOSTAT version 9.2 at Department of Genetics and Plant Breeding, KSNUAHS, Shivamogga.

Source of variation	df	SS	MSS	F Ratio
Replication	(r-1)	SSr	SSR/(r-1)=MSSR	MSSR/MSSE
Genotype	(t-1)	SSg	SSG/(t-1)=MSSG	MSSG/MSSE
Error	(r-1)(t-1)	SSE	SSG/(t-1)=MSSG	
Total	(rt-1)	TSt		

Where,

- r = Number of replications
- t = Number of genotypes
- MSSR= Replication mean sum of squares
- MSSG= Genotype mean sum of squares
- MSSE= Error mean sum of squares
- df = Degrees of freedom

Sum of squares can be obtained as follows,

$$\text{Total sum of squares (TSS)} = \Sigma (\text{No. of observations})^2 - \text{CF}$$

Where,

CF= Correction factor

$$\text{Genotype sum of squares (SSG)} = \Sigma (Ti)^2/n - \text{CF}$$

Where,

n= Number of replications

$$\text{Replication sum of squares (SSR)} = \Sigma (Rj)^2/s - \text{CF}$$

Where,

s= Number of genotypes

$$\text{Error sum of squares (SSE)} = \text{TSS} - \text{SSG} - \text{SSR}$$

3.4.1.1 Mean

Mean is the sum of all observations in a sample divided by the number of observations.

$$\bar{X} = \frac{[\Sigma_{i=1}^n X_i]}{n}$$

Where,

- \bar{x} = Population mean
- X_i = i^{th} observation of a sample
- n= Number of observations

3.4.1.2 Range

Range is the difference between maximum and minimum values of the observations in a sample of a genotype.

3.4.1.3 Standard error

It is the measure of uncontrolled variation present in a sample which is estimated by dividing the standard deviation (SD) by the square root of number of observations (n) in the sample and is denoted by SE.

$$\text{SE} = \frac{\text{SD}}{\sqrt{n}}$$

3.4.1.4 Standard error difference between two means (S.Ed.m)

It is calculated with the help of error mean sum of square from ANOVA table.

$$\text{S. Ed. m} = \sqrt{\frac{2\text{MSSE}}{r}}$$

Where,

r = Number of replications

MSSE= Error mean sum of square

3.4.1.5 Critical difference (CD)

It is calculated to judge whether the difference between two particular treatments is significant or not.

$$\text{CD at 1\% or 5\% probability level} = \sqrt{\frac{2 \text{ MSSE}}{r}} \times t^*$$

t* (value) at 1 per cent or 5 per cent probability level for error degrees of freedom

3.4.1.6 Coefficient of variation (CV)

It is the ratio of standard deviation of a sample to its mean and expressed in percentage.

$$\text{CV(\%)} = \frac{\text{Standard deviation}}{\text{Mean}} \times 100$$

3.4.1.7 Variance

Mean of squared deviations of individual values from their mean is called variance.

$$\text{Variance} = \frac{\sum(X - \bar{X})^2}{n}$$

3.4.2 Estimation of genetic parameters

The genotypic and phenotypic variances were estimated using the formula given by Weber and Murthy (1952).

$$\text{Genotypic variance } (\sigma_g^2) = \frac{\text{MSS (genotype)} - \text{MSS (error)}}{\text{Number of replications}}$$

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

3.4.3 Coefficient of variability

The coefficient of variability both at phenotypic and genotypic levels for all the characters were computed by applying the formula as suggested by Burton and De Vane (1953).

3.4.3.1 Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sigma_p}{\bar{X}} \times 100$$

3.4.3.2 Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sigma_g}{\bar{X}} \times 100$$

Where,

\bar{X} = Grand mean of the character

σ_p = Phenotypic standard deviation

σ_g = Genotypic standard deviation

PCV and GCV were classified as suggested by Shivasubramanian and Menon (1973) into low (<10 %), moderate (10-20 %) and high (>20 %).

3.4.4 Genetic advance (GA)

3.4.4.1 Predicted genetic advance

The predicted genetic advance was estimated according to the formula given by Johnson *et al.* (1955).

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

Where,

h^2 = Heritability

K = Selection differential at given intensity

σ_p = Phenotypic standard deviation

h^2 = Heritability

K = Selection differential at given intensity

3.4.4.2 Genetic advance as per cent mean (GAM)

The expected GA as *per cent* of mean was estimated as given below

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

Where,

GA = Genetic advance

\bar{X} = General mean of the character

The genetic advance as *per cent* of mean was categorized as suggested by Johnson *et al.* (1955) as low (<10 %), moderate (10-20 %) and high (>20 %).

3.4.5 Heritability (h^2) broad sense

Heritability in broad sense for all the characters was computed by the formula suggested by Lush (1945).

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

σ_g^2 = genotypic variance

σ_p^2 = phenotypic variance

Heritability was classified as suggested by Robinson *et al.* (1949) into low (0-30%), moderate (30-60 %) and high (>60 %).

3.4.6 Genetic diversity

3.4.6.1 Mahalanobis' D^2 analysis

Mahalanobis' (1936) D^2 statistic was used for assessing the genetic divergence between populations which was done by using the WINDOSTAT version 9.2 software installed at Department of Genetics and Plant Breeding, COA, Shivamogga. The generalized distance between any two populations is given by formula,

$$D^2 = \sum \sum \lambda_{ij} \sigma_{ai} \sigma_{aj}$$

Where,

D^2 = Square of generalized distance

λ_{ij} = Reciprocal of the common dispersal matrix

$$\sigma_{ai} = (\mu_{i1} - \mu_{i2})$$

$$\sigma_{aj} = (\mu_{j1} - \mu_{j2})$$

μ = General mean

Since, the formula for computation requires inversion of higher order determinant, transformation of the original correlated unstandardized character mean (Xs) to standardized uncorrelated variable (Ys) was done to simplify the computational procedure. The D^2 values were obtained as the corresponding uncorrelated (Ys) values of any two uncorrelated genotypes (Rao, 1952).

3.4.6.2 Clustering of D^2 values

All the $(n-1)/2$ D^2 values were clustered using Tocher's method as described by Rao (1952).

3.4.6.2.1 Intra cluster distance

$$\text{Square of inter cluster distance} = \frac{\sum D_i^2}{n}$$

The intra cluster distances were calculated using the formula given by Singh and Chaudhary (1977).

Where,

$\sum D_i^2$ = sum of distance between all possible combinations of the entries included in a cluster.

n = number of all the possible combinations

3.4.6.2.2 Inter cluster distance

The inter cluster distances were calculated by the formula described by Singh and Chaudhary (1977).

$$\text{Square of intra cluster distance} = \frac{\sum D_i^2}{n_i n_j}$$

Where,

$\sum D_i^2$ = Distances between all possible combinations of the ($n_i n_j$) of the entries included in the cluster study.

n_i = Number of entries in cluster i

n_j = Number of entries in cluster j

3.4.7 Correlation analysis

The correlation coefficients were calculated to determine the degree of association of the characters with yield and also among the different yield components.

To estimate the degree of association between the traits studied, phenotypic correlation was computed by using the formula given by Weber and Murthy (1952).

The analysis was done by using the WINDOSTAT version 9.2 software.

$$r_{g(x,y)} = \frac{Cov_{g(x,y)}}{\sqrt{\sigma_{g(x)}^2 \cdot \sigma_{g(y)}^2}}$$

where,

$$r_{p(x,y)} = \frac{Cov_{p(x,y)}}{\sqrt{\sigma_{g(x)}^2 \cdot \sigma_{g(y)}^2}}$$

r_p and r_g are phenotypic and genotypic correlations, respectively.

$Cov_p(x,y)$ and $Cov_g(x,y)$ are phenotypic and genotypic covariance between the characters x and y .

$\sigma_{g(x)}^2$ and $\sigma_{g(y)}^2$ are the genotypic variances of the characters x and y

$\sigma_{p(x)}^2$ and $\sigma_{p(y)}^2$ are the phenotypic variances of the characters x and y

The calculated value of 'r' was compared with 'r' table value for (n-2) degree of freedom given by Snedecor (1974) at five and one *per cent* level of significance, where 'n' refers to number of pairs of observations.

3.4.8 Path coefficient analysis

To study the direct or indirect effect of yield attributing traits to yield was calculated using correlation coefficients as given by Wright (1921). Analysis was done using WINDOSTAT software (Version 9.2).

$$P_{01} + P_{02}r_{12} + \dots P_{0p}r_{1p} = r_{01}$$

$$P_{01}r_{21} + P_{02}r_{22} + \dots P_{0p}r_{2p} = r_{02}$$

$$P_{0p}r_{1p} + P_{0p}r_{2p} + \dots P_{0p} = r_{0p}$$

Where,

P_{01}, P_{02}, P_{0p} are the direct path coefficients of variables 1, 2, 3.....p on the dependent variable 0. $r_{12}, r_{13}, \dots, r_{1p}, \dots, r_{(p-1)p}$ are the possible correlation coefficients between various independent variables and $r_{01}, r_{02}, \dots, r_{0p}$ are the correlations between dependent and independent variables. The indirect effects of the i^{th} variable via j^{th} variable were obtained $p_{0j} \times r_{ij}$.

The contribution of the remaining unknown factors was measured as the residual factor and calculated as,

$$P_{0x}^2 = 1 - (P_{01}^2 + 2 P_{01} P_{02} r_{12} + 2 P_{01} P_{03} r_{13} + \dots + P_{02}^2 + 2 P_{02} P_{03} + \dots + P_{0p}^2)$$

$$\text{Residual factor}(R^2) = \sqrt{P_{0x}^2}$$

Scale for path coefficients (Lenka and Mishra, 1973)

Value of direct or indirect effects	Scale
0.0 to 0.09	Negligible
0.10 to 0.19	Low
0.20 to 0.29	Moderate
0.30 to 0.99	High
More than 1.00	Very high

EXPERIMENTAL RESULTS

IV EXPERIMENTAL RESULTS

More than half of the world's population consumes rice as a staple food. Despite the progress made in recent years in improving the yield level by using high yielding varieties, still there is a need to continue increasing production to support an increase in population. So, in order to meet the demand high yielding varieties coupled with resistance to biotic stress must be developed.

Under the following sections, the findings of the current study on variability and genetic diversity studies for yield and yield component traits in 39 (*Oryza sativa* L.) advanced breeding lines, as well as screening for blast disease reaction, are reported.

4.1 Genetic variability in rice advanced breeding lines for yield and its contributing traits

4.2 Correlation coefficient analysis for yield and its contributing traits

4.3 Path coefficient analysis among yield and its contributing traits

4.4 Genetic divergence among the rice advanced breeding lines

4.5 Screening of rice advanced breeding lines for blast disease reaction

4.6 Performance of top advanced breeding lines for yield and yield related traits

4.1 Genetic variability in rice advanced breeding lines for yield and its contributing traits

The mean values for all the characters studied are presented in Appendix I and the analysis of variance is depicted in Table 2. The analysis of variance for thirteen yield and yield component characters were statistically tested and found to be significant for all the characters evaluated. The genetic variability parameter *viz.*, mean, range, standard deviation, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) and genetic advance as *per cent* mean for all the 13 characters are presented in Table 3.

4.1.1 Days to fifty per cent flowering

The mean number of days to fifty *per cent* flowering was 118 days with the range of 100 to 131 days. The genotype IS × Hyd-3 was the earliest to flower, while KPR-2 × IS-9-2-2-1 was late to flower. The low phenotypic (5.95) and genotypic (5.89) coefficients of variability and high heritability estimates of 97.90 *per cent* coupled with moderate genetic advance as *per cent* mean (12.00) was observed for this trait.

Table 2. Analysis of Variance for yield and its attributing characters in advanced breeding lines of rice

Source of variation	Degrees of freedom	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Number of tillers per plant	Number of productive tillers per plant	Panicle length (cm)
Replication	1	0.05	1.55	8.21	1.52	0.97	0.36
Genotype	38	99.01**	99.67**	442.23**	3.07**	2.18**	4.84**
Error	38	1.05	0.74	2.91	0.48	0.36	0.14
CD (5%)		2.08	1.74	3.45	1.40	1.22	0.75
CD (1%)		2.78	2.33	4.63	1.87	1.63	1.00
CV (%)		0.86	0.58	1.97	3.68	3.64	1.71

Source of variation	Degrees of freedom	Total number of grains panicle ⁻¹	Panicle fertility (%)	Test weight(g)	Grain length and breadth ratio	Straw yield(kg)	Grain yield (kg)	Harvest index
Replication	1	480.52	0.25	0.02	0.02	1399514.00	237952.90	0.000399
Genotype	38	4862.57**	11.84**	62.83**	0.42**	3706581.94**	2969534.61**	0.007172**
Error	38	882.26	0.49	0.22	0.02	579304.33	217855.70	0.001079
CD (5%)		60.13	1.42	0.95	0.25	1540.81	944.88	0.06
CD (1%)		80.54	1.90	1.27	0.34	2063.82	1265.61	0.09
CV (%)		10.79	0.82	2.50	3.46	10.03	9.00	8.12

** - Significance at 1% level

Table 3. Genetic variability parameters for yield and yield related characters in rice advanced breeding lines

Sl. No.	Character	Mean \pm SEM	Range		PCV (%)	GCV (%)	h ² (bs) (%)	GAM (%)
			Min	Max				
1	Days to 50 per cent flowering	118.87 \pm 0.72	100.00	131.00	5.95	5.89	97.90	12.00
2	Days to maturity	148.98 \pm 0.60	130.00	161.00	4.76	4.72	98.53	9.65
3	Plant height (cm)	86.62 \pm 1.20	58.65	123.00	17.22	17.11	98.69	35.01
4	Number of tillers plant ⁻¹	18.73 \pm 0.48	17.00	22.00	7.10	6.07	73.12	10.69
5	Number of productive tillers plant ⁻¹	16.51 \pm 0.42	15.00	19.00	6.83	5.78	71.64	10.07
6	Panicle length (cm)	21.57 \pm 0.26	18.60	24.60	7.31	7.11	94.54	14.24
7	Total number of grains panicle ⁻¹	275.24 \pm 21.00	183.00	413.00	19.47	16.21	69.29	27.79
8	Panicle fertility (%)	85.12 \pm 0.49	80.75	91.87	2.92	2.80	92.04	5.53
9	Test weight (g)	18.73 \pm 0.33	10.25	31.10	19.97	19.86	99.30	21.31
10	Grain length and breadth ratio	3.60 \pm 0.08	2.83	4.50	12.96	12.49	92.90	24.80
11	Straw yield (kg ha ⁻¹)	7586.90 \pm 538.19	4412.52	11141.04	19.29	16.48	72.97	29.00
12	Grain yield (kg ha ⁻¹)	5184.30 \pm 330.04	2632.50	7150.00	24.35	22.63	86.33	43.30
13	Harvest index	0.41 \pm 0.02	0.32	0.48	15.89	13.65	73.84	24.18

4.1.2 Days to maturity

With a range of 130 to 161 days, the average number of days to maturity was 149 days. The IS × Hyd-3 was the first to mature, while the KPR-2 × IS-9-2-2-1 was the last to do so. The low phenotypic and genotypic coefficients of variability were 4.76 and 4.72 *per cent*, respectively. This trait had a high heritability of 98.53 *per cent* and a low genetic advance of 9.65 *per cent*.

4.1.3 Plant height (cm)

Plant height was 86.62 cm on average among genotypes. KHP-10 had the maximum plant height (123.00 cm), whereas IS × Hyd-3-2-1-2-2 had the lowest (58.65 cm). The phenotypic and genotypic coefficients of variability were found to be moderate (17.22 and 17.11). This trait had a high broad sense heritability of 98.69 *per cent* and a high genetic advance as *per cent* mean (35.01).

4.1.4 Number of tillers per plant

The average number of tillers counted was 18.73, ranging from 17 to 22. The highest number of tillers (22) was detected in KPR-2 × IS-1-4-1-2, and the lowest (16) in JGL-1798 × KPR-2-2-6-3-1 and KPR-2 × Basu-2-1-6-2. For number of tillers per plant, low phenotypic coefficients of variability (7.10) and genotypic coefficients of variability (6.07) were reported, respectively, and high heritability of 73.12 *per cent* with a moderate genetic advance as *per cent* of mean (10.69).

4.1.5 Number of productive tillers per plant

With a mean of 16.51, the genotype Gandhsali × HYD-5-1-4-1-4 (19) had the most productive tillers and the genotype KPR-2 × Basu-1-5-1-4 (15) had the least. This characteristic had a low phenotypic (6.83) and genotypic (5.78) coefficient of variability. The number of productive tillers had a high heritability of 71.64 *per cent* and a moderate genetic advance as *per cent* mean of 10.07.

4.1.6 Panicle length (cm)

The average panicle length was 21.57 cm, ranging from 18.60 cm to 24.60 cm. KPR-2 × Basu-1-2-2-1 had the longest panicle length, whereas IS × Hyd-3-2-1-2-2 had the shortest panicle length. For this trait, low phenotypic and genotypic coefficients of variability were 7.31 and 7.11 *per cent*, respectively, and high heritability of 94.54 *per cent* was reported, with a moderate genetic advance as a *per cent* mean of 14.24 *per cent*.

4.1.7 Total number of grains per panicle

With a mean value of 275.24, the total number of grains per panicle ranged from 183 to 413. The genotype JGL-1798 × KPR-2-3-7-3-1-2 had the highest total number of grains per panicle, while Jyothi × Tunga-4-3 had the lowest total number of grains per panicle. This characteristic had moderate phenotypic (19.47) and genotypic (16.21) coefficients of variability along with a high heritability of 69.29 *per cent* and a high genetic advance of 27.79 *per cent*.

4.1.8 Panicle fertility (per cent)

This trait was shown to have a high heritability of 92.04 *per cent* and a low GAM (5.53 *per cent*). Low phenotypic and genotypic coefficients of variability observed were 2.92 and 2.80 *per cent*, respectively. In advanced breeding lines, panicle fertility ranged from 80.75 to 91.87 *per cent*, with an average of 85.12 *per cent*. JGL-1798 × KPR-2-2-4-1-1 had the highest spikelet fertility, while IS × Hyd-3 had the lowest panicle fertility.

