

**ASSESSMENT OF GENETIC VARIABILITY IN ADVANCED
BREEDING LINES OF RICE (*Oryza sativa* L.) AND SCREENING FOR
SUBMERGENCE TOLERANCE**

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***DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE, SHIVAMOGGA***

**KELADI SHIVAPPA NAYAKA
UNIVERSITY OF AGRICULTURAL AND HORTICULTURAL SCIENCES
SHIVAMOGGA**

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COLLEGE OF AGRICULTURE, SHIVAMOGGA**

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CERTIFICATE

This is to certify that the thesis entitled '**ASSESSMENT OF GENETIC VARIABILITY IN ADVANCED BREEDING LINES OF RICE (*Oryza sativa* L.) AND SCREENING FOR SUBMERGENCE TOLERANCE**' 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 **PAVANA D. SINGH, ID. No. MA1TBA0465** (pavanadsingh66@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.

**Shivamogga
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Assessment of Genetic Variability in Advanced Breeding Lines of Rice (*Oryza sativa* L.) and Screening for Submergence Tolerance

(PAVANA, D. SINGH)

ABSTRACT

The present investigation was conducted during *Kharif* 2022. Thirty two advanced breeding lines of rice cross RNR-15048 × KPR-1 and five checks were studied under randomised complete block design for genetic variability, character association and genetic diversity under non- submergence condition at AHRS, Kathalagere. Same advanced breeding lines and four checks were screened for submergence tolerance under submerged condition at ZAHRS, Navile, Shivamogga. Under non-submergence, analysis of variance revealed high significant differences for all the characters studied. Genetic variability revealed moderate to high estimates of PCV, GCV, heritability and genetic advance for the traits viz.. plant height, number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle and grain yield. Correlation study revealed significant positive association with grain yield for number of tillers per plant, number of productive tillers, number of spikelets per panicle, number of filled grains per panicle, panicle length, spikelet fertility, test weight and length breadth ratio. Mahalanobis D² statistics grouped 32 advanced breeding lines with five checks into six clusters. Maximum inter-cluster distance was observed between cluster IV and VI. Among advanced breeding lines screened under submerged condition, highest survival percentage was observed for R×K-1-4-5 and R×K-1-4-17. Genetic variability revealed high PCV, GCV, heritability and genetic advance for survival and stem elongation percentage. Phenotypic correlation for physiological traits revealed significant positive correlation of survival percentage with grain yield. Advanced breeding lines R×K-1-4-5 and R×K-1-4-17 could be proposed for further screening in different locations of hill zone of Karnataka.

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ಭತ್ತದ ಸುಧಾರಿತ ಪ್ರಜನನ ಸಾಲುಗಳಲ್ಲಿ ಅನುವಂಶೀಯ ಭಿನ್ನತೆ ಹಾಗೂ ಮುಳುಗುವಿಕೆಯ ಸಹಿಷ್ಣುತೆಯ ಅಧ್ಯಯನ
(ಪಾವನ, ಡಿ. ಸಿಂಗ್)