4.1.9 Test weight (g)

The grain test weight ranged from 10.25 to 31.10 g, with an average of 18.73 g. Tunga had the highest test weight while Gandhsali × HYD-5-3-4-1-3-4 had the lowest test weight. This trait had a moderate PCV (19.97), GCV (19.86), high heritability (99.30), and high genetic advance as a *per cent* mean (21.31).

4.1.10 L/B ratio

The L/B ratio ranged from 2.83 to 4.50, with an average of 3.60. Jyothi × Tunga-4-3 had the lowest L/B ratio, whereas KPR-1 × Jyothi 1-6-2-1-1-2 had the highest L/B ratio. For this characteristic, the moderate phenotypic and genotypic coefficients of variation were 12.96 and 12.49 *per cent*, respectively. This character has a high heritability of 92.90 *per cent* and a high genetic advance of 24.80 *per cent*.

4.1.11 Straw yield (kg/ha)

The average straw yield was 7586.90 kg ha⁻¹, with a range of 4412.52 kg ha⁻¹ to 11141.04 kg ha⁻¹. KPR-1 × Jyothi 1-6-2-1-1-2 had the lowest straw yield, while KPR-2 × IS-9-2-2-1 had the greatest. For this characteristic, the phenotypic (19.29) and genotypic (16.48) coefficients of variability were moderate. This character had a high heritability of 72.97 *per cent* and a high genetic advance as a *per cent* mean (29.00).

4.1.12 Grain yield (kg/ha)

Grain yields ranged from 2632.50 kg ha⁻¹ to 7150.00 kg ha⁻¹ with a mean of 5184.30 kg ha⁻¹. The lowest grain yield was found in KPR-2 × Basu-1-5-1-4, whereas the highest grain yield was found in KPR-2 × IS-1-4-1-2. For this characteristic, high phenotypic (24.35) and genotypic (22.63) coefficients of variability were observed, as well as high heritability (86.33) and high genetic advance as a *per cent* mean (43.30).

4.1.13 Harvest Index

With a mean of 0.41, the harvest index ranged from 0.32 to 0.48. Jyothi × Tunga-2-6-2 had the lowest harvest index, while KPR-2 × Basu-1-4-1-1 had the highest. This character has moderate phenotypic (15.89) and genotypic (13.65) coefficients of variability. Harvest index has a high heritability of 73.84 *per cent* and a high genetic advance of 24.18 *per cent*.

4.2 Correlation coefficient analysis for yield and its contributing traits

To determine the nature of the association between the characters, phenotypic correlation was calculated among 13 characters. Table 4. summarizes the findings. The results of the correlation between grain yield and other associated traits at the phenotypic level are presented first, followed by the correlation among the characters.

4.2.1 Correlation of grain yield with other characters

Grain yield was found to have a significant and positive phenotypic association with number of tillers per plant (0.3864**), number of productive tillers per plant (0.6717**), panicle length (0.2734*), panicle fertility (0.6281**), straw yield (0.3312**), and harvest index (0.7345**), where other yield components included days to fifty *per cent* flowering (0.1883), days to maturity (0.1866), plant height (0.2006), and total number of grains per panicle (0.1792) showed positive non-significant association. Characters such as test weight (-0.0137) and grain L/B ratio (-0.0695), on the other hand, displayed a negative and non-significant relationship with grain yield.

Table 4. Phenotypic correlation for grain yield and yield contributing traits in advanced breeding lines of rice

	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃
X ₁	1.00	0.9938**	0.1403	-0.0040	0.2000	0.1185	0.1675	0.1164	-0.0573	0.2370*	0.0266	0.2233*	0.1883
X ₂		1.00	0.1467	0.0021	0.2224	0.1144	0.1310	0.1073	-0.0519	0.2545*	0.0357	0.2137	0.1866
X ₃			1.00	0.1622	0.1981	0.4338**	-0.1643	0.1174	0.4378**	-0.3374**	0.2001	0.0489	0.2006
X ₄				1.00	0.5947**	0.0481	-0.0861	0.2658*	0.1700	0.1505	0.2020	0.1967	0.3864**
X ₅					1.00	0.0891	-0.0081	0.3373**	0.1065	-0.0169	0.2817*	0.4383**	0.6717**
X ₆						1.00	0.1804	0.2877*	0.0567	-0.0033	-0.0548	0.3122**	0.2734*
X ₇							1.00	0.2694*	-0.4497**	0.2595*	-0.0735	0.2211	0.1792
X ₈								1.00	-0.0423	0.1150	0.0853	0.5457**	0.6281**
X ₉									1.00	-0.3758**	0.0265	-0.0429	-0.0137
X ₁₀										1.00	-0.0851	-0.0265	-0.0695
X ₁₁											1.00	-0.3774**	0.3312**
X ₁₂												1.00	0.7345**
X ₁₃													1.00

*, ** Significance at 5% and 1% levels respectively

Where,

X₁ = Days to 50 per cent flowering

X₂ = Days to maturity

X₃ = Plant height (cm)

X₄ = Number of tillers per plant

X₅ = Number of productive tillers per plant

X₆ = Panicle length (cm)

X₇ = Total number of grains panicle⁻¹

X₈ = Panicle fertility (%)

X₉ = Test weight (g)

X₁₀ = Grain length and breadth ratio

X₁₁ = Straw yield (kg ha⁻¹)

X₁₂ = Harvest index

X₁₃ = Grain yield (kg ha⁻¹)

4.2.2 Correlation among yield components

4.2.2.1 Days to fifty per cent flowering

At the phenotypic level, days to fifty *per cent* flowering had positive and significant relationships with days to maturity (0.9938), grain L/B ratio (0.2370), and harvest index (0.2233). Plant height (0.1403), number of productive tillers per plant (0.2000), panicle length (0.1185), total number of grains per panicle (0.1675), panicle fertility (0.1164), and straw yield all showed non-significant positive correlations (0.0266). Number of tillers per plant (-0.0040) and test weight had a negative and non-significant relationship (-0.0573).

4.2.2.2 Days to maturity

Days to maturity were found to have a significant positive correlation with days to 50 *per cent* flowering (0.9938) and grain L/B ratio at phenotypic levels (0.2545). Plant height (0.1467), number of tillers per plant (0.0021), number of productive tillers per plant (0.2224), panicle length (0.1144), total number of grains per panicle (0.1310), panicle fertility (0.1073), straw yield (0.0357), and harvest index (0.2137) were all found to have a non-significant positive association. For the character test weight, there was a negative non-significant association (-0.0519).

4.2.2.3 Plant height (cm)

Plant height was found to have a significant positive correlation with panicle length (0.4338) and test weight (0.4378) at the phenotypic level. Days to fifty *per cent* flowering (0.1403), days to maturity (0.1467), number of tillers per plant (0.1622), number of productive tillers per plant (0.1981), panicle fertility (0.1174), straw yield (0.2001), and harvest index (0.0489) all exhibited a non-significant positive association. The character total number of grains per panicle showed a negative non-significant relationship (-0.1643). At the phenotypic level, this characteristic displays a negative significant correlation with grain L/B ratio (-0.3374).

4.2.2.4 Number of tillers per plant

At phenotypic levels, there was a significant positive correlation between the number of tillers per plant with the number of productive tillers per plant (0.5947) and panicle fertility (0.2658). Days to maturity (0.0021), plant height (0.1622), panicle length (0.0481), test weight (0.1700), grain L/B ratio (0.1505), straw yield (0.2020), and harvest index (0.1967) were all shown to have a non-significant positive association. The character days to fifty *per cent* flowering (-0.0040) and total number of grains per panicle had a negative non-significant correlation (-0.0861).

4.2.2.5 Number of productive tillers per plant

Number of productive tillers per plant was found to have significant positive correlation at phenotypic levels with number of tillers per plant (0.5947), panicle fertility (0.3373), straw yield (0.2817) and harvest index (0.4383). Days to fifty *per cent* flowering (0.2000), days to maturity (0.2224), plant height (0.1981), panicle length (0.0891), test weight (0.1065) had showed non-significant positive association. Negative non-significant association was observed for the character total number of grains per panicle (-0.0081) and grain L/B ratio (-0.0169).

4.2.2.6 Panicle length (cm)

Plant height (0.4338), panicle fertility (0.2877), and harvest index (0.3122) all had substantial positive phenotypic correlations with panicle length. There was a non-significant positive correlation between days to fifty *per cent* flowering (0.1185), days to maturity (0.1144), number of tillers per plant (0.0481), number of productive tillers per plant (0.0891), total number of grains per panicle (0.1804), and test weight (0.0567). The character grain L/B ratio (-0.0033) and straw yield (-0.0548) had a negative non-significant correlation.

4.2.2.7 Total number of grains per panicle

Total number of grains per panicle had a significant positive correlation with panicle fertility (0.2694) and grain L/B ratio (0.2595). Days to fifty *per cent* flowering (0.1675), days to maturity (0.1310), panicle length (0.1804), and harvest index (0.2211) were all shown to have a non-significant positive correlation. Character plant height (-0.1643), number of tillers per plant (-0.0861), number of productive tillers per plant (-0.0081), and straw yield (-0.0735) all had a negative non-significant relationship. At the phenotypic level, this trait displays a negative significant correlation with test weight (-0.4497).

4.2.2.8 Panicle fertility (%)

Panicle fertility was reported to have a significant positive correlation with number of tillers per plant (0.2658), number of productive tillers per plant (0.3373), panicle length (0.2877), total number of grains per panicle (0.2694), and harvest index at the phenotypic level (0.5457). Days to fifty *per cent* flowering (0.1164), days to maturity (0.1073), plant height (0.1174), grain L/B ratio (0.1150), and straw yield (0.0853) were all found to have a non-significant positive relationship. For the character test weight, there was a negative non-significant association (-0.0423) with panicle fertility.

4.2.2.9 Test weight (g)

At phenotypic levels, test weight was found to have a significant positive correlation with plant height (0.4378). The number of tillers per plant (0.1700), productive tillers per plant (0.1065), panicle length (0.0567) and straw yield (0.0265) were all found to have a non-significant positive association. The characters days to fifty *per cent* flowering (-0.0573), days to maturity (-0.0519), panicle fertility (-0.0423), and harvest index (-0.0429) all had a negative non-significant association. At the phenotypic level, this trait has a negative significant correlation with total number of grains per panicle (-0.4497) and grain L/B ratio (-0.0429).

4.2.2.10 Grain L/B ratio

At phenotypic levels, the grain L/B ratio was found to have a significant positive correlation with characters such as days to fifty *per cent* flowering (0.2370), days to maturity (0.2545), and total number of grains per panicle (0.2595). There was a non-significant positive relationship between the number of tillers per plant (0.1505) and panicle fertility (0.1150). For the characters number of productive tillers per plant (-0.0169), panicle length (-0.0033), straw yield (-0.0851), and harvest index (-0.0265), there was a negative non-significant correlation. At the phenotypic level, this character displays a negative significant correlation with plant height (-0.3374) and test weight (-0.0265).

4.2.2.11 Straw yield (kg/ha)

Straw yield was found to have significant positive correlation at phenotypic levels with number of productive tillers per plant (0.2817). Days to fifty *per cent* flowering (0.0266), days to maturity (0.0357), plant height (0.2001), number of tillers per plant (0.2020), panicle fertility (0.0853) and test weight (0.0265) had showed non-significant positive association. Negative non-significant association was observed for the character panicle length (-0.0548), total number of grains per panicle (-0.0735) and grain L/B ratio (-0.0851). This trait has negative significant correlation at phenotypic level with harvest index (-0.3774).

4.2.2.12 Harvest index

At phenotypic levels, harvest index was found to have a significant positive correlation with days to fifty *per cent* flowering (0.2233), number of productive tillers per plant (0.4383), panicle length (0.3122), and panicle fertility (0.5457). Days to maturity (0.2137), plant height (0.0489), number of tillers per plant (0.1967), and total number of grains per panicle (0.2211) were all shown to have a non-significant positive association. The character test weight (-0.0429) and grain L/B ratio had a negative non-significant correlation (-0.0265). At the phenotypic level, this characteristic displays a negative significant correlation with straw yield (-0.3774).

4.3 Path coefficient analysis among yield and its contributing traits

Wright (1921) created a statistical technique for path analysis that divides the correlation coefficient into direct and indirect effects of experimental variables on the direct variable. Table 5. depicts the findings. Because grain yield is a complicated trait that is heavily influenced by other traits, selecting purely on simple correlation without considering the component traits is ineffective. As a result, path analysis is critical for any plant breeding programme. The direct and indirect effects of characteristics on yield can aid in crop improvement programme.

4.3.1 Direct effect of yield contributing characters on grain yield

Positive and direct effect on grain yield at phenotypic level observed for ten characters out of twelve character *viz.*, days to maturity (0.0015), plant height (0.0283), number of tillers per plant (0.0146), number of productive tillers per plant (0.0499), total number of grains per panicle (0.0269), panicle fertility (0.0177), test weight (0.0122), grain L/B ratio (0.0351), straw yield (0.6792) and harvest index (0.9706). While the characters *viz.*, days to fifty *per cent* flowering (-0.0746) and panicle length (-0.0116) have direct and negative effect. Harvest index (0.9706) had shown highest positive direct effect whereas days to fifty *per cent* flowering (-0.0746) had the highest negative direct effect on grain yield.

4.3.2 Indirect effect of yield contributing characters on grain yield

4.3.2.1 Days to fifty per cent flowering

The indirect and positive effect of days to fifty *per cent* flowering on grain yield was displayed by number of tillers per plant (0.0003) and test weight (0.0043). Whereas it showed indirect and negative effect through days to maturity (-0.0742), plant height (-0.0105), number of productive tillers per plant (-0.0149), panicle length (-0.0088), total number of grains per panicle (-0.0125), panicle fertility (-0.0087), grain L/B ratio (-0.0177), straw yield (-0.0020) and harvest index (-0.0167).

4.3.2.2 Days to maturity

Days to 50 *per cent* flowering (0.0015), plant height (0.0002), number of productive tillers per plant (0.0003), panicle length (0.0002), total number of grains per panicle (0.0002), panicle fertility (0.0002), grain L/B ratio (0.0004), straw yield (0.0001), and harvest index (0.0003) all had indirect positive effects of days to maturity on grain yield. Through test weight (-0.0001), the indirect negative influence of days to maturity on grain yield was detected. Days to maturity is unaffected by the number of tillers per plant.

Table 5. Path matrix for grain yield and yield contributing traits in advanced breeding lines of rice

	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂
X ₁	-0.0746	-0.0742	-0.0105	0.0003	-0.0149	-0.0088	-0.0125	-0.0087	0.0043	-0.0177	-0.0020	-0.0167
X ₂	0.0015	0.0015	0.0002	0.0000	0.0003	0.0002	0.0002	0.0002	-0.0001	0.0004	0.0001	0.0003
X ₃	0.0040	0.0041	0.0283	0.0046	0.0056	0.0123	-0.0046	0.0033	0.0124	-0.0095	0.0057	0.0014
X ₄	-0.0001	0.0000	0.0024	0.0146	0.0087	0.0007	-0.0013	0.0039	0.0025	0.0022	0.0029	0.0029
X ₅	0.0100	0.0111	0.0099	0.0296	0.0499	0.0044	-0.0004	0.0168	0.0053	-0.0008	0.0140	0.0219
X ₆	-0.0014	-0.0013	-0.0050	-0.0006	-0.0010	-0.0116	-0.0021	-0.0033	-0.0007	0.0000	0.0006	-0.0036
X ₇	0.0045	0.0035	-0.0044	0.0023	-0.0002	0.0048	0.0269	0.0072	-0.0121	0.0070	-0.0020	0.0059
X ₈	0.0021	0.0019	0.0021	0.0047	0.0060	0.0051	0.0048	0.0177	-0.0007	0.0020	0.0015	0.0096
X ₉	-0.0007	-0.0006	0.0054	0.0021	0.0013	0.0007	-0.0055	-0.0005	0.0122	-0.0046	0.0003	-0.0005
X ₁₀	0.0083	0.0089	-0.0118	0.0053	-0.0006	-0.0001	0.0091	0.0040	-0.0132	0.0351	-0.0030	-0.0009
X ₁₁	0.0181	0.0242	0.1359	0.1372	0.1913	-0.0372	-0.0499	0.0579	0.0180	-0.0578	0.6792	-0.2563
X ₁₂	0.2167	0.2074	0.0483	0.1909	0.4254	0.3030	0.2146	0.5296	-0.0416	-0.0257	-0.3663	0.9706
r value	0.1883	0.1866	0.2006	0.3864	0.6717	0.2734	0.1792	0.6281	-0.0137	-0.0695	0.3312	0.7345

Residual effect = **0.1450** r = correlation coefficient of component traits with grain yield

Where,

X₁ = Days to 50 per cent flowering

X₂ = Days to maturity

X₃ = Plant height (cm)

X₄ = Number of tillers per plant

X₅ = Number of productive tillers per plant

X₆ = Panicle length (cm)

X₇ = Total number of grains panicle⁻¹

X₈ = Panicle fertility (%)

X₉ = Test weight(g)

X₁₀ = Grain length and breadth ratio

X₁₁ = Straw yield (kg)

X₁₂ = Harvest index

4.3.2.3 Plant height (cm)

The trait plant height has showed indirect and positive effect on grain yield *viz.*, days to fifty *per cent* flowering (0.0040), days to maturity (0.0041), number of tillers per plant (0.0046), number of productive tillers per plant (0.0056), panicle length (0.0123), panicle fertility (0.0033), test weight (0.0124), straw yield (0.0057), harvest index (0.0014) and it had indirect negative influence via total number of grains per panicle (-0.0046) and grain L/B ratio (-0.0095).

4.3.2.4 Number of tillers per plant

Number of tillers per plant had shown indirect positive effect on plant height (0.0024), number of productive tillers per plant (0.0087), panicle length (0.0007), panicle fertility (0.0039), test weight (0.0025), grain L/B ratio (0.0022), straw yield (0.0029) and harvest index (0.0029). Days to fifty *per cent* flowering (-0.0001) and number of grains per panicle (-0.0013) had negative indirect effects on yield. The number of tillers per plant is not affected by the days to maturity.

4.3.2.5 Number of productive tillers per plant

Number of productive tillers per plant had shown indirect positive effect on grain yield through the traits like days to fifty *per cent* flowering (0.0100), days to maturity (0.0111), plant height (0.0099), number of tillers per plant (0.0296), panicle length (0.0044), panicle fertility (0.0168), test weight (0.0053), straw yield (0.0140) and harvest index (0.0219). A negative indirect effect of the trait can be observed via total number of grains per panicle (-0.0004) and grain L/B ratio (-0.0008).

4.3.2.6 Panicle length (cm)

It showed positive indirect effect on yield through the character straw yield (0.0006). However, it had also shown negative indirect effect via days to fifty *per cent* flowering (-0.0014), days to maturity (-0.0013), plant height (-0.0050), number of tillers per plant (-0.0006), number of productive tillers per plant (-0.0010), total number of grains per panicle (-0.0021), panicle fertility (-0.0033), test weight (-0.0007) and harvest index (-0.0036). Grain L/B ratio has no effect on panicle length.

4.3.2.7 Total number of grains per panicle

It had indirect and positive effect on grain yield through days to fifty *per cent* flowering (0.0045), days to maturity (0.0035), number of tillers per plant (0.0023), panicle length (0.0048), panicle fertility (0.0072), grain L/B ratio (0.0070) and harvest index (0.0059). A negative indirect effect of the trait can be observed via plant height (-0.0044), number of productive tillers per plant (-0.0002), test weight (-0.0121) and straw yield (-0.0020).

4.3.2.8 Panicle fertility (%)

Panicle fertility had indirect and positive effect on grain yield through days to fifty *per cent* flowering (0.0021), days to maturity (0.0019), plant height (0.0021), number of tillers per plant (0.0047), number of productive tillers per plant (0.0060), panicle length (0.0051), total number of grains per panicle (0.0048), grain L/B ratio (0.0020), straw yield (0.0015) and harvest index (0.0096). Test weight showed a negative effect (-0.0007).

4.3.2.9 Test weight (g)

Plant height (0.0054), number of tillers per plant (0.0021), number of productive tillers per plant (0.0013), panicle length (0.0007) and straw yield (0.0003) had a positive indirect effect on grain yield, while days to 50 *per cent* flowering (-0.0007), days to maturity (-0.0006), total number of grains per panicle (-0.0055), panicle fertility (-0.0005), grain L/B ratio (-0.0046) and harvest index (-0.0005).

4.3.2.10 Grain L/B ratio

Grain L/B ratio had an indirect positive effect on grain yield through days to fifty *per cent* flowering (0.0083), days to maturity (0.0089), number of tillers per plant (0.0053), total number of grains per panicle (0.0091), panicle fertility (0.0040) and negative indirect effect through plant height (-0.0118), number of productive tillers per plant (-0.0006), panicle length (-0.0001), test weight (-0.0132), straw yield (-0.0030) and harvest index (-0.0009).

4.3.2.11 Straw yield (kg/ha)

Straw yield showed indirect positive effect on grain yield through days to fifty *per cent* flowering (0.0181), days to maturity (0.0242), plant height (0.1359), number of tillers per plant (0.1372), number of productive tillers per plant (0.1913), panicle fertility (0.0579), test weight (0.0180) and negative indirect effect through panicle length (-0.0372), total number of grains per panicle (-0.0499), grain L/B ratio (-0.0578) and harvest index (-0.2563).

4.3.2.12 Harvest index

Harvest index had indirect positive effect on grain yield via days to fifty *per cent* flowering (0.2167), days to maturity (0.2074), plant height (0.0483), number of tillers per plant (0.1909), number of productive tillers per plant (0.4254), panicle length (0.3030), total number of grains per panicle (0.2146), panicle fertility (0.5296) and negative indirect effect through test weight (-0.0416), grain L/B ratio (-0.0257) and straw yield (-0.3663).

4.4 Genetic divergence among the rice advanced breeding lines

Analyzing genetic diversity can help to determine how diverse the genotypes are, in order to identify genetically diverse genotypes for use in recombination breeding programs thirteen characters were studied for Mahalanobis' generalized distance analysis (D^2).

4.4.1 Group constellation

On the basis of the genotype distribution pattern, 39 advanced breeding lines are grouped into six clusters in Table 6. During a cluster analysis, all 39 rice advanced breeding lines were grouped together, such that advanced breeding lines within each cluster were closely related and their D^2 statistics were smaller than those belonging to other clusters. Based on cluster pattern, most advanced breeding lines are grouped in cluster I which comprises 18 advanced breeding lines, 11 advanced breeding lines in cluster III, seven advanced breeding lines in cluster II, and one advanced breeding line in each of clusters IV, V, and VI.

4.4.2 Intra and Inter relation of clusters

Table 7. shows the average D^2 values for intra and inter cluster distances. Cluster III (383.13) had the highest intra cluster distance, followed by cluster-II (221.58) and cluster-I (142.97), while clusters IV, V, and VI had the lowest intra cluster distance.

The diversity of the clusters ranged from 251.22 to 2039.53. Cluster-IV and cluster-V had the highest inter-cluster distance (2039.53), followed by cluster-V and VI (1567.19), and cluster-I and IV had the lowest inter-cluster distance (251.22).

4.4.3 Cluster mean analysis

Tocher's approach was used to generate cluster means for 13 yield and yield-related characteristics. Table 8. shows the cluster means for yield and yield-related factors recorded.

4.4.3.1 Days to fifty per cent flowering

Cluster-VI consists of genotypes taking less days to fifty *per cent* flowering (107.50 days) whereas cluster-V genotypes exhibited the more mean days to fifty *per cent* flowering (122.50 days).

Table 6. Clustering pattern of advanced breeding lines of rice based on D² values

Clusters	No. of advanced breeding lines	Advanced breeding lines
I	18	KPR-2 × Basu-1-6-1-1, KPR-2 × Basu-1-4-3-1, JGL-1798 × KPR-2-3-7-4-1, KPR-2 × Basu-1-4-2-1, KPR-1 × Jyothi 1-6-2-1-1-2, JGL-1798 × KPR-2-2-6-3-1, JGL-1798 × KPR-2-3-7-3-1-2, KPR-2 × Basu-1-5-1-4, KPR-2 × Basu-2-1-6-2, JGL-1798 × KPR-2-2-6-3-2, JGL-1798 × KPR-2-7-2-3-1-1-1, KPR-2 × Jyothi-2-5-6-1, KPR-2 × Basu-1-4-1-1, KPR-2 × IS-1-4-1-2, JGL-1798 × KPR-2-7-2-2-7-2, Jyothi × Tungga-2-6-2, KPR-2 × Jyothi-2-1-4-1, JGL-1798 × KPR-2-2-4-1-1
II	7	KPR-2 × IS × Gandhsali-2-4-4-3, Jyothi × Tungga-4-5, Jyothi × Tungga-2-4, Tungga, KPR-2 × IS-9-2-2-2, Jyothi × Tungga-4-3, KHP-13
III	11	Gandhsali × HYD-5-1-4-1-4, KHP-11, KPR-2 × IS-9-2-2-1, JGL-1798 × KPR-2-2-6-5-2, KPR-2 × Basu-1-2-2-1, KPR-2 × IS-1-4-2-1, Jyothi × Tungga-4-6, KPR-2 × Jyothi-2-1-8-5-3, Jyothi × Tungga-2-6-1, IS × Hyd-3, Gandhsali × HYD-5-2-2-4-2-2
IV	1	IS × Hyd-3-2-1-2-2
V	1	KHP-10
VI	1	Gandhsali × HYD-5-3-4-1-3-4

Table 7. Intra and inter cluster distances for yield and its component characters in advanced breeding lines of rice

Clusters	I	II	III	IV	V	VI
I	142.97	737.91	509.24	251.22	1491.34	766.72
II		221.58	564.15	910.48	424.25	1371.38
III			383.13	851.25	844.23	539.22
IV				0.00	2039.53	1329.24
V					0.00	1567.19
VI						0.00

Table 8. Cluster means for yield and its component characters in advanced breeding lines of rice

Cluster / Character	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃
I	121.53	151.53	77.05	18.29	16.31	21.34	296.16	85.13	15.26	3.76	7080.62	5053.72	0.41
II	120.93	151.36	35.79	19.21	16.82	21.71	222.56	84.61	27.36	3.40	7729.13	5212.00	0.40
III	113.95	144.09	94.30	19.05	16.61	21.94	269.45	84.90	18.76	3.43	8320.86	5334.18	0.39
IV	118.50	148.50	58.65	19.25	16.30	18.60	259.20	85.88	18.10	4.36	7665.12	4712.50	0.38
V	122.50	152.50	123.00	18.75	17.15	24.30	285.00	88.44	29.65	3.15	6830.45	5667.50	0.45
VI	107.50	137.50	102.00	19.50	16.50	20.90	337.80	87.05	10.25	3.69	8309.16	5681.00	0.41

Where,

X₁ = Days to 50 per cent flowering

X₂ = Days to maturity

X₃ = Plant height(cm)

X₄ = Number of tillers per plant

X₅ = Number of productive tillers per plant

X₆ = Panicle length (cm)

X₇ = Total number of grains panicle⁻¹

X₈ = Panicle fertility (%)

X₉ = Test weight(g)

X₁₀ = Grain length and breadth ratio

X₁₁ = Straw yield(kg)

X₁₂ = Grain yield (kg)

X₁₃ = Harvest index

4.3.2.2 Days to maturity

When the cluster means for days to maturity were examined, cluster-V had the highest mean of 152.50 days. Cluster VI had the shortest average time to maturity, at 137.50 days.

4.4.3.3 Plant height (cm)

Cluster V genotypes had the highest mean plant height (123.00 cm), while cluster II genotypes had the lowest mean plant height (35.79 cm).

4.4.3.4 Number of tillers per plant

Cluster VI genotypes had the largest mean number of tillers per plant (19.50), while genotypes in cluster I (18.29) had the lowest.

4.4.3.5 Productive tillers per plant

Cluster V (17.15) had the highest mean number of productive tillers per plant, while cluster I had the lowest (16.31).

4.4.3.6 Panicle length (cm)

The genotypes belonging to the cluster V was recorded highest mean panicle length (24.30 cm) and lowest mean panicle length was recorded by the genotypes in cluster IV (18.60 cm).

4.4.3.7 Total number of grains per panicle

The genotypes in cluster-VI have the highest mean for total number of grains per panicle (337.80), whereas genotypes in cluster II have the lowest mean for total number of grains per panicle (222.56).

4.4.3.8 Panicle fertility (%)

Cluster-V genotypes had the highest mean panicle fertility (88.44), while genotypes in cluster II had the lowest mean panicle fertility (84.61).

4.4.3.9 Test weight (g)

Cluster V genotypes had the highest mean test weight (29.65), whereas cluster VI genotypes had the lowest mean test weight (10.25).

4.4.3.10 Grain L/B ratio

Cluster-IV (4.36) had the largest mean number of grain L/B ratio while cluster V had the lowest (3.15).

4.4.3.11 Straw yield (kg/ha)

Cluster-V genotypes recorded the highest mean straw yield III (8320.86 kg ha⁻¹), while genotypes in cluster V recorded the lowest mean straw yield (6830.45 kg ha⁻¹).

4.4.3.12 Grain yield (kg/ha)

Genes in cluster-VI have the highest mean grain yield (5681.00 kg ha⁻¹) and those in cluster-II have the lowest mean grain yield (4712.50 kg ha⁻¹).

4.4.3.13 Harvest index

Cluster-V genotypes recorded the highest panicle fertility (0.45), while cluster IV genotypes recorded the lowest panicle fertility (0.38).

4.4.4 Contribution of different characters towards divergence

Differences in the proportion of each character's contribution to overall D² statistics were found, as shown in Fig 1. In the genotypes studied, the test weight (39.68) contributed the most to the total divergence. The plant height (23.75), number of days to fifty *per cent* flowering (13.66), panicle length (5.80) and other traits (17.41) followed.

4.5 Screening of rice advanced breeding lines for blast reaction

Blast is caused by fungi, *Magnaporthe grisea* (Herbert) Borr. (anamorph = *Pyricularia oryzae*). Long periods of free moisture, where leaf wetness is required for infection, and high humidity all are favorable to rice blast. Initially appearing as small necrotic lesions on rice seedlings, blast symptoms continue growing and spread to other parts of the plant. Rice blast is controlled using a various methods, including resistant varieties, cultural practices, biological, and chemical management. The development of disease-resistant cultivars, on the other hand, is regarded to be the most environmentally friendly and practical way to combat the disease.

In *kharif* 2020, rice genotypes were field tested for leaf blast disease reaction at Agricultural and Horticultural Research Station (AHRS) Ponnampet (hotspot for blast disease). Table 9. presents the results on leaf blast disease incidence for 39 advanced breeding lines of rice.

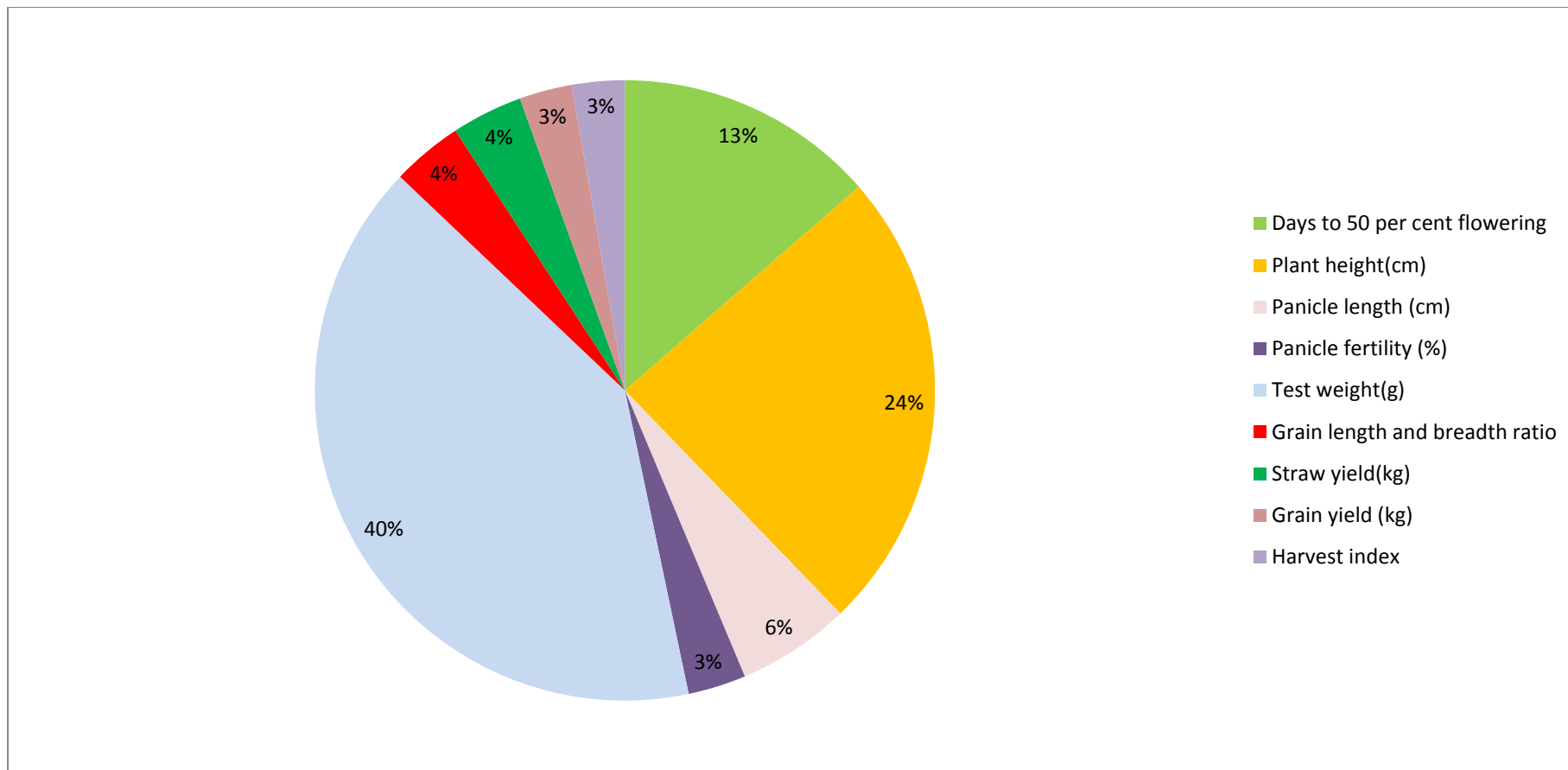


Fig 1: Per cent contribution of yield and yield related traits towards genetic divergence of advanced breeding lines of rice

Table 9. Scoring of advanced breeding lines of rice for blast disease

Sl. No.	Disease scale	Disease reaction	Advanced breeding lines	No. of Advanced breeding lines
1	0	HR	Nil	-
2	1	R	Nil	-
3	2 and 3	MR	JGL-1798 × KPR-2-2-6-3-2, KPR-2 × Basu-1-2-2-1, KPR-2 × Basu-1-4-1-1, KPR-2 × Basu-2-1-6-2, KPR-2 × Basu-1-5-1-4, KPR-2 × IS-1-4-1-2, Jyothi × Tungga-4-6, Jyothi × Tungga-2-6-1, Gandhsali × HYD-5-1-4-1-4, KPR-1 × Jyothi-1-6-2-1-1-2, JGL-1798 × KPR-2-2-4-1-1, KPR-2 × IS-1-4-1-2, KPR-2 × IS × Gandhsali-2-4-4-3, KPR-2 × Basu-1-4-3-1, Gandhsali × HYD-5-2-2-4-2-2, IR-64(check), Tetep(check).	16
4	4.5 and 6	MS	JGL-1798 × KPR-2-2-6-3-1, JGL-1798 × KPR-2-7-2-2-7-2, JGL-1798 × KPR-2-2-6-5-2, KPR-2 × IS-1-4-2-1, KPR-2 × Jyothi-2-1-4-1, KPR-2 × Jyothi-2-1-8-5-3, KPR-2 × Jyothi-2-5-6-1, Jyothi × Tungga-4-3, Jyothi × Tungga-2-4, JGL-1798 × KPR-2-7-2-3-1-1-1, JGL-1798 × KPR-2-3-7-3-1-2, KPR-2 × IS-9-2-2-2, KPR-2 × IS-9-2-2-1, KPR-2 × Basu-1-6-1-1, Jyothi × Tungga-4-5, Jyothi × Tungga-2-6-2, JGL-1798 × KPR-2-3-7-4-1, Gandhsali × HYD-5-3-4-1-3-4, IS × Hyd-3, IS × Hyd-3-2-1-2-2, Intan(check).	21
5	7	S	KPR-2 × Basu-1-4-2-1, HR-12(check)	2
6	8 and 9	HS	Nil	-
Total number of advanced breeding lines				39

None of the advanced breeding lines exhibited resistance with a disease score of one, whereas 16 advanced breeding lines namely JGL-1798 × KPR-2-2-6-3-2, JGL-1798 × KPR-2-3-7-4-1, KPR-2 × Basu-1-2-2-1, KPR-2 × Basu-1-4-1-1, KPR-2 × Basu-2-1-6-2, KPR-2 × Basu-1-5-1-4, KPR-2 × IS-1-4-1-2, Jyothi × Tunga-4-6, Jyothi × Tunga-2-6-1, Gandhsali × HYD-5-3-4-1-3-4, Gandhsali × HYD-5-1-4-1-4, IS × Hyd-3, KPR-1 × Jyothi 1-6-2-1-1-2, IS × Hyd-3-2-1-2-2, IR-64 (check), Tetep (check) exhibited moderate resistance with a disease score of two and three, 21 advanced breeding lines exhibited moderately susceptible reaction namely with a disease score of four, five and six, two advanced breeding lines exhibited susceptible reaction with a disease score of seven, and none of the advanced breeding lines exhibited highly susceptible reaction with a disease score of eight and nine.