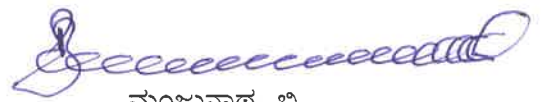
ಸಾರಾಂಶ

ಪ್ರಸ್ತುತ ಅಧ್ಯಯನವನ್ನು ೨೦೨೨ ರ ಮುಂಗಾರಿನಲ್ಲಿ ಕೈಗೊಳ್ಳಲಾಯಿತು. ಮೂವತ್ತೆರಡು ಭತ್ತದ ಸಂಯೋಜಿತ ಆರ್.ಎನ್.ಆರ್- ೧೫೦೪೮ x ಕೆ.ಪಿ.ಆರ್-೧ದ ಸುಧಾರಿತ ಪ್ರಜನನ ಸಾಲುಗಳು ಮತ್ತು ಐದು ಚೆಕ್‌ಗಳನ್ನು ಯಾದೃಚ್ಛಿಕ ಸಂಪೂರ್ಣ ಬ್ಲಾಕ್ ವಿನ್ಯಾಸದ ಪರಿಸ್ಥಿತಿಯಲ್ಲಿ ಅನುವಂಶಿಕ ವ್ಯತ್ಯಾಸ ಗುಣಲಕ್ಷಣಗಳ ಪರಸ್ಪರ ಸಂಬಂಧ ಮತ್ತು ಅನುವಂಶಿಕ ವೈವಿಧ್ಯತೆಗಾಗಿ ಮುಳುಗಿಸಿದ ಸ್ಥಿತಿಯಲ್ಲಿ ಕೃ.ತೋ.ಸಂ.ಕೇ, ಕತ್ತಲಗೆರೆಯಲ್ಲಿ ಅಧ್ಯಯನ ಮಾಡಲಾಗಿದೆ. ವ.ಕೃ.ತೋ.ಸಂ. ಕೇ ನವಿಲೆ, ಶಿವಮೊಗ್ಗದಲ್ಲಿ ಮುಳುಗಿದ ಸ್ಥಿತಿಯಲ್ಲಿ ಮುಳುಗುವಿಕೆ ಸಹಿಷ್ಣುತೆಗಾಗಿ ಅದೇ ಸುಧಾರಿತ ಪ್ರಜನನ ಸಾಲುಗಳು ಮತ್ತು ನಾಲ್ಕು ಚೆಕ್ ಗಳನ್ನು ಪ್ರದರ್ಶಿಸಲಾಯಿತು. ಮುಳುಗದ ಸಾಮಾನ್ಯ ಭತ್ತ ಬೆಳೆಯುವ ಸ್ಥಿತಿಯಲ್ಲಿ ವ್ಯತ್ಯಾಸದ ವಿಶ್ಲೇಷಣೆಯ ಅಧ್ಯಯನ ಮಾಡಿದ ಎಲ್ಲಾ ಗುಣಗಳಿಗೆ ಗಮನಾರ್ಹ ವ್ಯತ್ಯಾಸ ಕಂಡುಬಂದಿದೆ. ಗಿಡದ ಎತ್ತರ, ಪ್ರತಿ ಗಿಡದಲ್ಲಿನ ತೆಂಡೆಗಳ ಸಂಖ್ಯೆ, ಪ್ರತಿ ಗಿಡದಲ್ಲಿನ ಉತ್ಪಾದಕ ತೆಂಡೆಗಳ ಸಂಖ್ಯೆ, ಪ್ರತಿ ತೆನೆಗೆ ಧಾನ್ಯಗಳ ಸಂಖ್ಯೆ ಪ್ರತಿ ತೆನೆಗೆ ತುಂಬಿದ ಧಾನ್ಯಗಳ ಸಂಖ್ಯೆ ಮತ್ತು ಧಾನ್ಯದ ಇಳುವರಿ ಮಧ್ಯಮದಿಂದ ಹೆಚ್ಚಿನ ವಿಭಿನ್ನಾರ್ಥದ ಗುಣಾಂಕ (ಪಿ.ಸಿ.ವಿ) ವ್ಯತ್ಯಾಸದ ವಂಶವಾಹಿ ಬಗೆಯ ಗುಣಾಂಕ (ಜಿ.ಸಿ.ವಿ), ಹೆಚ್ಚಿನ ಅನುವಂಶೀಯತೆ ಮತ್ತು ಸರಾಸರಿ ಶೇಕಡಾವಾರು ಅನುವಂಶಿಕ ಮುಂಗಡವನ್ನು ಹೊಂದಿದೆ. ಪರಸ್ಪರ ಸಂಬಂಧದ ಅಧ್ಯಯನದಲ್ಲಿ ಪ್ರತಿ ಗಿಡದಲ್ಲಿನ ತೆಂಡೆಗಳ ಸಂಖ್ಯೆ, ಪ್ರತಿ ತೆನೆಗೆ ಧಾನ್ಯಗಳ ಸಂಖ್ಯೆ, ತೆನೆಯ ಉದ್ದ, ತೆನೆಯ ಫಲವತ್ತಿಕೆ, ೧೦೦೦ ಧಾನುಗಳ ತೂಕ, ಧಾನ್ಯದ ಉದ್ದ ಮತ್ತು ಅಗಲ ಪ್ರತಿ ಧಾನ್ಯದ ಇಳುವರಿಗೆ ಗಮನಾರ್ಹ ಸಕಾರಾತ್ಮಕ ಸಂಬಂಧ ಕಂಡುಬಂದಿದೆ. ಮಹಲನೋಬಿಸ್ ಡಿ^೨ ಅಂಕಿ ಅಂಶಗಳ ಅನುಸಾರ ೩೨ ಭತ್ತದ ಸುಧಾರಿತ ಪ್ರಜನನ ಸಾಲುಗಳು ಮತ್ತು ೫ ಚೆಕ್‌ಗಳನ್ನು ೫ ಗುಂಪುಗಳಾಗಿ ವರ್ಗೀಕರಿಸಿದೆ. ಗುಂಪು-೪ ಹಾಗೂ ೬ ರ ನಡುವೆ ಗರಿಷ್ಠ ಅಂತರ ಕಂಡು ಬಂದಿದೆ. ಮುಳುಗಿಸಿದ ಸ್ಥಿತಿಯಲ್ಲಿ, ತಳಿ ಆರ್ x ಕೆ -೧-೪-೫ ಮತ್ತು ಆರ್ x ಕೆ -೧-೪-೧೭ ಹೆಚ್ಚು ನೀರು ಮುಳುಗುವಿಕೆಗೆ ಸಹಿಷ್ಣುತೆ ತೋರಿದೆ. ಅನುವಂಶೀಯ ವ್ಯತ್ಯಾಸ ಅಧ್ಯಯನದಲ್ಲಿ ನೀರು ಮುಳುಗಡೆಯ ಸಹಿಷ್ಣುತೆ, ಕಾಂಡ ಉದ್ದವಾಗುವ ಸಾಮರ್ಥ್ಯವು ಹೆಚ್ಚಿನ ಪಿ.ಸಿ.ವಿ ಹಾಗೂ ಜಿ.ಸಿ.ವಿ ಹೊಂದಿರುತ್ತದೆ. ನೀರು ಮುಳುಗಡೆಯ ಸಹಿಷ್ಣುತೆ, ಪ್ರತಿ ಗಿಡದ ಧಾನ್ಯದ ಇಳುವರಿಗೆ ಗಮನಾರ್ಹ ಸಕಾರಾತ್ಮಕ ಸಂಬಂಧವನ್ನು ತೋರಿಸಿದೆ. ಆರ್ x ಕೆ.-೧-೪-೫ ಮತ್ತು ಆರ್ x ಕೆ.-೧-೪-೧೭ ತಳಿಗಳನ್ನು ಕರ್ನಾಟಕದ ಗುಡ್ಡಗಾಡು ವಲಯದ ವಿವಿಧ ಸ್ಥಳಗಳಲ್ಲಿ ನೀರು ಮುಳುಗುವಿಕೆಯ ಸಹಿಷ್ಣುತೆಗಾಗಿ ಪ್ರಸ್ತಾಪಿಸಬಹುದಾಗಿದೆ.