4.6 Performance of top advanced breeding lines for yield and yield related trait

The top performing superior advanced breeding lines for yield and yield related trait are depicted in Table 10. KPR-2 × IS-1-4-1-2 recorded highest grain yield (7150 kg/ha) with tillers per plant (22.00), productive tillers per plant (19.00), panicle length (21.80 cm), grains per panicle (391.00) with panicle fertility (88.41%) followed by KPR-2 × Basu-1-2-2-1 had grain yield (6850 kg ha⁻¹) with tillers per plant (21.00), productive tillers per plant (18.00), panicle length (24.60 cm), grains per panicle (320.00) with panicle fertility (89.59 %), KPR-2 × Basu-1-4-1-1 had grain yield (6826.50 kg/ha) with tillers per plant (20.00), productive tillers per plant (19.00), panicle length (22.90 cm), grains per panicle (324.00) with panicle fertility (87.48 %), JGL-1798 × KPR-2-2-4-1-1 had grain yield (6675 kg ha⁻¹) with tillers per plant (18.00), productive tillers per plant (17.00), panicle length (21.40 cm), grains per panicle (315.00) with panicle fertility (91.88 %) and Gandhsali × HYD-5-2-2-4-2-2 had grain yield (6575 kg ha⁻¹) with tillers per plant (21.00), productive tillers per plant (18.00), panicle length (21.90 cm), grains per panicle (300.00) with panicle fertility (89.30 %).

Table 10. Performance of top advanced breeding lines for yield and yield related trait

Sl No.	Advanced breeding lines	Number of tillers per plant	Number of productive tillers per plant	Panicle length (cm)	Total number of grains per panicle	Panicle fertility (%)	Grain yield (kg/ha)
1	KPR-2 × IS-1-4-1-2	22.00	19.00	23.80	391.00	88.41	7150.00
2	KPR-2 × Basu-1-2-2-1	21.00	18.00	24.60	320.00	89.59	6850.00
3	KPR-2 × Basu-1-4-1-1	20.00	19.00	22.90	324.00	87.48	6826.50
4	JGL-1798 × KPR-2-2-4-1-1	18.00	17.00	21.40	315.00	91.88	6675.00
5	Gandhsali × HYD-5-2-2-4-2-2	21.00	18.00	21.90	300.00	89.35	6575.00

Checks :

1	KHP-10	18.00	16.00	18.30	265.00	84.43	5667.50
2	KHP-11	19.00	16.00	22.40	270.00	87.31	5407.00
3	KHIP-13	18.00	17.00	21.40	217.00	84.34	5370.83
4	Tunga	19.00	18.00	21.20	241.00	86.15	5397.00
	Mean	18.73	16.51	21.57	275.24	85.12	5184.30
	CD @ 5%	1.40	1.22	0.75	60.13	1.42	944.88
	CV	3.68	3.64	1.71	10.79	0.82	9.00

DISCUSSION

V DISCUSSION

Every form of crop improvement through breeding aims to augment genetic potential for yields in the future. The rate at which yield varies polygenically and is heavily dependent on the environment makes selection solely based on yield ineffective. Thus, breeders consider selection from highly heritable and yield associated traits after removing environmental components of phenotypic variation in order to achieve high crop yield.

The current study, entitled 'Assessment of Genetic Variability and Divergence in Advanced breeding lines of rice (*Oryza sativa* L.) in Lowlands of Hill Zone' was conducted in a Randomised Complete Block Design (RCBD) with two replications at ZAHRS, Mudigere, with the goals of estimating the genetic parameters of yield and yield associated traits among advanced breeding lines, studying the genetic diversity available in the advanced breeding lines and degree of association of grain yield with its component traits. The advanced breeding lines were screened for blast reaction at AHRS, Ponnampet.

The summary of the evidence obtained on variability parameters, genetic divergence, correlations, and path coefficients, as well as blast disease screening of rice advanced breeding lines under the following headings.

5.1 Genetic variability parameters for grain yield and yield attributing characters

5.2 Correlation coefficient analysis for yield and yield attributing characters

5.3 Path coefficient analysis among yield and yield attributing characters

5.4 Genetic divergence among grain yield and yield related attributes

5.5 Screening of rice advanced breeding lines for blast reaction

5.6 Performance of top advanced breeding lines for yield and yield related traits

5.1 Genetic variability parameters for grain yield and yield attributing characters

The most important factor for crop improvement programs is genetic variability. Yield is a polygenic trait that is largely influenced by the environment. The variability observed is the combined effect of hereditary and environmental factors. The variability is then partitioned into heritable and non-heritable components using suitable genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance as *per cent* mean (GAM). The estimation of this genetic variability parameter helps plant breeder in achieving the required crop improvement by selection.

A wide range of variations is observed among the genotypes, allowing for the selection of superior and desired genotypes for further improvement in rice. Assessing the genetic and non-genetic components of the total variability observed is crucial to select an appropriate breeding procedure. By studying factors such as coefficients of genotypic and phenotypic variability, heritability, and predicted genetic advance, the heritable portion of observed variation can be determined.

For days to fifty *per cent* flowering, the phenotypic and genotypic coefficients of variability were low, similar works were observed with the studies of Yadav *et al.* (2017), Vanisri *et al.* (2020) and Bhargava *et al.* (2021). A high heritability estimate was recorded for days to fifty *per cent* flowering. The results were in agreement with those of Acharya *et al.* (2018), Tiwari *et al.* (2019) and Donkor *et al.* (2021). Genetic advance of this trait was moderate, similar to that of Acharya *et al.* (2018).

PCV and GCV were low for days to maturity, paired with a high heritability and low GAM. The same results were found for days to maturity with high heritability and low GAM by Tiwari *et al.* (2019) and Donkor *et al.* (2021). GCV and PCV estimate are low in line with the findings of Rashid *et al.* (2017) and Yadav *et al.* (2017) suggested that selection based on them would be inappropriate for crop improvement programs.

The variability of plant height was moderate in both phenotypic and genotypic traits. Similar results were recorded by Manohara and Singh (2015), Longkho *et al.* (2020) and Vanisri *et al.* (2020). High heritability coupled with high genetic advance *per cent* mean was observed for this trait. Similar estimates were recorded by Balat (2018) Choudhary *et al.* (2018) and Bhargava *et al.* (2021).

For the number of tillers and number of productive tillers per plant, the phenotypic and genotypic coefficients of variation were low. These findings were consistent with those of Rashid *et al.* (2017) and Behera *et al.* (2018). The number of tillers and productive tillers had a high heritability and moderate genetic advance, which are in line with the works of Tiwari *et al.* (2019) and Longkho *et al.* (2020).

For panicle length, phenotypic and genotypic coefficients of variability were low. The results were also consistent with those obtained by Gampala *et al.* (2015), Longkho *et al.* (2020) and Bhargava *et al.* (2021). As in the study conducted by Ranjith *et al.* (2018), Bhargavi *et al.* (2021) and Donkor *et al.* (2021) these results revealed moderate genetic advance and high heritability estimates.

For total number of grains per panicle, the phenotypic and genotypic coefficients of variability were medium. These results were also similar to those of Manohara and Singh (2015), Bagati *et al.* (2016) and Longkho *et al.* (2020). Genetic advance as *per cent* mean and heritability were high, which agrees with the observations of Acharya *et al.* (2018), Longkho *et al.* (2020) and Gupta *et al.* (2021).

Panicle fertility is characterized by low genotypic and phenotypic coefficients of variation. The findings of are in line with those of Bagati *et al.* (2016), Longkho *et al.* (2020) and Vanisri *et al.* (2020). A high heritability for panicle fertility is reported and observed a low genetic advance as percent of mean, which is similar to the results of Manohara and Singh (2015) and Longkho *et al.* (2020).

For test weight, there was moderate phenotypic and genotypic variability, and the results were similar to those of Gampala *et al.* (2015), Sameera *et al.* (2016) and Longkho *et al.* (2020). This character exhibited high heritability and genetic advance as *per cent* mean results were in accordance with Tiwari *et al.* (2019) and Bhargavi *et al.* (2021).

For grain L/B ratio, moderate genotypic and phenotypic variability was recorded, which correspond to those found in Srivastava *et al.* (2017). High estimates of heritability along with high genetic advance as *per cent* of mean was recorded, that agrees with the findings of Gangashetty *et al.* (2013) and Vanisree *et al.* (2013).

Straw yield displayed moderate genotypic and phenotypic coefficients of variation. These findings are in line with those of Pal and Sabesan (2010) and Basavaraj (2013). Heritability and genetic advance as a *per cent* of mean were high, which are similar to the results of Yadav *et al.* (2017) and Gupta *et al.* (2021).

The study found high phenotypic and genotypic coefficients of variability for grain yield. Similar results were obtained by Balat *et al.* (2018), Patel *et al.* (2018) and Bhargava *et al.* (2021). For this trait, there was a high heritability coupled with a high genetic advance. The results were consistent with those of Longkho *et al.* (2020), Bhargavi *et al.* (2021) and Gupta *et al.* (2021). Higher PCV and GCV value indicated that there is scope for the selection of these traits during yield improvement as they possess high genetic variability.

For harvest index, the phenotypic and genotypic coefficients of variability are moderate. Dhanwani *et al.* (2013) and Behera *et al.* (2018) found similar results. For this trait, high heritability and genetic advance were recorded. Similar results were obtained by Gupta *et al.* (2021).

The analysis of variance (ANOVA) was performed in Randomized Complete Block Design depicting that highly significant difference was found among all the characters of rice advanced breeding lines. This indicates that there is high amount of variability present in the advanced breeding lines for all the traits.

Using the coefficient of variation analysis, it was found that the phenotypic coefficient of variation (PCV) for all traits was greater than the genotypic coefficient of variation (GCV), suggesting they were all less influenced by the environment. The

same result was also reported in rice by Balat *et al.* (2018) and Bhargava *et al.* (2021). However, the difference between PCV and GCV was considerable, suggesting low levels of environmental impact and a dominant role for genetic factors.

According to Johnson *et al.* (1955), instead of considering only heritability, high heritability coupled with high genetic advance as *per cent* mean would be more suitable in estimating the effectiveness of selecting the best individual. Therefore, along with heritability, it is essential to consider the estimated genetic advance as a tool for selection in the breeding program for better efficiency. Genetic advance as *per cent* of mean helps to better understand the measure of genetic gain under selection.

Estimates of high heritability along with high genetic advance as *per cent* of mean observed for plant height, total number of grains per panicle, test weight, grain L/B ratio, straw yield, grain yield and harvest index (Behera *et al.* 2018). As a result, the predominance of additive gene action in controlling these traits was revealed. Those characters can perhaps be improved in the future simply by selection. At most, having genetic variation in a crop is a requirement for enhancing economically important qualities like rice yield. The results of the analysis showed that advanced breeding lines had enough variability for yield and its associated traits.

High heritability coupled with moderate genetic advance as *per cent* of mean was observed for the traits *viz.*, days to fifty *per cent* flowering, number of tillers per plant, number of productive tillers per plant and panicle length indicating the presence of both additive and non-additive genetic effects and genetic improvement of these characters can be exploited through heterosis breeding.

5.2 Correlation coefficient analysis for yield and yield attributing characters

The correlation analysis reveals the characteristics that influence the grain yield. The breeder needs to understand the inter-relationships of plant characters with grain yield and among themselves in order to prioritize complex characters like grain yield, for which direct selection is not very effective. Such knowledge aids plant breeders in selecting elite genotypes from diverse genetic populations, and hence association analysis must be used to establish the direction of selection and the number of variables to be considered in enhancing grain yield (Chandramohan *et al.*, 2016).

5.2.1 Correlation of grain yield with other character

Yield is defined as a quantitative character. Hence, it is important to consider its association with other traits. A positive and significant phenotypic association was found between grain yield and number of tillers per plant, number of productive tillers per plant, panicle length, panicle fertility, straw yield, and harvest index. The results obtained by were in line with those obtained by Lakshmi *et al.* (2019) and Vanisri

et al. (2020) for panicle length, number of tillers per plant, panicle fertility, Fentie *et al.* (2021) for panicle length, straw yield and harvest index, Islam *et al.* (2021) for panicle length, panicle fertility and harvest index. Consequently, the enhancement of these traits by selection would result in improved grain yield.

By contrast, a positive non-significant correlation was found with a grain yield by days to fifty *per cent* flowering, days to maturity, plant height and number of grains per panicle. Based on the results, the findings are comparable to those reported by Gayathri and Padmalatha (2015) and Tiwari *et al.* (2019). The traits test weight, grain length and breadth ratio had showed non-significant negative association with grain yield. The results were similar to those obtained by Allam *et al.* (2015) and Fentie *et al.* (2021). The genetic cause of negative association could be the result of pleiotropy or linkage. In a crop improvement program, it is difficult to improve two negatively correlated traits simultaneously. A careful selection is thus required for improvement of such component traits at a time.

5.2.2 Correlation among yield components

At the phenotypic level, days to fifty *per cent* flowering revealed positive and significant correlations with days to maturity, grain L/B ratio, and harvest index. Plant height, number of productive tillers per plant, panicle length, total number of grains per panicle, panicle fertility, and straw yield all exhibited a non-significant positive correlation. Number of tillers per plant and test weight had a negative and non-significant correlation. Results are in confirmation with the findings of Dhurai *et al.* (2016) for grain L/B ratio, Fentie *et al.* (2021) for days to maturity and grain yield.

At phenotypic levels, days to maturity found to have a significant positive correlation with days to fifty *per cent* flowering and grain L/B ratio. Plant height, number of tillers per plant, number of productive tillers per plant, panicle length, total number of grains per panicle, panicle fertility, straw yield and harvest index all exhibited a non-significant positive association. For the character test weight, there was a negative non-significant association. Similar findings were found by Gayathri and Padmalatha (2015) and Shrestha *et al.* (2018) for plant height and total number of grains per panicle, Mutturaj *et al.* (2019) for days to fifty *per cent* flowering, grain L/B ratio, plant height and panicle length.

Plant height was found to have significant positive correlation at phenotypic level with panicle length and test weight. Days to fifty *per cent* flowering, days to maturity, number of tillers per plant, number of productive tillers per plant, panicle fertility, straw yield and harvest index had showed non-significant positive association. Negative non-significant association was observed for the character total number of grains per panicle. This trait has negative significant correlation at phenotypic level

with grain L/B ratio. Reports are in conformity with the above results of Kumar *et al.* (2017) for days to maturity and panicle fertility, Lakshmi *et al.* (2019) and Islam *et al.* (2021) for panicle length.

At phenotypic levels, there was a significant positive correlation between number of tillers per plant with the number of productive tillers per plant and panicle fertility. Sarwar *et al.* (2015) and Singh *et al.* (2018) reported similar findings. Days to maturity, plant height, panicle length, test weight, grain L/B ratio, straw yield, and harvest index were all found to have a non-significant positive correlation. Characters days to fifty *per cent* flowering and total number of grains per panicle were found to have a negative non-significant association. Similar findings were reported by Allam *et al.* (2015) and Vanisri *et al.* (2020).

Number of productive tillers per plant was found to have significant positive correlation at phenotypic level with number of tillers per plant, panicle fertility, straw yield and harvest index. Days to fifty *per cent* flowering, days to maturity, plant height, panicle length, test weight had showed non-significant positive association. Negative non-significant association was observed for the character total number of grains per panicle and grain L/B ratio. The results are in confirmation with the findings of Gayathri and Padmalatha (2015), Dhurai *et al.* (2016) and Mutturaj *et al.* (2019).

Plant height, panicle fertility, and harvest index were all found to have a significant positive correlation with panicle length. Days to fifty *per cent* flowering, days to maturity, number of tillers per plant, number of productive tillers per plant, total number of grains per panicle, and test weight all indicated a non-significant positive association. The character grain L/B ratio and straw yield had a negative non-significant relationship. This result is consistent with Venkatalakshmi *et al.* (2014) and Muthuramu and Sakthivel (2016) for days to maturity, number of productive tillers per plant and Islam *et al.* (2021) for plant height.

At phenotypic level, the total number of grains per panicle was found to have a significant positive correlation with panicle fertility and grain L/B ratio. The days to fifty *per cent* flowering, days to maturity, panicle length, and harvest index all revealed a non-significant positive association. The results obtained by Priya *et al.* (2017) for days to maturity and harvest index, Kamana *et al.* (2019) for panicle fertility, panicle length, and harvest index were all the same. Characters such as plant height, number of tillers per plant, number of productive tillers per plant, and straw yield showed a negative non-significant correlation. At the phenotypic level, this trait exhibits a negative significant correlation with test weight. This was previously reported by Kumar *et al.* (2017) and Singh *et al.* (2018).

Number of tillers per plant, number of productive tillers per plant, panicle length, total number of grains per panicle, and harvest index were found to have a significant positive correlation at phenotypic levels with panicle fertility. Whereas, plant height, harvest index and total number of grains per panicle Islam *et al.* (2021) came up with the same conclusions. Days to fifty *per cent* flowering, days to maturity, plant height, grain L/B ratio, and straw yield were all found to have a non-significant positive association. For the character test weight, there was a negative non-significant association. The same results were obtained by Muthuramu and Sakthivel (2016) and Rachana *et al.* (2018).

At phenotypic level, test weight was found to have a significant positive correlation with plant height. The number of tillers per plant, the number of productive tillers per plant, the panicle length, and the straw yield all indicated a non-significant positive association. For panicle fertility, similar results were obtained by Mahendrabhati *et al.* (2015) and Vanisri *et al.* (2020) for plant height and number of productive tillers per plant. For the characters days to fifty *per cent* flowering, days to maturity, panicle fertility, and harvest index there was a negative non-significant correlation. At the phenotypic level, this characteristic displays a negative significant correlation with total number of grains per panicle and grain L/B ratio. This is consistent with the findings Sarwar *et al.* (2015) and Bhujel *et al.* (2018).

The grain L/B ratio was found to have a significant positive correlation with traits such as days to fifty *per cent* flowering, days to maturity, and total number of grains per panicle. There was a non-significant positive relationship between the number of tillers per plant and panicle fertility. For the characters number of productive tillers per plant, panicle length, straw yield, and harvest index, there was a negative non-significant correlation. At the phenotypic level, this characteristic displays a negative significant correlation with plant height and test weight. Similar findings were discovered by Bhujel *et al.* (2018), Kamana *et al.* (2019) and Mutturaj *et al.* (2019).

Straw yield was found to have significant positive correlation at phenotypic levels with number of productive tillers per plant, it agrees with the results of Muthuramu and Sakthivel (2016) and Rachana *et al.* (2018). Days to fifty *per cent* flowering, days to maturity, plant height, number of tillers per plant, panicle fertility and test weight had showed non-significant positive association. Negative non-significant association was observed for the character panicle length, total number of grains per panicle and grain L/B ratio. This trait has negative significant correlation at phenotypic level with harvest index. Similar results were reported by Lakshmi *et al.* (2017) for panicle length and Fentie *et al.* (2021) for grain yield and harvest index.

Harvest index was found to have a significant positive correlation with days to fifty *per cent* flowering, number of productive tillers per plant, panicle length, and panicle fertility. Days to maturity, plant height, number of tillers per plant, and total number of grains per panicle were all found to have a non-significant positive correlation. Similarly, Islam *et al.* (2021) found similar results for panicle fertility. The character test weight and grain L/B ratio had a negative non-significant association. At the phenotypic level, this characteristic exhibits a negative significant correlation with straw yield. It is consistent with the findings of Mahendra Bhati *et al.* (2015) and Vanisri *et al.* (2020).

5.3 Path coefficient analysis among yield and yield attributing characters

Dewey and Lu (1959) proposed the path coefficient analysis, which specifies the effective measure of direct and indirect causes of association as well as illustrates the relative value of each element involved in contributing to the final product, *i.e.* yield.

In considering simple correlation coefficients, path analysis is an effective technique to understand the association between different variables. It assists in partitioning the overall association of particular variables with dependent variables into direct and indirect effects. When one wants to understand the influence of a set of variables on a dependent variable, path analysis can be used to estimate the direct and indirect contribution of each variable to the total influence each variable has on the dependent variable. While dealing with a more complex character like yield, it helps the breeders to identify the important component traits of such a nature so that differential emphasis can be laid on such component characters for selection.

In the current investigation, results of path coefficient analysis unveiled that days to maturity, plant height, number of tillers per plant, number of productive tillers per plant, total number of grains per panicle, panicle fertility, test weight, grain L/B ratio, straw yield and harvest index showed direct positive effect on grain yield and also displayed positive direct effect with grain yield at phenotypic level, similar results were obtained by Shrestha *et al.* (2018) for plant height and number of tillers per plant. Results imply that these characters can be considered as a selection criteria in yield improvement program.

The traits *viz.*, days to fifty percent flowering and panicle length had negative direct effect on yield, similar results obtained by Donkor *et al.* (2021) for days to fifty percent flowering. The negative direct effect indicates that the direct selection through these traits would not prove to be useful for the improvement of yield of rice. In spite of possessing negative direct effect on yield, these characters appear to be the potential traits in improving the grain yield as these exerts indirect effect via, other component characters.

The highest indirect positive effect on grain yield was exhibited by harvest index through panicle fertility followed by harvest index through number of productive tillers per plant. Similar findings were obtained by Vanisri *et al.* (2020). The highest indirect negative effect on grain yield was observed by days to fifty *per cent* flowering through days to maturity. Thus, indirect selection of those traits which displayed indirect effect on yield through other component characters would also contribute for yield improvement in breeding programs.

The residual effect was found 0.1450, which indicated that 85.50 *per cent* of the variability was accounted for grain yield and yield contributing traits included in the present study. Rest 14.50 *per cent* variability might be controlled by other yield contributing traits that were not included in the present investigation.

5.4 Genetic divergence among grain yield and yield related attributes

Any crop improvement strategy depends on the genetic diversity and relationships between breeding materials. Genetic diversity determines the inherent capacity of a cross for heterosis and the frequency of desirable recombinants in advanced generations (Chanbeni *et al.* 2012).

As a result of the complementary interactions between divergent genes in parents, the hybridization program involving genetically diverse parents of different clusters could provide an opportunity to bring together gene constellations of diverse nature. Several researchers have emphasized the importance of genetic divergence in the selection of desirable parents (Kumar *et al.* 2014). Many researchers have emphasized the use of Mahalanobis' D^2 statistics to estimate genetic divergence (Garg *et al.* 2011). As a result, 39 advanced breeding lines of rice were evaluated to assess the nature and magnitude of genetic diversity among the genotypes for future use in breeding programs.

5.4.1 Genetic diversity in different groups

Based on D^2 value 39 advanced breeding lines were grouped into six clusters. The cluster pattern revealed that more number of advanced breeding lines (18) in cluster-I followed by 11 advanced breeding lines in cluster-III, seven advanced breeding lines in cluster II and one advanced breeding line in cluster-IV, V and VI. Less diversity was observed among the advanced breeding lines of rice having one of the parents in common. In cluster I, it is observed that majority of the advanced breeding lines had KPR-2 and JGL-1798 as one of their parents. In cluster II and III, majority of the advanced breeding lines derived from Jyothi \times Tunga which deviates significantly from other clusters.

5.4.2 Average inter and intra cluster distances

The highest intra cluster distance was shown by cluster-III (383.13). Hence the advanced breeding lines falling into cluster III (Gandhsali × HYD-5-1-4-1-4, KHP-11, KPR-2 × IS-9-2-2-1, JGL-1798 × KPR-2-2-6-5-2, KPR-2 × Basu-1-2-2-1, KPR-2 × IS-1-4-2-1, Jyothi × Tunga-4-6, KPR-2 × Jyothi-2-1-8-5-3, Jyothi × Tunga-2-6-1, IS × Hyd-3 and Gandhsali × HYD-5-2-2-4-2-2) can be considered during selection owing to the presence of greater diversity within these advanced breeding lines.

Cluster-IV and cluster-V showed highest inter cluster distance (2039.53) followed by cluster-V and cluster-VI (1567.19) whereas the lowest inter cluster distance was noticed between cluster-I and cluster-IV (251.22) followed by cluster-II and cluster-IV (424.25).

The maximum inter cluster distance indicates the wider genetic diversity among the advanced breeding lines falling into the groups which can be utilized in selection of diverse advanced breeding lines, while the minimum inter cluster distance indicates that the advanced breeding lines falling in such clusters are closely related and thus selection among such advanced breeding lines will not give any fruitful result. The greater distance between the two clusters indicates the wider genetic diversity between the genotypes (Solanki *et al.*, 2019). Hence it is desirable to select advanced breeding lines from the clusters showing high inter cluster distance coupled with high grain yield as parents in future breeding programs for developing varieties with wider variability and desirable quality for lowland situations in hill zone.

5.4.3 Analysis of cluster means

Yield improvement in any crop through indirect selection depends on selection of traits having direct positive effect on yield. Cluster-V exhibited high mean values for days to fifty percent flowering, days to maturity, plant height, number of productive tillers per plant, panicle length, panicle fertility, test weight, harvest index and cluster-VI showed high mean values for number of tillers per plant, total number of grains per panicle, grain yield and cluster-III showed high mean values for straw yield and cluster IV showed high mean values for grain length and breadth ratio.

Sudeepthi *et al.* (2020) and Vanisri *et al.* (2020) found similar findings, recommending that selection of parents for hybridization should be from two clusters having wider inter cluster distance to get maximum variability for economically important traits.

5.4.4 Contribution of different characters towards divergence

The maximum *per cent* contribution towards divergence was made by test weight followed by plant height, days to fifty *per cent* flowering, panicle length, grain length and breadth ratio and straw yield. Similar result was also obtained by Shivani *et al.* (2018). Hence these traits should be given foremost importance while selecting parents for further breeding programs.

5.5 Screening of rice genotypes for blast reaction

Among various fungal diseases infecting the rice plant, rice blast is a major disease in terms of geographic distribution. Rice blast, also known as rice fever disease, has been reported in all the rice growing countries of the world. The causative agent of the disease is *Magnaporthe grisea*, a filamentous ascomycete fungus. It infects leaves, culm and panicles of the rice plants, thus reducing photosynthetic efficiency and grain yield. Various integrated approaches are followed to control the disease severity in which development of resistant varieties proved to be eco-friendly and most effective method.

In the present study, 39 advanced breeding lines including four checks (IR-64 and Tetep as resistant checks, Intan and HR-12 as susceptible checks) were screened for the rice leaf blast disease reaction at AHRS, Ponnampet (hot spot for rice blast) during *kharif* 2020 under natural infection conditions.

None of the lines showed resistant reaction, 16 lines showed moderately resistant reaction, 21 lines showed moderately susceptible reaction, two lines showed susceptible reaction and none of the lines showed highly susceptible reaction to leaf blast during *kharif* 2020.

The yield is not only a major criterion for sustainable agriculture. Hence, it is also essential to identify the genotypes resistant to major pest and diseases. It is well known that blast disease is leading to major loss in rice ecosystem. In the present study it was identified that the genotype are high yielding and also showed moderate to high level of resistance to blast disease.

5.6 Performance of top advanced breeding lines for yield and yield related traits

In the present study the advanced breeding lines are derived from the different crosses *viz.*, JGL-1798 × KPR-2, KPR-2 × IS, KPR-2 × Jyothi, KPR-2 × Basu, Jyothi × Tunga and Gandhsali × HYD, among the 39 advanced breeding lines, the identified best performing lines are KPR-2 × IS-1-4-1-2 followed by KPR-2 × Basu-1-2-2-1, KPR-2 × Basu-1-4-1-1, JGL-1798 × KPR-2-2-4-1-1 and Gandhsali × HYD-5-2-2-4-2-2 showed significantly higher mean performance for grain

yield and for other yield related traits viz., number of tillers per plant, number of productive tillers per plant, panicle length and panicle fertility compared to the checks. It is therefore necessary to advance these lines to the next generation and assess their stability and adaptability. The same results were also obtained by Lakshmi *et al.* (2019) and Vanisri *et al.* (2020) they also identified best performing advanced breeding lines in their study for grain yield and yield related traits panicle length, tillers per plant and panicle fertility.

Conclusion

The rice advanced breeding lines evaluated in this study have the potential for economic trait variation. For yield improvement, early generation selection schemes would be effective, and there is scope for isolating promising lines from advanced breeding lines under study. It is suggested that selection of advanced breeding lines possessing different combinations of such traits is the most useful approach for obtaining desirable high yielding varieties, based on characters showing significant correlation with yield, high heritability and high genetic advance *per cent* of mean.

Among the 39 advanced breeding lines studied in the present investigation, the top advanced breeding lines *viz.*, KPR-2 × IS-1-4-1-2 followed by KPR-2 × Basu-1-2-2-1, KPR-2 × Basu-1-4-1-1, JGL-1798 × KPR-2-2-4-1-1, Gandhsali × HYD-5-2-2-4-2-2 and Gandhsali × HYD-5-1-4-1-4 exhibited significantly higher mean performance for number of tillers per plant, number of productive tillers per plant, panicle length, total number of grains per panicle, panicle fertility, test weight, grain yield and straw yield compared to the checks. Hence, these lines may be evaluated for their stability and adaptability.

The advanced breeding line KPR-2 × IS-1-4-1-2 was found to be superior in terms of number of tillers per plant (22.00), number of productive tillers per plant (19.00), panicle length (23.80), grain yield (7150 kg/ha) and straw yield (8303 kg/ha) which are ideal characteristics to be considered while selecting for low land situations of hill zone.

Rice advanced breeding lines *viz.*, JGL-1798 × KPR-2-2-6-3-2, JGL-1798 × KPR-2-3-7-4-1, KPR-2 × Basu-1-2-2-1, KPR-2 × Basu-1-4-1-1, KPR-2 × Basu-2-1-6-2, KPR-2 × Basu-1-5-1-4, KPR-2 × IS × Gandhsali-2-4-4-3, Jyothi × Tunga-4-6, Jyothi × Tunga-2-6-1, Gandhsali × HYD-5-3-4-1-3-4, Gandhsali × HYD-5-1-4-1-4, IS × Hyd-3, KPR-1 × Jyothi-1-6-2-1-1-2, IS × Hyd-3-2-1-2-2 exhibited moderate blast resistance with a disease score of two and three. Hence, these advanced breeding lines could be used to mitigate blast disease under lowland ecosystem.

Future line of work

Based on the information available and results obtained in the present study following future line of work has been proposed.

- The rice advanced breeding lines KPR-2 × IS-1-4-1-2, KPR-2 × Basu-1-2-2-1 and KPR-2 × Basu-1-4-1-1 found to be superior for grain yield and are moderately blast resistant. These advanced lines are proposed to assess the stability and also to be evaluated in farm trails.
- The blast resistance among the advanced breeding lines of rice should be confirmed through molecular analysis.
- Further, these rice advanced breeding lines could be evaluated for nutritional quality traits.

SUMMARY

VI SUMMARY

The present investigation entitled ‘Assessment of genetic variability and divergence in advanced breeding lines of rice (*Oryza sativa* L.) in lowlands of hill zone’ was carried out in order to study the genetic variability, character association, genetic diversity and screening for blast reaction among 39 advanced breeding lines of rice including four checks. The experiment was carried out at two locations viz., ZAHRS, Mudigere and AHRS, Ponnampet (Hotspot for rice blast) with the objective to assess the extent of genetic variability, to study the correlation and path coefficient analysis and genetic diversity analysis in 39 advanced breeding lines of rice including four checks for yield and yield attributing traits. Screening of 39 advanced breeding lines along with four checks for blast reaction was also done.

In the present investigation, grain yield recorded high PCV and GCV values indicates presence of high amount of variability and better scope for improvement of this character and plant height, total number of grains per panicle, test weight, grain L/B ratio, straw yield and harvest index reported moderate PCV and GCV, this suggests the presence of relatively moderate variability for these traits, which could be utilized for improvement of these characters through selection.

High heritability coupled with high genetic advance was observed for plant height, total number of grains per panicle, test weight, grain L/B ratio, straw yield, grain yield and harvest index suggesting the presence of considerable variation and additive gene effect, along with this it is also indicating that on the expression of these traits there is low environmental influence and hence these traits can be considered during the selection.

Positive correlation recorded between grain yield with number of tillers per plant, number of productive tillers per plant, panicle length, panicle fertility, straw yield and harvest index. Hence, these traits can also be considered to select for the higher yields, as they were mutually and directly related to yield.

Path matrix revealed that ten out of twelve traits had a positive and direct effect on grain yield viz., days to maturity, plant height, number of tillers per plant, number of productive tillers per plant, total number of grains per panicle, panicle fertility, test weight, grain L/B ratio, straw yield and harvest index.

The advanced breeding lines IS × HYD-3 and Gandhsali × HYD-5-2-2-4-2-2 had lowest mean value for days to fifty *per cent* flowering and days to maturity. Hence, these lines may be utilized in low lands of hill zone as short duration varieties.

The highest number of tillers (22.00) was recorded in KPR-2 × IS-1-4-1-2, panicle length was highest for KPR-2 × Basu-1-2-2-1 and total number of grains per panicle was maximum in JGL-1798 × KPR-2-3-7-3-1-2. These advanced breeding lines can be utilized for development of high yielding varieties in the rice breeding programme.

Based on Mahalanobis' D^2 statistic and Tocher method, the 39 rice advanced breeding lines were grouped into six clusters. The maximum number of genotypes was observed in cluster I followed by clusters III and II. The maximum intra cluster distance was shown by cluster III. Cluster IV and cluster V followed by cluster V and cluster-VI showed highest inter cluster distance.