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INTRODUCTION

I INTRODUCTION

Rice scientifically known as *Oryza sativa* L. having chromosome number $2n=24$. It is the most important cereal crop cultivated widely in many parts of the world. Genus *Oryza* belongs to the tribe Oryzeae in the family Poaceae. Out of 24 species of rice, 22 species are wild and only two species are cultivated, *i.e.*, *Oryza sativa* and *Oryza glaberrima*. It is a staple food for more than half of the world's population and is a major source of income in many Asian countries. It is grown in more than 100 countries in 154 million hectares with 90 per cent of the total global production from Asia (Bista, 2018).

Rice provides 21 per cent of global human per capita energy and 15 per cent of per capita protein. It is the primary source of food and protein (30%) providing 50-60 per cent of the total calories for about half of the mankind with an enormous nutritional and economic impact. The protein quality is around 0.55 which is also higher compared to other cereals. Apart from carbohydrates and proteins rice also provides essential amino acids, minerals (P, Mg, Ca), vitamins (Folic acid) and fibre. It is the crucial dietary and food security source of many Asian countries like China, India, Indonesia, Bangladesh and Vietnam. China and India are the largest producers and consumers of rice. India ranks the highest area of cultivation of rice in the world, next being China. In India, West Bengal has highest total rice production followed by Uttar Pradesh. The other major rice producing states in India are Punjab, Andhra Pradesh, Tamil Nadu, Bihar, Chhattisgarh, Odisha (Ashraf *et al.*, 2016). In 2021-22, the rice area, production and productivity in India was 46.38 Mha, 130.29 mt and 2.81 t/ha respectively. In Karnataka, rice occupies 1.39 million hectares with 4.29 million tonnes of production and 3.72 t/ha productivity (Anonymous, 2022).

The existence of genetic variability is essential for selection in plant breeding as the significant amount of variability among the breeding materials will lead to effective selection. Rice shows an array of genetic variability which helps in effective selection for desirable traits. Yield improvement is the major objective in rice breeding programmes. The information about the extent of several genetic parameters *viz.*, Phenotypic Co-efficient of Variation (PCV), Genotypic Co-efficient of Variation (GCV), broad- sense heritability and genetic advance is essential for the successful genetic improvement of a genotype (Kishore *et al.*, 2015).

Correlation is a very important factor for any selection program. Success in selection depends on the knowledge of the association of component traits with grain yield hence indirect selection for yield component traits are more reliable than selection for yield (Nath and Kole, 2021). Therefore, character association studies help to

understand the nature of physical linkage and also provide information on the nature and direction of correlation which exists between the variables.

Assessing genetic diversity is a fundamental aspect for the development of new genotypes with a desired combination of traits. Moreover, it hastens the revelation of promising genotypes without the need to evaluate all possible cross combinations in breeding programs. Multivariate analysis tool like Mahalanobis D^2 statistic is functional for measuring genetic diversity by considering morphological and quantitative characteristics in a given population. It is utilized in detecting clustering patterns, to establish a link between genetic and environmental divergence, to study quantitative traits which determines maximum divergence and also to identify the characters which significantly contribute to divergence among the genotypes (Jangala *et al.*, 2022).