Thirty nine advanced breeding lines including four checks were screened for the rice leaf blast reaction at AHRS, Ponnampet. None of the advanced breeding lines showed resistant reaction, 16 advanced breeding lines were showed moderately resistant reaction, 21 advanced breeding lines showed moderately susceptible reaction, two advanced breeding lines showed susceptible reaction and none of the genotypes showed highly susceptible reaction to leaf blast.

Out of 39 advanced breeding lines, superior advanced breeding line was KPR-2 × IS-1-4-1-2 followed by KPR-2 × Basu-1-2-2-1, KPR-2 × Basu-1-4-1-1, JGL-1798 × KPR-2-2-4-1-1 and Gandhsali × HYD-5-2-2-4-2-2. They displayed significantly higher mean performance of about 20 to 25 *per cent* for grain yield and for other yield related traits *viz.*, number of tillers per plant, number of productive tillers per plant, panicle length and panicle fertility compared to the checks. Therefore they are utilized to assess their stability and adaptability in lowlands of hill zone of Karnataka.

REFERENCES

VII REFERENCES

- ACHARYA, S., SHRESTHA, A., ACHARYA, N. AND POUDEL, A., 2018, Genetic variability, heritability and correlation analysis in quantitative traits of irrigated rice (*Oryza sativa* L.). *Biosci. Biotechnol. Res. Asia*, **15**(3): 729-735.
- ADITYA, J. P. AND BHARTIYA, A., 2013, Genetic variability, correlation and path analysis for quantitative characters in rain fed upland rice of Uttarakhand hills. *J. Rice. Res.*, **6**(2): 24-34.
- AKHTAR, N., NAZIR, M. F., RABNAWAZ, A., MAHMOOD, T., SAFDAR, M. E., ASIF, M. AND REHMAN, A., 2011, Estimation of heritability, correlation and path coefficient analysis in fine grain rice (*Oryza sativa* L.). *The J. Animal & Plant Sci.*, **21**(4): 660-664.
- AKINWALE, M. G., GREGORIO, N. F., AKINYEL, B. O., OGUNBAYA, S. A. AND ODIYI. C., 2011, Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). *Afr. J. Plant Sci.*, **5**(3): 207-212.
- ALLAM, C. R., JAISWAL, H. K. AND QAMAR, A., 2015, Character association and path analysis studies of yield and quality parameters in basmati rice (*Oryza sativa* L.). *The Bioscan*, **9**(4): 1733-1737.
- AMIT, K. M., SINGH, P. K., RISHAV, K., PAWAN, K., RAHUL, S., ANAND, K. AND ALOK, K., 2018, Genetic divergence study in advance indica rice (*Oryza sativa* L.) lines for yield and quality attributes. *Int. J. Curr. Microbiol. App. Sci.*, **7**: 2924-2933.
- AMIT, P. R., SINGH, A. G., BABU, S. G. R., LAVANYA AND YADAV, Y., 2014, Diversity analysis of local land races and improved germplasm of rice (*Oryza sativa* L.). *Ind. J. Applied res.*, **4**: 2249-555.
- ANIS, G., EL-SABAGH, A., GHAREB, A. AND EL-REWAINY, I., 2016, Evaluation of promising lines in rice (*Oryza sativa* L.) to agronomic and genetic performance under Egyptian conditions. *Int. J. Agron. Agric. Res.*, **8**(3): 52-57.
- ANONYMOUS, 2019, First advance estimates of production of food grains for 2019-20, Ministry of Agriculture and Farmers Welfare, pp. 1. <http://agricoop.gov.in>
- ANONYMOUS, 2021, Whatare sustainable rice ecosystems, Food and Agriculture Organizations of the United Nations, pp. 1.<http://www.fao.org>

- AUKAOMA, A., AUGUSTINA, OKOCHA, P., IWUNOR, OKECHUKWU, R. AND IJEOMA, 2013, Heritability and character correlation among some rice genotypes for yield and yield components. *J. Pl. Breed. Genet.*, **1**(2): 73-84.
- BABU, R. P. AND SREELAKSHMI, C. H., 2017, Genetic divergence studies for yield and quality traits in rice (*Oryza sativa* L.). *J. Rice Res.*, **10**(1): 17-20.
- BABU, R. V., SHREYA, K., DANGI, K. S., USHARANI, G. AND SHANKAR, S. A., 2012, Correlation and path analysis studies in popular rice hybrids of India. *Int. J. Sci. Res.*, **2**(3): 2250-3153.
- BAGATI, S., SINGH, A. K., SALGOTRA, R. K., BHARDWAJ, R., SHARMA, M., RAI, S.K. AND BHAT, A., 2016, Genetic variability, heritability and correlation coefficients of yield and its component traits in basmati rice (*Oryza sativa* L.). *SABRAO J. Breed. Genet.* **48**(4).
- BAGHERI, N., JELODAR, B. N. AND PASHA, A., 2011, Path coefficient analysis for yield and yield components in diverse rice (*Oryza sativa* L.) genotypes. *Biharean Biol.*, **5**(1): 32-35.
- BALAT, J. R., PATEL, V. P., VISAT, M. L. AND BHAGORA, R. N., 2018, Variability analysis in F₂ population of rice (*Oryza sativa* L.) for yield and related traits. *Ind. J. Pure App. Biosci.*, **6**(1): 1021-1027.
- BARHATE, K. K., JADHAV, M. S. AND BHAVSAR, V. V., 2021, Genetic diversity analysis in aromatic lines of rice (*Oryza sativa* L.). *Int. J. Pharmacogn. Phytochem.*, **10**(3): 367-370.
- BARNWAL, M. K., VAIBHAV, K., SHARMA, R. B. AND SINGH, B. N., 2014, Field evaluation of rice genotypes for resistance and new fungicides for control of blast (*Pyricularia oryzae*). *Ind. Phytopath.*, **65**(1): 56-59.
- BASAVARAJ, K., 2013, Assessment of genetic diversity for grain yield and its components in rice (*Oryza sativa* L.) genotypes under submergence. *M.Sc. (Agri.) Thesis*, Unvi. Agric. Sci., Bengaluru.
- BASHIR, S. A., APURVA, K., GOPALA, K. S., SINGH, U. D., RATHOUR, R., TONAPI, V., SHARMA, T. R., NAGARAJAN, M., PRABHU, K. V. AND SINGH, A. K., 2013, Molecular analysis and phenotypic validation of blast resistance genes Pita and Pita2 in landraces of rice (*Oryza sativa* L.). *Ind. J. Genet. Plant Breed.*, **73**(2): 131-141.
- BEHERA, B., SAHU, S., KAR, R. K. AND PANDEY, R. K., 2018, Studies on genetic variability for some metric traits in slender grain rice genotypes. *J. Pharmacogn. Phytochem.*, **10**(1): 375 – 378.

- BHARGAVA, K., SHIVANI, D., PUSHPAVALLI, S. L., SUNDARAM, R. M., BEULAH, P. AND SENGUTTUVEL, P., 2021, Genetic variability, correlation and path coefficient analysis in segregating population of rice. *Electron. J. Plant Breed.*, **12**(2): 549-555.
- BHARGAVI, M., SHANTHI, P., REDDY, V. N., REDDY, D. M. AND RAVINDRA, B., 2021, Estimates of genetic variability, heritability and genetic advance for grain yield and other yield attributing traits in rice (*Oryza sativa* L.). *J. Pharm. Innov.*, **10**(5): 507-511.
- BHATT, B. P., ARYAL, N., NEUPANE, S. S. AND POUDEL, S., 2016, Variability, correlation and path coefficient analysis of rice (*Oryza sativa* L.). *J. sci. eng. res.*, **7**(6): 2107-2176.
- BHINDA, M. S. AND KARNWAL, M. K., 2017, Estimates of genetic divergence in advance breeding lines of rice (*Oryza sativa* L.). *J. Environ. Ecol.*, **35**: 3289-3292.
- BHUJEL, J., SHARMA, S., SHRESTHA, J. AND BHATTARAI, A., 2018, Correlation and path coefficient analysis in normal irrigated rice (*Oryza sativa* L.). *Fmg. Mngmt.*, **3**(1): 19-22.
- BURTON, G. W. AND DE VANE, E. H., 1953, Estimating heritability in tall Fescue (*Festuca aurundinacea*) from replicated clonal material. *Agron. J.*, **45**: 478- 481.
- CHAKMA, S. P., HUQ, H., MAHMUD, F. AND HUSAN, A., 2012, Genetic diversity analysis in rice (*Oryza sativa* L.). *Bangladesh J. Pl. Breed. Genet.*, **25**(1): 31-39.
- CHAKRABORTY, S. AND CHATURVEDI, H. P., 2014, Genetic variability in upland Rice (*Oryza sativa* L.) genotypes of Nagaland. *Indian Res. J. Genet. & Biotech.*, **6**(2): 374-378.
- CHANBENI, Y., OVUNG, G. M., LAL AND RAI. P. K., 2012, Studies on genetic diversity in Rice (*Oryza sativa* L.). *J. of Agric. Technol.*, **8**(3): 1059-1065.
- CHANDRAMOHAN, Y., SRINIVAS, B., THIPPESWAMY, S. AND PADMAJA, D., 2016, Diversity and variability analysis for yield parameters in rice (*Oryza sativa* L.) genotypes. *Ind. J. Agric. Res.*, **50**(6): 609-613.

- CHOUHDARY, A. K., HAIDER, Z. A., MISHRA, S. B., PRASAD, K., BHUSHAN, S., KUMAR, S., CHOUHDARY, V. K., BHUSHAN, M. AND PRASAD, J. P., 2018, Assessment of genetic variability for yield and yield attributing traits in F₂ and F₃ population of rice (*Oryza sativa* L.) cross. *Curr. j. appl.*, 1-5.
- COCHRAN, W. G. AND COX, G. M., 1957. Experimental designs. pp. 127-131.
- DAR, S. H., RATHER, A. G., NAJEEB, S. AND AHANGAR, M. A., 2015, Screening of rice germplasm against blast disease under temperate conditions. *Mol. Plant Breed.*, **6**(13): 1-4.
- DEWEY, D. R. AND LU, K. H., 1959, A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.*, **51**: 515-518.
- DHAKAL, A., POKHREL, A., SHARMA, S. AND POUDEL, A., 2020, Multivariate analysis of phenotypic diversity of rice (*Oryza sativa* L.) landraces from Lamjung and Tanahun districts, Nepal. *Int. J. Agron.*, **10**(6): 7-12.
- DHANWANI, R. K., SARAWGI, A. K., SOLANKI, A. AND TIWARI, K. J., 2013, Genetic variability analysis for various yield attributing and quality traits in rice (*Oryza sativa* L.). *The Bioscan*, **8**(4): 1403-1407.
- DHURAI, D., SAMIR, Y., REDDY, M. AND RAVI, S., 2016, Correlation and path analysis for yield and quality characters in rice (*Oryza sativa* L.). *Rice Omic. Gen.*, **7**(4): 1-6.
- DONKOR, E. F., ADJEI, R. R., BOADU, S. E., BOATENG, A. S. AND DUROWAA, A., 2021, Genetic variability, heritability and path analyses of yield and yield related traits of newly developed rice (*Oryza sativa* L.) genotypes in lowland ecology in Ghana. *Int. J. Innov. Agric. Sci.*, **8**(1):16-20.
- EDUKONDALU, B., REDDY, V. R., RANI, T. S., KUMARI, C. A. AND SOUNDHARYA, B., 2017, Variability, heritability, correlation and path analysis for yield, yield attributes in rice (*Oryza sativa* L.). *Int. J. Curr. Microbiol. App. Sci.*, **6**(10): 2369-2376.
- EKKA, R. E., SARAWGI, A. K. AND KANWAR, R. R., 2015, Genetic variability and inter-relationship analysis for various yield attributing and quality traits in traditional germplasm of rice (*Oryza sativa* L.). *Plant Arch.*, **15**(2): 637-645.
- ELIZABETH, R. E., SARWAGI, A. K., RAJA, R. AND KANWAR, 2011, Correlation and path analysis in traditional rice accessions of Chhattisgarh. *J. Rice Res.*, **4**: 11-18.

- FENTIE, D. B., ABERA, B. B. AND ALI, H. M., 2021, Association of agronomic traits with grain yield of lowland rice (*Oryza Sativa* L.) genotypes. *Int. J. Res. Agric. Sci.*, **8**(3): 2348-3997.
- FIYAZ, A. R., RAMYA, K. T., CHIKKALINGAIAH, AJAY, B. C., GIREESH, C. AND KULKARNI, R. S., 2011, Genetic variability, correlation and path coefficient analysis studies in rice (*Oryza sativa* L.) under alkaline soil condition. *Electron. J. Plant Breed.*, **2**(4): 531-537.
- GAMPALA, S., SINGH, V. J., PATHAK, S. K., SRIVASTAVA, N., KAUSHIK, S. K. AND RANGARE, N. R., 2015, Estimation of genetic variability for yield and quality traits in rice (*Oryza sativa* L.) genotypes. *J. Environ. Ecol.*, **33**(1A): 303-305.
- GANGASHETTY, P. I., SALIMATH, P. M. AND HANAMARATTI, N. G., 2013, Genetic variability studies in genetically diverse non-basmati local aromatic genotypes of rice (*Oryza sativa* L.). *Rice Genomics and Genetics*, **4**(2): 4-8.
- GARG, P., PANDEY, D. P. AND KAUSHIK, R. P., 2011, Genetic divergence for yield and quality traits in rice (*Oryza sativa* L.). *J. Rice Res.*, **4**: 1-2.
- GAYATHRI, N. K. AND PADMALATHA, Y., 2015, Correlation and path analysis studies in medium duration rice varieties of Andhra Pradesh. *J. Nutr. Sci.*, **5**: 2-5.
- GHALEY, B. B., CHRISTIANSEN, J. L. AND ANDERSEN, B. S., 2012, Genetic diversity in blast resistance of Bhutan rice landrace. *Euphytica.*, **184**: 119-130.
- GHOSH, S. C. AND SHARMA, D., 2012, Genetic parameters of agro morpho physiological traits in rice (*Oryza sativa* L.). *Electr. J. Pl. Breed.*, **3**(1): 711-714.
- GOUR, L., KOUTU, G. K., SINGH, S. K., PATEL, D. D., SHRIVASTAVA, A. AND SINGH, Y., 2017, Genetic variability, correlation and path analyses for selection in elite breeding materials of rice (*Oryza sativa* L.) genotypes in Madhya Pradesh. *J. Pharm. Innov.*, **6**(11): 693-696.
- GULZAR, S., SANGHER, A., SUBHASH, C., KASHYAP, GHULAM, A. AND PARRAY., 2013, Genetic variation for grain yield and related traits in temperate red rice (*Oryza sativa* L.). *Ecotypes. Not. Sci. Biol.*, **5**(3): 400-406.
- GUPTA, S., GAURHA, D., SAO, A. AND RANI, P., 2021, Assessment of genetic variability, heritability and genetic advance in accessions of rice (*Oryza sativa* L.). *J. Pharm. Innov.* **10**(6): 1231-1233.

- GURU, T., PADMA, D. V., REDDY, P. R., SANJEEVA, R., RAMESH, T. AND RADHAKRISHNA, K. V., 2017, Genetic diversity analysis for yield attributing traits in rice genotypes. *Res. on Crops.*, **18**(2): 311-315.
- HARISH, D., 2016, Variability and genetic divergence studies for yield and yield component traits in rice (*Oryza sativa* L.) genotypes in hill zone. *M.Sc. Thesis*. COA, UAHS, Shivamogga.
- HASAN, M. J., KULSUM, M. U., AKTER, A., MASUDUZZAMAN, A. S. M. AND RAMESHA, M. S., 2011, Genetic variability and character association for agronomic traits in hybrid rice (*Oryza sativa* L.). *Bangladesh J. Pl. Breed. Genet.*, **24**(1): 45-51.
- HASAN SHAHRIAR, M. D., ARIF HASAN KHAN., ROBIN. AND AHASANUL HOQUE., 2014, diversity assessment of yield, yield contributing traits, and earliness of advanced T-aman rice (*Oryza sativa* L.) lines. *J. Biosci. Agric. Res.*, **1**(2): 102-112.
- HOSAGOUDAR, G. N. AND BABU, U., 2018, Genetic variability and blast resistance studies in rice genotypes under rainfed shallow lowland conditions. *J. Pharmacogn. Phytochem.*, **7**(5): 2127-2131.
- HOSSAIN, M. M. AND HEGDE, H. R., 2016, Screening of rice germplasm against *Pyricularia oryzae* the cause agent of rice blast fungus in upland areas. *J. Environ. Ecol.*, **34**(1): 8-11.
- IDOWU, O. O., SALAMI, A. O., AJAYI, S. A., AKINWALE, R. O. AND SERE, Y., 2013, Varietal resistance of rice to blast fungus *Magnaporthe oryzae* at two sites in southwestern Nigeria. *Afr. J. Biotechnol.*, **12**(33): 5173-5182.
- IQBAL, T., IQBAL, H., AHMAD, N., NAUMAN, M., ALI, M., SAEED, S., ZIA, M. AND ALI, F., 2018, Genetic variability, correlation and cluster analysis in elite lines of rice. *J. Agric. Sci.*, **2**: 85-91.
- ISLAM, S.S., NUALSRI, C. AND HASAN, A.K., 2021, Character association and path analysis studies in upland rice (*Oryza sativa*) genotypes. *Res. on Crops.*, **22**(2): 239-245.
- JACKSON, S. A., 2016, Rice: the first crop genome. *Rice*, **9**(1): 1-3.
- JAYAWARDANA, W. A. D., JAYASEKERA, G. A. U., WIJESUNDERA, R. L. C., DISSANAYAKE, D. M. N., SOORIYAPATHIRANA, S. D. S. S., WEEBADDE, C. K., PERERA, K. L. N. S., GUNAPALA, K. R. D. AND HETTIGE, P., 2014, Evaluation of DNA markers linked to blast resistant genes, Pikh, Pit (p), and Pita, for parental selection in Sri Lankan rice breeding. *Tropical Agril. Res.*, **26**(1): 82-93.

- JOHANNSEN, W. L., 1909, Elementadorexakten Erbk. *Int. Jena: Gustav Tisher.*, **515**.
- JOHNSON, H. W., ROBINSON, H. I. AND COMSTOCK, R. E., 1955, Estimation of genetic and environmental variability in soybean. *Agron. J.*, **47**: 314-318.
- KAMANA, B., ANKUR, P., SUBARNA, S., PRASAD, K. B. AND KOSHRAJ, U., 2019, Genetic variability, correlation and path analysis of rice genotypes in rainfed condition at Lamjung, Nepal. *Russ. J. agric. soc.-econ. sci.*, **92**(8): 274-280.
- KAZIPYO, C. S., SURESH, B. G., PRIYATHAM, K. AND PRAVEEN, K., 2018, Genetic diversity analysis in elite rice (*Oryza sativa* L.) germplasm using agromorphological traits. *J. Pharmacogn. Phytochem.*, **7**(4): 1687-1690.
- KHAIRE, A. R., KUNKERKAR, R. L., THORAT, B. S., GAVAI, M. P. AND BHAVE, S. G., 2017, Studies on genetic variability for yield and yield contributing traits in local rice (*Oryza sativa* L.). *J. Pharmacogn. Phytochem.*, **6**(5): 1376-1378.
- KHALID, A. O., AHMED, M. M., FARHAN, A., ZHENG, Y. AND QIU, F., 2012, Genetic variability for yield and related attributes of upland rice genotypes in semi-arid zone (Sudan). *Afri. J. Agric. Res.*, **7**(33): 4613-4619.
- KHRIEDINUO, P. F., AMIT, K., WRICHA, T., MYANK, R. A. AND PATTANAYAK, 2011, Genetic variability in yield and its components in upland rice grown in acid soils of north east India. *J. Rice Res.*, **4**: 4-7.
- KHUSH, G. S., 2005, What it will take to feed 5.0 billion rice consumers in 2030. *Plant Mol. Biol.*, **59**: 1-6.
- KISHORE, N.S., SRINIVAS, T., NAGABHUSHANAM, U., PALLAVI, M. AND SAMEERA, S.K., 2015, Genetic variability, correlation and path analysis for yield and yield components in promising rice (*Oryza sativa* L.) genotypes. *SAARC J. Agric.*, **13**(1): 99-108.
- KRISHNA, K., MOHAN, Y.C., SHANKAR, V.G., RANI, C.D., KRISHNA, L. AND KIRANBABU, T., 2020, Screening of maintainer lines for leaf blast resistance through uniform blast nursery method in rice (*Oryza sativa* L.). *Int. J. Ecol. Environ. Sci.*, **2**(3): 213-217.
- KUMAR, P. V. AND SONALI, K., 2018, Association analysis of native rice (*Oryza sativa* L.) of Bastar. *Electron. J. Plant Breed.*, **9**(1): 199-212.

- KUMAR, S., BHUVANESWARI, S., DEVI, E. L., SHARMA, S. K., ANSARI, M. A., SINGH, I. M., SINGH, Y. R. AND PRAKASH, N., 2017, Estimation of genetic variability, correlation and path analysis in short duration rice genotypes of Manipur. *J. Agri. Search.*, **4**(2): 112-118.
- KUMAR, V, KOSHTA, N., SOHGAURA, N. AND KOUTU, G. K., 2014, Genetic evaluation of RILS population for yield and quality attributing traits in rice (*Oryza sativa* L.). *J. Agric. Technol.*, **1**(1): 43-51.
- KUMARI, B. K., KUMAR, B. R., JYOTHULA, D. P. B. AND RAO, N. M., 2021, Diversity analysis in rice breeding lines for yield and its components using principal component analysis. *J. Pharmacogn. Phytochem.*, **10**(1): 905-909.
- LAKSHMI, L., BRAHMESWARA, M, V., SURENDER, R. AND NARENDRA, S., 2017, Variability, correlation and path analysis in advanced generation of aromatic rice. *Int. J. Curr. Microbiol. App. Sci.*, **6**(7): 1798-1806.
- LAKSHMI, V., SREEDHAR, M., VANISRI, S., ANANTHA, M. S., RAO, L. S., GIREESH, C., 2019, Multivariate analysis and selection criteria for identification of African rice (*Oryza globerrima*) for genetic improvement of Indica rice cultivars. *Pl. Genet. Res.* **17**(6): 499-505.
- LAL, M. AND CHAUHAN, D. K., 2012, Studies of genetic diversity and cluster analysis in rice. *Int. J. Agril. Stat. Sci.*, **8**(1):293-297.
- LENKA, D. AND MISHRA, B., 1973, Path coefficient analysis in rice varieties. *Ind. J. Agric. Sci.*, **43**: 376-379.
- LONGKHO, K., KOLE, P.C. AND BEHERA, P.P., 2020, Genetic parameter studies in F₄ segregating generation of rice. *J. Pharmacogn. Phytochem.*, **9**(1): 1647-1651.
- LOPEZ, S. AND JOSEPH, K., 2008, TaqMan based real time PCR method for quantitative detection of basmati rice adulteration with non-basmati rice. *European Food Res. Technol.*, **227**(2): 619-622.
- LUSH, J.L., 1945, Inter generation correlation and regression of offspring on dams as a method of estimating heritability of characters. *Proc. American. Soc. Anim. Prod.*, **33**: 293-301.
- MADHAVILATHA, L., SEKHAR, M. R., SUNEETHA, Y. AND SRINIVAS, T., 2005, Genetic variability, correlation and path analysis for yield and quality traits in rice (*Oryza sativa* L.). *Res. Crops*, **6**(3): 527-534.
- MAHALANOBIS, P. C., 1936, On the generalized distance in statistics. *Proc. Nat. Inst. Sci. India.*, **2**: 49-55.

- MAHENDRA BHATI, G., SURESH BABU AND AISHWARYA SINGH RAJPUT., 2015, Genetic variability, correlation and path coefficient for grain yield and quantitative traits of elite rice (*Oryza sativa* L.) genotypes at Uttar Pradesh. *Electron. J. Plant Breed.*, **6**(2): 586-591.
- MANJUNATHA, B., 2020, Estimation of genetic diversity for yield and yield attributing traits in rice (*Oryza sativa* L.). *J. Pharmacogn. Phytochem.*, **9**(4): 3078-3080.
- MANJUNATH, B., MALLESHAPPA, C. AND NIRANJANA, K. B., 2018, Studies on variability, heritability and genetic advance for quantitative traits in rice (*Oryza sativa* L.). *Int. J. Agr. Sci.*, **10**(11): 6192-6194.
- MANOHARA, K. K. AND SINGH, N. P., 2015, Genetic variability, correlation and path analysis in rice (*Oryza sativa* L.) under coastal salinity conditions of Goa. *ISCAR*, **33**: 34-39.
- MANOJ, K. P., CHANDRA, M. S., SURESH, B. G., ROOPA, G., LAVANYA AND PRIYADARSHINI, J., 2011, Genetic parameters for grain yield and its component characters in rice (*Oryza sativa* L.). *Electron. J. Plant Breed.*, **2**(2): 235-238.
- MINA, A., BABAK, R., HABIBOLLAH, S. AND LAGHI., 2011, Genetic variability, correlation and path analysis in rice under optimum and stress irrigation regimes. *Not. Sci. Biol.*, **3**(4): 134-142.
- MUHAMMAD ASHFAQ, ABDUS SALAM KHAN, SULTAN HABIB ULLAH KHAN AND RASHID AHMAD., 2012, Association of various morphological traits with yield and genetic divergence in rice (*Oryza sativa*). *Int. J. Agric. Biol.*, **14**(1): 55-62.
- MUTHURAMU, S. AND SAKTHIVEL, S., 2016, Correlation and path analysis for yield traits in upland rice (*Oryza sativa*). *Res. J. Agrl. Sci.*, **7**: 763-765.
- MUTTURAJ, D., MALLESHAPPA, C. AND DUSHYANTH KUMAR, B. M., 2019, Variability, correlation and path analysis studies of yield and yield attributing traits in advanced breeding lines of rice (*Oryza sativa* L.). *Int. J. Pure App. Biosci.*, **7**(1): 267-273.
- NAGARAJU, C., REDDI, S., HARIPRASAD, K. AND SUDHAKAR, P., 2013, Correlation between traits and path analysis coefficient for grain yield and other components in rice (*Oryza sativa* L.) genotypes. *Int. J. Appl.*, **4**(3): 137-142.

- NAVEENKUMAR, SINGH, D., GUPTA, S., SIROHI, A., RAMESH, B., SIROHI, P., RAJENDRAKUMAR, SIROHI, P., SINGH, A., SINGH, J., KUMAR, N., KUMAR, PURUSHOTTAM, A., KUMAR, R., KUMAR, P., CHAUHAN, P. AND CHAND, S., 2013, Determination and expression of genes for resistance to blast (*Magnaporthe oryza*) in basmati and non-basmati indica rice (*Oryza sativa* L.). *African J. Biotech.*, **12**(26): 4098.
- NEERAJ, K., RAJESH, K. AND BINOD, K., 2015, Genetic diversity for agromorphological traits in rice (*Oryza sativa* L.). *Environ. Ecol.*, **33**(4A): 1754-1757.
- NIKHIL, B. S. K., RANGARE, N. R. AND SAIDAIHAH, P., 2014, Correlation and path analysis in rice (*Oryza sativa* L.). *Int. J. Tropical Agri.*, **32**: 1-5.
- NUSRAT, J., EUGENIA, L., SUBHASH, K., ARPIT, G., PARRAY, G. A. AND RAMTEKE, P. W., 2017, Genetic variability, character association and path analysis studies for grain yield and contributing traits in rice (*Oryza sativa* L.) under temperate conditions of Kashmir. *Int. J. Plant Res.*, **30**(2): 87-93.
- ODILE, F. R., GIANLUCA, B., PAMELA, A., STEFANO, C., ANNA, M. P., LAETITIA, B., ELISABETTA, L. AND PIETSO, P., 2011, Assessment of genetic diversity in Italian rice germplasm related to agronomic traits and blast resistance (*Magnaporthe oryzae*). *Mol. Breed.*, **27**: 233-246.
- OGUNBAYO, S. A., SIE, M., OJO, D. K., SANNI, K. A., AKINWALE, M. G., TOULOU, B., SHITTU, A., IDEHEN, E. O., POPOOLA, A. R., DANIEL, I. O. AND GREGORIO, G. B., 2014, Genetic variation and heritability of yield and related traits in promising rice genotypes (*Oryza sativa* L.). *J. Plant Breed. Crop Sci.*, **6**(11): 153-159.
- OSMAN, K. A., MUSTAFA, A. M., ALI, F., YONGLAIN, Z. AND FAZHAN, Q., 2012, Genetic variability for yield and related attributes of upland rice genotypes in semiarid zone (Sudan). *Afri. J. Agric.*, **7**(33): 4613-4619.
- PADMAJA, D., RADHIKA, K., RAO, L. S. AND PADMA, V., 2011, Correlation and path analysis in rice germplasm. *Oryza*, **48**(1): 69-72.
- PAIKHOMBA, N., ARVIND KUMAR., CHAURASIA, A. K. AND PRASHANT KUMAR RAI., 2014, Assessment of genetic parameters for yield and yield components in hybrid rice and parents. *J. Rice Res.*, **2**(1): 1-3.
- PAL, A. AND SABESAN, T., 2010, Studies on genetic variability for lodging related traits in rice (*Oryza sativa* L.). *Electron. J. Plant Breed.*, **1**(3): 301-304.

- PANDEY, S., 2016, Screening of rice cultivars for quantification of apparent infection rate of leaf blast. *Middle East J. Agric. Res.*, **5**: 430-434.
- PANDEY, V. R., SINGH, P. K., VERMA, O. P. AND PANDEY.P., 2012, Interrelationship and path coefficient estimation in rice under salt stress environment. *Int. J. Agric. Res.*, **7**(4): 169-184.
- PATEL, H. R., PATEL, V. P., PATEL, P. B., RATHOD, A. J. AND PAMPANIYA, A. G., 2018, Genetic variability, correlation and path analysis for grain yield and component traits in F₃ segregating population of rice (*Oryza sativa* L.). *Int. J. Chem. Stud.*, **6**(2): 2327-2331.
- PRAVEEN, K. U., SURESH, B. G., ANKIT, K. AND SWAMY, M., 2015, Genetic divergence among advanced breeding lines of medium duration rice (*Oryza sativa* L.). *Int. J. Sci. Res.*, **4**(7): 2585-2587.
- PRIYA, C. S., SUNEETHA, Y., BABU, D. R. AND RAO, V. S., 2017, Inter-relationship and path analysis for yield and, quality characters in rice (*Oryza sativa* L.). *Int. J. Environ. Sci. Technol.*, **6**: 381-390.
- QUDSIA, H., RIAZ, A. AND AKHTAR, M., 2017, Evaluation of rice germplasm of resistance against *Pyricularia oryzae* the cause of rice leaf blast. *Asian J. Agric. Res.* **4**(3): 1-6.
- RACHANA, B., ESWARI, K. B., JYOTHI, B. AND RAGHUVeer, P. R., 2018, Correlation and path analysis for yield and its component traits in NPT core set of rice (*Oryza sativa* L.). *Int. J. Curr. Microbiol. App. Sci.*, **7**(9): 97-108.
- RAMANJANEYULU, A. V., GOURI SHANKAR, V., NEELIMA, T. L. and SHASHIBHUSAHN, D., 2014, Genetic analysis of rice (*Oryza sativa* L.) genotypes in aerobic conditions on alfisols. *SABRAO J. Breed. Genet.*, **46**(1): 99-111.
- RAMYA, B., SARAVANAN, K. AND SATHEESH, K. P., 2012, Genetic parameters of variability, correlation and path coefficient studies for grain yield and other yield attributes traits in rice (*Oryza sativa* L.). *Plant Arch.*, **12**: 711-715.
- RAMYA, R., SANJEEVA, D., RAVINDRA, V. AND BHARATHI, M., 2017, Correlation and path coefficient analysis for yield, yield attributing and nutritional traits in rice (*Oryza sativa* L.). *Int. J. Curr. Microbiol. App. Sci.*, **6**(11): 183-188.
- RANJITH, P., SAHU, S., DASH, K. S., BASTIA, D. N. AND PRADHAN, B. D., 2018 Genetic diversity studies in rice (*Oryza sativa* L.). *J. Pharmacogn. Phytochem.*, **7**(2): 2529-2531.

- RAO, C. R., 1952, Advance statistical methods in biometric research. *John Wiley and Sons Inc., New York*.
- RASHID, M. M., NURUZZAMAN, M., HASSAN, L. AND BEGUM, S. N., 2017, Genetic variability analysis for various yield attributing traits in rice genotypes. *J. Bangladesh Agril. Univ.*, **15**: 1.
- RASHMI, K. P., DUSHYANTHAKUMAR, B. M., JAGADEESH, G. B., GANGAPRASAD, S. AND NISHANTH, G. K., 2017, Genetic diversity studies in advanced breeding lines of rice. *Biosci. Trends.*, **10**(36): 7554-7557.
- RAVINDRA BABU, V., SHREYA, KULDEEP SINGH DANGI, K., USHARANI, G. AND NAGESH, P., 2012, Genetic variability studies for qualitative and quantitative traits in popular rice hybrids of India. *Int. J. Sci. and Res.*, **2**(4): 112-126.
- ROBINSON, H. F., COMSTOCK, R. E. AND HARNEY, P. H., 1949, Estimates of heritability and degree in corn. *Agron. J.*, **41**: 353-359.
- RIJAL, T. R., HAMAL, G. B., JHA, P., AND KOIRALA, K. B., 2017, Identification of resistant genotypes on rice against blast disease under field condition at Rampur, Chitwan. *Int. J. Appl. Sci. Biotechnol.*, **5**(4): 505-510.
- SABIN, K., BIJAY, S., AMRIT, B., RAMAN, G. D., BHUWAN, S., PRIYANKA, N., MAN, S. S. AND PRASAD, G. S., 2016, Screening of different rice genotypes against (*pyricularia grisea*) sacc. in natural epidemic condition at seedling stage in Chitwan, Nepal. *Adv. Crop Sci. Technol.*, **4**: 1-6.
- SAIKIRAN, V., KRISHNA, L., JAGADEESHWAR, R., MOHAN, Y. C. AND GOURI, V., 2019, Identification of superior hybrids and parents for blast resistance in rice (*Oryza sativa* L.). *J. Pharmacogn. Phytochem.*, **8**(3): 3010-3013.
- SAMEERA, S. K., SRINIVAS, T., RAJESH, A. P., JAYALAKSHMI V. AND NIRMALA, P. J., 2016, Variability and path co-efficient for yield and yield components in rice. *Bangladesh J. Agric. Res.*, **41**(2): 259-271.
- SANGAM, K. S., CHANDRA, M. S. AND LAL, G. M., 2011, Assessment of genetic variability for yield and its components. *Res. in Plant Bio.*, **1**(4): 73-77.
- SANTOSH KUMAR, SINGH S. S., ANIL KUMAR SINGH, ELANCHEZHIAN, R., SANGALE U. R. AND SUNDARAM P. K., 2012, Evaluation of rice genotypes for resistance to blast disease under rainfed lowland ecosystem. *J. Pl. Dis. Sci.*, **7**(2): 175-178.