Among the 42 biotic and abiotic stresses affecting rice production, submergence or flooding is considered the third most important constraint for higher productivity, which is mostly seen in lowland rice growing areas of south and southeast Asia. Heavy rainfall, tides in coastal areas, overflow of rivers and canals result in floods. Crop losses are seen due the interference in normal gas exchange and light interception due to submergence (Singh *et al.*, 2022). Flooding which causes complete or partial submergence of the crop which affects about 10 – 15 million hectares of rice fields every year (Anonymous, 2020).

To identify and develop the best genotypes to environmental conditions like submergence, it demands a proper screening and evaluation of the genotypes under similar environmental conditions. Because of their sessile nature, plants cannot escape easily from different kinds of biotic and abiotic factors.

Further, it is anticipated that area under floods will increase considerably as a consequence of rise in sea level caused by melting of polar ice caps. Hence, the lowland farmers have no other option better than rice, as it is semi aquatic and capable of surviving under submerged conditions as it is capable of overcoming oxygen limitation for a considerable period of time. Under submerged conditions rice manages to survive either by resistance (inherent metabolic adaptations) or by avoidance i.e., by elongation of stem to keep the leaves above water surface (Das *et al.*, 2005).

Therefore, in the present study, an effort is being made to identify and develop the best genotypes to environmental conditions like submergence, which involves a proper screening and evaluation of the advanced breeding lines under similar environmental conditions as that of natural submergence situations under the title **“Assessment of Genetic Variability in Advanced Breeding Lines of Rice**

(*Oryza sativa* L.) and Screening for Submergence Tolerance” is carried out with the following objectives:

- 1) To study the genetic variability in advanced breeding lines of rice
- 2) To study correlation for grain yield and yield attributing traits
- 3) To study the genetic divergence in advanced breeding lines of rice
- 4) Phenotypic evaluation of advanced breeding lines of rice for submergence tolerance

REVIEW OF LITERATURE

II REVIEW OF LITERATURE

Rice is the second most vital staple food crop of the world next to wheat and is referred to as “Global Grain” (Abodolereza and Rainozer, 2009). It is widely recognized as an ideal model plant for the study of grass genetics and genome organization due to its diploid origin ($2n = 24$), relatively small genome size (430 Mb) and availability of vast germplasm collections (Panwar and Mathur, 2007). To meet the food needs of the increasing population, the development of high yielding varieties is essential.

The success of any plant breeding programme mainly depends on the selection of parents for hybridization. The parents involved in the development of varieties/hybrids should be divergent. Knowledge on the nature and degree of genetic divergence would help the plant breeder in choosing the right parents for breeding programme (Vivekanandan and Giridharan, 1998).

The research work done in India and elsewhere in recent years related to “Assessment of Genetic Variability in Advanced Breeding Lines of Rice (*Oryza sativa* L.) and Screening for Submergence Tolerance” is reviewed and presented under the following headings;

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

Genetic improvement of any crop depends on the amount of variability present in the population and the heritability of the desirable traits. So, magnitude of variability in gene pool is of utmost importance to take up any breeding programme. Hence, the knowledge of estimation of variability using different parameters is necessary to take up breeding programme in crops like rice.

Vanaja and Babu, (2007) evaluated genetic variability of 10 quality parameters in a set of 56 high yielding diverse rice genotypes. Phenotypic and genotypic coefficients of variation revealed the existence of large variability in alkali-spreading value and moderate variability in length/breadth ratio (L/B) ratio of grain, milling percentage, amylose content, water uptake, and volume expansion. High heritability, high expected genetic gain, and moderate genotypic coefficient of variation were noted for alkali spreading value, L/B ratio of grain, milling percentage, amylose content, volume expansion ratio and water uptake.

Pandey *et al.* (2009) evaluated 40 rice genotypes for genetic variability by studying 12 quantitative characters. Analysis of variance revealed the existence of sufficient amount of variability in the gene pool for all the traits. High magnitude of genotypic and phenotypic coefficients of variation was recorded for plant height, grain yield per hill, harvest index and biological yield per hill. High heritability along with

high genetic advance as per cent of mean was registered for harvest index, grain yield, plant height, biological yield, test weight, number of tillers per hill and number of spikelets per panicle suggesting preponderance of additive gene action in the expression of these characters.

Fiyaz *et al.* (2011) conducted an experiment to study the response of rice genotypes and their quantitative traits to examine the nature and magnitude of variability, heritability and genetic advance. Variability studies revealed significant differences among the genotypes for the traits studied. High values of heritability and genetic advance were observed for total spikelet per panicle, thousand grain weight and total biomass.

Adilakshmi and Rani (2012) studied variability and heritability among 64 rice genotypes. Variability studies revealed the existence of significant differences for all the characteristics indicating wide variability among the genotypes. Variability was found high for shoot elongation, while it was low in days to 50 per cent flowering. Total shoot elongation, relative shoot elongation, plant survival per cent and grain yield per plant registered high heritability coupled with high genetic advance giving scope for phenotypic selection as additive gene action under submergence. Ear bearing tillers recorded low genetic advance along with heritability indicated that this character was highly influenced by environment.

Pratap *et al.* (2012) evaluated 100 high yielding rice genotypes to determine variability for grain yield and its components. There was significant variation among the genotypes for all the traits studied. High estimates of heritability, genetic advance, genotypic and phenotypic coefficients of variation were recorded for number of panicles per hill, flag leaf area and grain yield per hill.

Sravan *et al.* (2012) studied genetic variation in 36 exotic rice breeding lines. There was significant difference reported among the lines indicating the presence of high variability among them. High genotypic coefficient of variation was exhibited for grain yield followed by harvest index and flag leaf length.

Dhanwani *et al.* (2013) conducted an experiment in rice genotypes to study variability. The analysis of variance was found to be highly significant for all the traits in rice indicating that enough variability is present in the material. Among them, grain yield per plant, filled grain per panicle, were found to have high GCV and PCV. The characters showing high GCV and PCV were found to be highly heritable coupled with high genetic advance revealing that they are governed by additive gene action and direct selection for these traits can be done.

Gangashetty *et al.* (2013) carried out an experiment to know the extent of genetic variability present in 42 genetically diverse rice genotypes. Analysis of

variance was found to be significant for all the traits. Higher values of genotypic and phenotypic coefficient of variability were observed for plant height, number of tillers per plant, number of productive tillers per plant, panicle weight, grain length, test weight, iron and zinc content and grain yield per plant. High heritability with high genetic advance was observed for all traits except days to 50 per cent flowering.

Patel *et al.* (2014) conducted a study with 44 diverse rice genotypes. The analysis of variance revealed the significant differences among the genotypes for all the traits. High estimates of genotypic and phenotypic coefficient of variation were observed for number of grains per panicle, grain yield per plant, straw yield per plant and harvest index indicating wider genetic variation for these traits. High values of heritability coupled with high genetic advance as per cent of mean were observed for number of grains per panicle, grain yield per plant, straw yield per plant, harvest index, 1000-grain weight, grain length/breadth ratio (L/B) ratio and amylose content indicating selection may be effective for these characters.

Pradhan *et al.* (2015) evaluated 30 rice cultivars to study the genetic basis of yield variations. The majority of traits exhibited higher magnitude of both GCV and PCV under sub-merged conditions except for panicle length and plot yield. High heritability estimates associated with moderate to high genetic gain for days to 50 per cent flowering, plant height, grain number and 100-grain weight indicate the presence of additive gene effects and hence selection based on phenotypic performance would be effective.

Devi *et al.* (2016) studied variability on 27 rice genotypes. Higher estimates of PCV and GCV were observed for yield per plant and filled seeds per panicle indicating possibility of genetic improvement through direct selection. High heritability in broad sense coupled with high genetic advance as per cent of mean was exhibited by effective tillers, plant height, flag leaf length, filled grains per panicle, test weight, yield per plant, head rice recovery and length/breadth ratio indicating the preponderance of additive gene action which provide good scope for further improvement by selection.

Venkatesan *et al.* (2016) conducted an investigation to study the submergence tolerance of 26 rice genotypes. Based on eleven characters namely, days to first flowering, plant height, number of tillers per plant, number of panicles per plant, panicle length, test weight, photosynthetic rate, stomatal conductance, intercellular CO₂ conc., transpiration rate and grain yield per plant, diversity analysis was made. The analysis of variance revealed the presence of variability among the genotypes for all the eleven characters taken under studies both in normal and submergence conditions.

Edukondalu *et al.* (2017) carried out an investigation to study the heritability, correlation and path analysis for 15 characters in 40 genotypes of rice. Analysis of variability parameters revealed that the phenotypic coefficient of variation was higher than genotypic coefficient variation. The magnitude of PCV and GCV was high for number of grains per panicle. High heritability coupled with high genetic advance as per cent of mean was observed for number of grains per panicle, number of tillers per plant, 1000-grain weight, length/breadth ratio (L/B) ratio, plant height, kernel length, grain yield per plant, kernel breadth and days to flowering.

Gour *et al.* (2017) conducted an investigation to estimate variability parameters in 83 rice genotypes. High GCV and PCV were observed for grain yield per plant, panicle weight/plant, biological yield/plant, filled spikletes/plant, test weight, harvest index, number of tillers/plant, whereas moderate GCV and PCV was observed for plant height. High heritability coupled with high genetic advance as per cent of mean was observed for grain yield per plant, panicle weight/plant, biological yield/plant, filled spikletes/plant, harvest index, test weight, number of tillers/plant and panicle length/plant. The filled spikletes/plant, harvest index, biological yield per plant showed high genetic advance.

Lahari, (2017) carried out the investigation with 49 genotypes for evaluating genetic variability. The analysis of variance revealed a significant difference among the genotypes for all the characters under study. High PCV and GCV coupled with high heritability and high GAM was recorded in number of tillers per plant, number of productive tillers per plant, grain yield per plant, straw yield per plant and absolute growth rate.