- SARAWGI, A. K., PACHAURI, A. K. AND NAIR, S. K., 2017, Correlation path analysis and assessment of genetic diversity for yield attributing traits in rice (*Oryza sativa* L.) genotypes. *Agril. Res. J.*, **54**(4): 449-454.
- SARKER, U., 2020, Variability, heritability, character association, and path coefficient analysis in advanced breeding lines of rice (*Oryza sativa* L.). *Genetika*, **52**(2): 711-726.
- SARWAR, G., HOSSAIN, S., RASHID, M, H. AND PARVEEN, S., 2015, Assessment of genetic variability for agro-morphological important traits in aman rice (*Oryza sativa* L.). *Int. J. Appl. Sci. Biotechnol.*, **3**(1): 73-79.
- SATHEESHKUMAR, P. AND SARAVANAN, K., 2012, Genetic variability, correlation and path analysis in rice (*Oryza sativa* L.). *Int. J. Curr. Res.*, **4**(9): 082-085.
- SELVARAJ, C. I., NAGARAJAN, P., THIYAGARAJAN, K., BHARATHI, M. AND RABINDRAN, R., 2011, Genetic parameters of variability, correlation and path coefficient studies for grain yield and other yield attributes among rice blast disease resistant genotypes of rice (*Oryza sativa* L.). *African J. Biotech.*, **10**(17): 3322–3334.
- SHARMA, S., SINGH, S., KULDEEP, R. AND BENIWAL, D. C., 2014, Assessment of genetic variability in rice (*Oryza sativa* L.) genotypes under rainfed conditions. *Agron. Sustain. Dev.*, **2**(2): 137-140.
- SHESHAIAH, DUSHYANTHAKUMAR, GANGAPRASAD, S., GOWDA, T. H., HOSAGOUDAR, G. N. AND SHASHIDHAR, H. E., 2018, Assessment of rice germplasm lines for leaf blast resistance and yield related parameters under blast hot spot locality. *J. Pharmacogn. Phytochem.*, **7**(5): 3102-3106.
- SHIVANI, D. K., DWIVEDI, HUSAIN, R., GYANENDRA, K. AND KHAN, N. A., 2018, Genetic divergence for yield and other quantitative traits in rice (*Oryza sativa* L.). *Int. J. Curr. Microbiol. App. Sci.*, **7**(1): 1201-1207.
- SHIVAPRASAD, G., RADHA KRISHNA, K. V., SUBBA RAO, L. V. AND CHAITHANYA, U., 2013, Quantitative analysis of rice genotypes (*Oryza sativa* L.). *Int. J. Inn. Res. Dvt.*, **2**(9): 14-17.
- SHIVASUBRAMANIAN, S. AND MENON, N., 1973, Heterosis and inbreeding depression in rice. *Madras Agric. J.*, **60**: 1134-1144.
- SHRESTHA, N., POUDEL, A., SHARMA ACHARYA, S., PARAJULI, A., BUDHATHOKI, S. AND SHRESTHA, K., 2018, Correlation coefficient and path analysis of advance rice genotypes in central mid-hills of Nepal. *Int. J. Agric. Res.*, 2348-3997.

- SINGH, A., NANDAN, R. AND SINGH, P., 2014, Genetic variability and association analysis in rice germplasm under rain fed conditions, *Crop Res.*, **47**: 7-11.
- SINGH, R. K. AND CHAUDHARY, B. D., 1977, Biometrical methods for quantitative genetic analysis, *Kalyani Publishers, New Delhi.*, **378**.
- SINGH, R., YADAV, V., MISHRA, N. D. AND YADAV, A., 2018, Correlation and path analysis studies in rice (*Oryza sativa* L.). *Int. J. Pharmacogn. Phytochem.*, **1**: 2084-2090.
- SINHA, N., SINGH, D. AND MOHANTY, T.A., 2020, Study of genetic divergence in lowland rice genotypes of Bihar. *Int. J. Curr. Microbiol. App. Sci.*, **9**(2): 88-94.
- SNEDECOR, G. W. AND COCHRAN, W. G., 1974, *Statistical methods*. Fifth edition. Iowa State University Press. Ames. Iowa, USA.
- SOLANKI, U. I., PARMAR, M. B. AND GEDIYA, L. N., 2019, Assessment of genetic divergence in rice genotypes under middle Gujarat condition. *IJCS*, **7**(3): 2825-2828.
- SRAVAN, T., RANGARE, N. R., SURESH, B. G. AND RAMESH KUMAR, S., 2012, Genetic variability and character association in rainfed upland rice (*Oryza sativa* L.). *J. of Rice Res.*, **5**: 24-29.
- SRIVASTAVA, N., BABU, G. S., SINGH, O. N., VERMA, R., PATHAK, S. K., BEHRA, M., JENA, D. AND CHANDA, M., 2017, Genetic variation, heritability and diversity analysis of exotic upland rice (*Oryza sativa* L.) germplasms based on quantitative traits. *J. Pharm. Innov.*, **6**(12): 316-320.
- SRUJANA, G., SURESH, B. G., LAVANYA, B., JALANDHAR, R. AND SUMANTH, V., 2017, Genetic variability, heritability and genetic advance for yield and quality components in rice (*Oryza sativa* L.). *J. Pharmacogn. Phytochem.*, **6**(4): 564-566.
- SUDEEPTHI, K., SRINIVAS, T., KUMAR, B. R. AND UMAR, S. N., 2020, Anaerobic germination tolerance based genetic diversity analysis in rice (*Oryza sativa* L.). *J. Pharm. Innov.*, **9**(1): 467-471.
- SUJITHA, R., PILLAI, M. A., KANNAN, R. AND SHOBA, D., 2020, Genetic diversity and association studies in rice (*Oryza sativa* L.). *J. Pharmacogn. Phytochem.*, **9**(6): 487-492.
- SUWANSA, C., NUALSRI, C., NATTAPON, J. AND WATCHARIN, S., 2018, Genetic diversity, genetic variability, and path analysis for yield and its components in indigenous upland rice (*Oryza sativa* L. var *glutinosa*). *J. Sci. Technol.*, **40**(3): 609-616.

- TEJASWINI, K. L. Y., MANUKONDA, S., RAMANA RAO, P. V., RAVI KUMAR, B. N. V. S. R., MOHAMMAD, L. A. AND RAJU, S. K., 2016, Cluster analysis studies in rice (*Oryza sativa* L.) using wards minimum variance method. *J. Agril. Crop Res.*, **4**(9): 129-139.
- THOMAS, N. AND GABRIEL, 2012, Genetic divergence in rice genotypes under irrigated conditions. *Ann. Pl. Soil Res.*, **14**(2): 109-112.
- TIWARI, D. N., TRIPATHI, S. R., TRIPATHI, M. P., KHATRI, N. AND BASTOLA, B. R., 2019, Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. *J. Adv. Agric.*, **5**(6): 125-130.
- VANISREE, S. K., ANJALI, C. H., DAMODAR RAJU, C. H., SURENDER RAJU AND SREEDHAR, M., 2013, Variability, heritability and association analysis in scented rice. *J. Bio. Sci.*, **1**(4): 347-352.
- VANISRI, S., PRIYANKA, B., CHARLES WESLY, K. AND SREEDHAR, M., 2020, Selection criteria for agronomic traits suitable for cold season through cluster and principal component analysis in rice (*Oryza Sativa* L.). *J. Pharmacogn. Phytochem.*, **9**(4): 1129-1137.
- VASUDEVAN, CASIANA, M., VERA CRUZ, WILHELM GRUISSEM, AND NAVREET, K. B., 2014, Large scale germplasm screening for identification of novel rice blast resistance sources. *Front. Plant Sci.*, **5**(505): 1-9.
- VENKATALAKSHMI, M., YUGANDHAR, G., VENKATALAKSHMI, N. AND SUNEETHA, Y., 2014, Correlation studies in rice (*Oryza sativa* L.). *Int. J. Genetic Eng. Biotechnol.*, **5**(2): 121-126.
- WEBER, C. R. AND MOORTHY, B. R., 1952, Heritable and non-heritable relationships and variability of oil content and agronomic characters in the F₂ generation of soybean crosses. *Agron. J.*, **44**: 202-209.
- WRIGHT, S., 1921, Correlation and causation. *J. Agric. Res.*, **20**: 557-585.
- YADAV, R., RAJPOOT, P., VERMA, O. P., SINGH, P. K., SINGH, P. AND PATHAK, V., 2017, Genetic variability, heritability and genetic advance in Rice (*Oryza sativa* L.) for grain yield and it's contributing attributes under sodic soil. *Int. J. Pharmacogn. Phytochem.*, **6**(5): 1294-1296.

APPENDICES

VIII APPENDICES

Appendix I. Means of thirteen characters of 39 advanced breeding lines of rice

Sl. No	Advanced breeding lines	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃
1	JGL-1798 × KPR-2-7-2-3-1-1-1	120.50	149.50	80.60	18.00	16.00	22.30	274.40	86.00	16.50	3.14	6856.22	6011.50	0.46
2	JGL-1798 × KPR-2-2-6-3-1	121.00	151.00	79.30	16.50	15.70	22.04	323.70	82.06	14.00	3.78	6050.08	4712.50	0.43
3	JGL-1798 × KPR-2-3-7-3-1-2	120.50	148.50	71.80	17.50	16.00	22.30	412.50	86.35	14.65	3.33	7109.12	6397.92	0.42
4	JGL-1798 × KPR-2-2-6-3-2	120.50	150.50	74.80	19.00	15.75	21.10	250.40	84.30	17.00	3.08	5862.47	4676.00	0.33
5	JGL-1798 × KPR-2-3-7-4-1	123.50	154.50	70.15	18.00	16.10	21.80	245.50	85.11	13.30	3.94	5325.20	3822.92	0.37
6	JGL-1798 × KPR-2-7-2-2-7-2	117.50	147.50	63.80	17.75	15.50	20.70	303.90	81.94	11.55	3.77	6479.04	4533.33	0.41
7	JGL-1798 × KPR-2-2-4-1-1	123.50	153.50	77.00	18.00	17.00	21.40	315.00	91.88	19.15	3.99	6276.19	6675.00	0.38
8	JGL-1798 × KPR-2-2-6-5-2	117.50	147.50	80.80	19.50	18.45	19.90	223.10	88.00	18.30	3.63	7667.24	6370.83	0.44
9	KPR-2 × IS-9-2-2-2	127.50	158.00	89.50	20.50	17.05	19.10	201.90	85.34	28.20	3.88	10863.18	5554.17	0.42
10	KPR-2 × IS-1-4-1-2	125.50	155.50	101.00	22.00	18.00	23.80	391.00	88.41	16.35	3.82	8303.08	7150.00	0.42
11	KPR-2 × IS-9-2-2-1	130.50	160.50	105.30	17.50	16.40	23.50	285.40	85.36	14.30	3.22	11141.03	5643.50	0.42
12	KPR-2 × IS-1-4-2-1	109.50	139.50	89.80	19.00	15.50	23.50	291.30	86.32	22.25	3.33	7510.33	5127.08	0.36
13	KPR-2 × Jyothi-2-1-4-1	122.50	152.50	82.15	18.40	17.50	22.10	279.70	84.84	19.75	3.02	8426.33	6262.50	0.38
14	KPR-2 × Jyothi-2-1-8-5-3	107.50	137.50	84.30	17.70	16.80	21.00	272.20	82.86	23.50	3.42	9099.99	5681.00	0.43
15	KPR-2 × Jyothi-2-5-6-1	123.50	154.00	88.50	18.50	15.85	23.60	289.80	83.82	13.85	4.01	6237.52	4111.50	0.39
16	KPR-2 × Basu-1-6-1-1	120.50	151.50	72.00	18.75	17.35	19.90	237.90	86.86	13.70	3.60	8220.33	6307.00	0.42
17	KPR-2 × Basu-1-4-2-1	124.50	154.50	71.30	19.50	15.90	22.70	283.50	84.48	15.40	4.42	7714.02	4862.50	0.36
18	KPR-2 × Basu-1-4-3-1	122.50	152.50	75.00	18.25	16.25	20.40	315.80	88.02	13.50	3.92	7748.38	4729.17	0.34
19	KPR-2 × Basu-1-2-2-1	110.50	140.50	86.80	21.00	18.00	24.60	320.00	89.59	15.90	4.23	8654.21	6850.00	0.42
20	KPR-2 × Basu-1-4-1-1	118.50	149.00	75.30	20.00	18.00	22.90	324.00	87.48	16.10	4.42	8554.96	6826.50	0.48
21	KPR-2 × Basu-2-1-6-2	123.00	153.00	85.30	16.50	15.50	19.70	264.60	83.63	15.90	3.73	7444.80	4891.00	0.35

Appendix I. Means of thirteen characters of 39 advanced breeding lines of rice (Contd.)

22	KPR-2 × Basu-1-5-1-4	120.50	150.50	81.15	17.35	14.55	20.40	299.60	83.02	16.55	4.23	8277.83	2632.50	0.37
23	KPR-2 × IS × Gandhsali-2-4-4-3	120.00	150.00	98.50	18.50	16.45	20.50	208.20	82.32	29.10	3.23	8216.73	4613.00	0.41
24	Jyothi × Tunga-4-3	109.50	139.50	90.00	17.50	15.55	23.20	182.70	87.02	26.65	2.83	7368.75	4860.50	0.43
25	Jyothi × Tunga-4-6	107.50	138.00	89.50	17.65	16.45	20.30	210.70	84.66	21.50	2.90	6365.73	4813.00	0.38
26	Jyothi × Tunga-2-6-1	109.00	139.00	90.80	19.50	15.20	19.00	242.90	81.55	23.95	3.31	7173.58	2682.50	0.43
27	Jyothi × Tunga-4-5	118.50	148.50	91.50	18.50	15.65	21.20	218.40	82.34	27.25	3.31	6784.34	3632.50	0.35
28	Jyothi × Tunga-2-4	120.50	150.50	99.70	20.50	16.30	23.40	289.70	84.78	28.00	3.26	7079.00	4878.00	0.36
29	Jyothi × Tunga-2-6-2	126.00	156.00	87.15	17.75	16.60	19.90	277.80	82.47	12.40	3.10	8788.98	4634.00	0.32
30	Gandhsali × HYD-5-2-2-4-2-2	106.50	137.00	66.50	21.00	18.00	21.90	300.00	89.35	14.65	3.07	9164.54	6575.00	0.40
31	Gandhsali × HYD-5-3-4-1-3-4	107.50	137.50	102.00	19.50	16.50	20.90	337.80	87.05	10.25	3.69	8309.16	5681.00	0.40
32	Gandhsali × HYD-5-1-4-1-4	123.50	153.50	112.30	20.50	18.65	23.80	295.00	86.73	15.95	3.78	9806.08	6371.00	0.43
33	IS × Hyd-3-2-1-2-2	118.50	148.50	58.65	19.25	16.30	18.60	259.20	85.87	18.10	4.36	7665.12	4712.50	0.42
34	IS × Hyd-3	99.50	130.00	89.00	17.50	15.25	21.50	206.80	80.75	19.65	3.38	7425.50	2721.00	0.41
35	KPR-1 × Jyothi 1-6-2-1-1-2	121.50	151.50	70.80	18.75	15.75	21.00	330.30	83.03	15.00	4.51	4412.53	2731.50	0.43
36	KHP-10 (Check)	122.50	152.50	123.00	18.00	16.00	18.65	265.00	84.43	29.65	3.15	6830.45	5667.50	0.39
37	KHP-11 (Check)	124.00	154.00	122.00	19.00	16.00	22.40	270.00	87.31	16.45	3.50	6885.36	5407.00	0.45
38	KHP-13 (Check)	124.00	156.50	98.80	18.00	17.00	21.40	217.00	84.34	21.25	4.02	6780.68	5370.83	0.43
39	Tunga (Check)	126.50	156.50	102.50	19.00	18.00	21.20	241.00	86.15	31.10	3.31	7011.22	5397.00	0.44

Where,

X₁ = Days to fifty per cent flowering

X₂ = Days to maturity

X₃ = Plant height (cm)

X₄ = Number of tillers per plant

X₅ = Number of productive tillers per plant

X₆ = Panicle length (cm)

X₇ = Total number of grains panicle⁻¹

X₈ = Panicle fertility (%)

X₉ = Test weight (g)

X₁₀ = Grain L/B ratio

X₁₁ = Straw yield (kg ha⁻¹)

X₁₂ = Harvest index

X₁₃ = Grain yield (kg ha⁻¹)

Appendix II. Scoring of 39 advanced breeding lines of rice for blast reaction

Sl. No	Advanced breeding lines	Blast disease scoring
1	JGL-1798 × KPR-2-7-2-3-1-1-1	6
2	JGL-1798 × KPR-2-2-6-3-1	5
3	JGL-1798 × KPR-2-3-7-3-1-2	4
4	JGL-1798 × KPR-2-2-6-3-2	3
5	JGL-1798 × KPR-2-3-7-4-1	4
6	JGL-1798 × KPR-2-7-2-2-7-2	5
7	JGL-1798 × KPR-2-2-4-1-1	3
8	JGL-1798 × KPR-2-2-6-5-2	5
9	KPR-2 × IS-9-2-2-2	4
10	KPR-2 × IS-1-4-1-2	2
11	KPR-2 × IS-9-2-2-1	5
12	KPR-2 × IS-1-4-2-1	6
13	KPR-2 × Jyothi-2-1-4-1	5
14	KPR-2 × Jyothi-2-1-8-5-3	6
15	KPR-2 × Jyothi-2-5-6-1	5
16	KPR-2 × Basu-1-6-1-1	6
17	KPR-2 × Basu-1-4-2-1	7
18	KPR-2 × Basu-1-4-3-1	3
19	KPR-2 × Basu-1-2-2-1	3
20	KPR-2 × Basu-1-4-1-1	2
21	KPR-2 × Basu-2-1-6-2	3
22	KPR-2 × Basu-1-5-1-4	3
23	KPR-2 × IS × Gandhsali-2-4-4-3	3
24	Jyothi × Tunga-4-3	4
25	Jyothi × Tunga-4-6	2
26	Jyothi × Tunga-2-6-1	3
27	Jyothi × Tunga-4-5	5
28	Jyothi × Tunga-2-4	4
29	Jyothi × Tunga-2-6-2	5
30	Gandhsali × HYD-5-2-2-4-2-2	3
31	Gandhsali × HYD-5-3-4-1-3-4	4
32	Gandhsali × HYD-5-1-4-1-4	2
33	IS × Hyd-3-2-1-2-2	5
34	IS × Hyd-3	4
35	KPR-1 × Jyothi 1-6-2-1-1-2	2
36	IR-64 (Check)	3
37	Intan (Check)	6
38	Tetep (Check)	3
39	HR-12 (Check)	7