Prasad *et al.* (2017) carried out the investigation with 50 boro rice genotypes to evaluate variability parameters. Analysis of variance indicated high GCV and PCV values for number of filled grains per panicle, number of unfilled grains per panicle and grain yield per plant. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, number of unfilled grains per panicle, 1000- grain weight and grain yield per plant which indicated additive type of gene action.

Ram *et al.* (2017) carried out the investigation to study the genetic parameters for yield and yield attributing characters in 100 rice genotypes. Analysis of variance revealed significant differences for all the traits under study, which indicated enough variability in the material. The characters, viz., grain yield/plant and biological yield exhibited high GCV and PCV. The characters viz., ear bearing tillers, number of grains per panicle, biological yield, test weight and grain yield/plant exhibited high heritability coupled with high genetic advance.

Rashid *et al.* (2017) conducted an experiment to estimate the genetic variability of ten rice genotypes. Analysis of variance for yield and yield contributing traits showed significant variation among the genotypes. High estimates of PCV and GCV were observed for number of filled grains per panicle, number of unfilled grains per panicle and plant height. High heritability values along with high genetic advance and genetic advance as percentage of mean were found for all the traits indicating the prevalence of additive gene action, which provides good scope for further improvement by selection.

Srujana *et al.* (2017) conducted variability studies for 13 quantitative characters in 29 rice genotypes including a check in RBD with three replications. According to the analysis of variance, there is a considerable amount of variability among genotypes. The difference between GCV and PCV was small indicating less environmental influence on the characters studied. High to moderate estimates of GCV and PCV were recorded for grain yield per hill, harvest index, spikelets per panicle, tillers per hill, flag leaf length and panicles per hill.

Sumanth *et al.* (2017) conducted the experiment with 23 rice genotypes for 13 quantitative characters to study genetic variability, heritability and genetic advance. Analysis of variance showed significant differences for all the characters studied. The highest genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) was observed for seed yield per plant followed by flag leaf length, number of spikelets per panicle, biological yield per plant and panicles per plant indicating that these characters could be used as selection for crop improvement. A high estimate of heritability was observed for plant height, flag leaf length, biological yield per plant, spikelets per panicle and panicles per plant. High genetic advance was observed for number of spikelets per panicle and plant height.

Anyaocha *et al.* (2018) characterized 77 upland rice genotypes collected from Nigeria and other rice-growing parts of the world for ten traits. Yield and most yield-related component traits showed higher PCV compared to growth parameters. The highest PCV was observed for yield. At the same time, all other parameters exhibited low to moderate GCV. The genetic advance was observed in the range of 9.88 per cent for plant height and 41.08 for yield. The traits 1000 grain weight, days to 50 per cent flowering and days to maturity showed high heritability.

Bandi *et al.* (2018) conducted experiment with a total of 36 rice entries consisting of 28 cross and eight parental lines to estimate the variability parameters for 24 traits of rice cultivars. High PCV coupled with GCV was recorded for gel consistency and alkali spreading value. Moderate PCV and GCV were observed for total number of tillers per plant, number of grains per panicle, LAI at maximum tillering stage, volume expansion ratio, water uptake, amylose content and grain yield

per plant. High heritability coupled with high genetic advance as per cent of means for total number of tillers per plant, number of grains per panicle, leaf area index at maximum tillering stage, water uptake, gel consistency, alkali spreading value, amylose content and grain yield per plant, revealing the role of additive gene effect.

Divya *et al.* (2018) conducted an experiment with 33 genetically diverse genotypes for variability studies. Analysis of variance revealed that the moderate genotypic and phenotypic coefficients of variance were recorded for number of productive tillers per plant, number of grains per panicle and seed yield per plant. High heritability with high genetic advance was observed for number of productive tillers per plant, 1000 grain weight, number of grains per panicle and seed yield per plant.

Gautam *et al.* (2018a) studied variability in *Sub1* introgressed lines of rice. The analysis of variance revealed the existence of significant variation among the genotypes for grain yield and all other morpho-physiological quantitative traits. High estimates of genotypic and phenotypic variation in case of stem thickness and panicle number per plant indicated that selection would be effective for these characters. Among all the traits, high heritability with high genetic advance as per cent of mean was recorded for leaf length, stem thickness, leaf width, test weight and grain width indicating these traits should be given priority in selection.

Sandeep *et al.* (2018) carried out an investigation to estimate genetic variability, heritability and genetic advance in 200 genotypes of rice. Genotypic and phenotypic coefficients of variability were high for single plant yield, number of grains per panicle, number of tillers per hill, pollen viability and spikelet fertility. The characters spikelet fertility, plant height, single plant yield, number of grains per panicle, number of tillers per hill, pollen viability, number of productive tillers per hill, panicle length and test weight exhibited high heritability estimates coupled with high genetic advance as per cent of mean which suggested for further improvement by simple selection methods.

Barik *et al.* (2019) evaluated 88 lowland indigenous landraces for submergence response. Variation in survival rate, shoot elongation, relative growth index, dry matter, chlorophyll, soluble sugar and starch were evaluated under well drained and completely submerged conditions for two years. The first three components showed 96.82 per cent of total variation among landraces showing wide variation among genotypes. PCV was more than GCV for all traits.

Manjunatha and Kumara (2019) conducted an experiment with 64 rice genotypes to study genetic variability, heritability and genetic advance for grain yield and yield-associated traits. The analysis of variance revealed significant differences indicating the existence of genetic variability among the genotypes for all the traits

studied. Higher PCV and GCV values were exhibited by panicles per square meter suggesting the possibility of improving this trait through selection. High to medium heritability with high GCV and high genetic advance as percentage of means were exhibited for plant height and panicles per square meter. High genetic advances as per cent of means were recorded by yield, panicles per square meter, plant height and days to 50 per cent flowering.

Tiwari *et al.* (2019) conducted an experiment to estimate the genetic variability in seven rice genotypes. All the genotypes showed significant variations for all the traits considered. The genotypic coefficient of variation was lower than phenotypic coefficient of variation for all the traits studied. The magnitudes of genotypic coefficient of variations were relatively higher for grain yield, 1000-grain weight, and days to heading. 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.

Nath and Kole, (2021) studied genetic variation in 26 diverse rice genotypes. The genotypes showed significant variation for all the characters. Genotypic and phenotypic coefficients of variation were high for the flag leaf area, spikelet number, grain number, test weight and grain yield, and moderate for plant height, days to flowering, the number of panicle and primary branches per panicle. Heritability was high for days to flowering, plant height and test weight. Genetic advance as per cent of mean was very high for test weight and grain yield, moderate for plant height, flag leaf area and number of grains, low for spikelet fertility (per cent).

Singh *et al.* (2021) studied 50 advanced breeding lines along with five checks for 11 yield and 19 quality traits. Variance studies showed extremely significant variations among all the advanced breeding lines for all the yield and quality traits, suggesting presence of significant amount of variance. Number of unfilled grains per panicle, alkali spreading value, amylose per cent, gel consistency, number of filled grains per panicle, grain yield per plant (g), head rice recovery per cent, biological yield per plant (g) and harvest index per cent showed high values of GCV and PCV. This indicates direct selection for these traits will result in genetic improvement.

Niharika *et al.* (2022) carried out investigation at ZAHRS, Shivamogga by using multi-parent advanced breeding lines of the MF₆ generation developed by crossing eight diverse varieties having desirable traits. The variability studies among the lines revealed a higher GCV, PCV, heritability and genetic advance as per cent of mean for majority of yield attributing traits. The knowledge about genetic variability of yield contributing characters, inter relationship among them and their relation with yield are necessary for an effective breeding programme.

Katkani *et al.* (2023) studied 32 advanced breeding lines of rice for three different techniques, viz., direct seeded condition (E-I), transplanting with spacing of 15 x 15 cm (E-II) and 25 x15 cm (E-III) to explore the parameters of heredity and variability for yield along with yield components. The analysis of variance from the experimental results documented significant changes amongst various genotypes for all studied traits with respect to the three-planting spacing. High GCV, high magnitude of broad sense heritability coupled with genetic advance as percentage of mean was detected for grain yield per plant and harvest index.

Murali *et al.* (2023) aimed on genetic variability studies for yield and its component traits using 45 accessions of Rice. The study found that PCV was higher than GCV. High PCV and GCV recorded for number of unfilled grains and harvest index. High heritability was observed for all the characters. High genetic advance as per cent of mean was recorded for number of spikelets per panicle and number of filled grains per panicle.

2.2 To study correlation for grain yield and yield attributing traits

The main aspect of any breeding programme is to increase the yield, so there is a great importance to have knowledge of the grain yield and its related traits. Hence, the characters which are positively associated with yield have to be identified.

Zahid *et al.* (2006) conducted correlation coefficient analysis for yield, yield components and grain quality characteristics in 14 genotypes of Basmati rice. Plant height had negative correlation with yield which indicated that taller Basmati plants have low yield. Grains per panicle have positive and significant genotypic and phenotypic correlation with yield. Plant height and test weight had positive correlations with grain length and cooked grain length while tillers per plant had negative correlation with these traits. Grain length had positive and significant correlation with cooked grain length.

Fiyaz *et al.* (2011) conducted an experiment to study the quantitative traits and their association with grain yield in rice genotypes. Studies showed that number of productive tillers, total spikelet per panicle, total biomass, days to 50 per cent flowering and plant height exhibited significant positive association with grain yield. Path analysis revealed their direct effects on grain yield. Direct effect of total biomass and harvest index was also high on grain yield. Thus, these traits contribute to the grain yield and can be exploited for further breeding programmes.

Adilakshmi and Rani (2012) conducted character association studies in 64 rice genotypes. The association analysis indicated negative association of plant survival per cent with total shoot elongation and relative shoot elongation, where as positive association with yield per plant indicated its importance. Path analysis revealed that the

traits viz., total shoot elongation, plant survival per cent, plant height at maturity, kernel length and test weight exhibited positive direct effects on grain yield per plant. The direct effects of plant survival and test weight were more and hence these traits could be considered for getting good yield under submergence conditions.

Babu *et al.* (2012) conducted an experiment to study the correlation and path analysis in 21 popular hybrids of rice. Character association of the yield attributing traits revealed significantly positive association of grain yield per plant with number of productive tillers per plant. Among all the characters, number of productive tillers per plant possessed both positive association and high direct effects. Hence, selection for this traits can improve the yield.

Pratap *et al.* (2012) evaluated 100 high yielding rice genotypes to determine character association for grain yield and its components. Majority of the traits showed significant and positive association between yield and yield components like biological yield per hill followed by harvest index.

Sravan *et al.* (2012) studied interrelationship of grain yield and its component traits using 36 exotic breeding lines. Grain yield per plant had significant positive correlation with biological yield per plant, harvest index, panicles per plant, plant height, spikelets per panicle, panicle length, test weight, spikelet fertility and flag leaf length. Path analysis revealed that the biological yield was the major contributor of grain yield per plant followed by harvest index and spikelets per panicle. It was suggested that selection of characters such as high biological yield, harvest index and number of spikelets per panicle for further crop improvement programmes will be beneficial.

Patel *et al.* (2014) conducted a study to obtain information on inter-relationship of grain yield and associated characters using 44 diverse rice genotypes. Grain yield per plant was found positively and significantly associated with plant height, panicle length, number of total tillers per plant, number of effective tillers per plant, number of grains per panicle, harvest index and 1000-grain weight at both genotypic and phenotypic levels indicating that these traits were main yield attributing traits. For maximizing the grain yield per plant, emphasis should be given in selection of characters such as number of grains per panicle, straw yield per plant, harvest index and 1000 grain weight.

Rashid *et al.* (2014) studied 20 diverse cultivars of rice for correlation. Among the traits days to heading, days to maturity, number of productive tillers, 1000-grain weight showed highly significant positive correlation with grain yield per plant whereas, flag leaf area, plant height and panicle length showed highly significant negative correlation with grain yield per plant. Number of grains per panicle was not correlated with grain yield per plant.

Pradhan *et al.* (2015) evaluated 30 rice cultivars under both normal and submerged situations to study the genetic association between yield and its attributing traits. Grain yield per plant was positively correlated with panicle number, fertile grain number, fertility percentage and harvest index under normal condition whereas it was only positively correlated with harvest index under submerged condition. Both plot yield and grain yield per plant showed positive association with panicle number, fertile grain number and fertility percentage, whereas grain yield per plant exhibited positive association with harvest index under both the conditions indicating the importance of such traits for realization of high yield.

Devi *et al.* (2016), studied correlation and path analysis for yield and quality traits in 27 rice genotypes. Grain yield per plant had the highest significant positive association with filled seeds per panicle, plant height, flag leaf length, effective tillers, flag leaf width and panicle length indicating importance of these characters for yield improvement, while head rice recovery was found to be significantly and positively correlated with milling per cent and hulling per cent.

Biswajit *et al.* (2017) evaluated 50 diverse rice genotypes in low land submerged field condition at two locations to study association between yield and yield components under submerged condition with more than 50 cm of water depth for 2 weeks at vegetative stage of crop. Fertile grains per panicle, panicle length and test weight (1000 seed weight) are consistently highly positively correlated with seed yield.

Gour *et al.* (2017) conducted an investigation to estimate correlation coefficient from data collected on 83 rice genotypes. Grain yield per plant showed positive association with panicle weight per plant, biological yield per plant, number of tillers per plant and harvest index, while, negative association with plant height. Hence, biological yield per plant, harvest index and number of seeds per plant were identified as key traits for developing high yielding genotypes of rice for future breeding programme.

Lahari, (2017) carried out an investigation with 49 genotypes using randomized complete block design with two replications under submergence during *kharif* 2016 for evaluating character association. Correlation studies revealed highly positive significant association of grain yield per plant with number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle and straw yield per plant.

Kar *et al.* (2018) carried out the experiment to establish the nature of relation between grain yield and yield components by using correlation analysis in 51 rice genotypes. The results indicated that grain yield was positively correlated with days to flowering, plant height, fertile grain number and fertility percentage indicating the importance of such traits for realization of high yield in rice.

Singh *et al.* (2018), carried out the study on correlation analysis in 84 rice varieties including checks. Biological yield per plant, harvest index, 1000-grain weight, panicle bearing tillers per plant and panicle length showed positive and significant correlation with grain yield per plant that emerged as most important associates of grain yield in rice.

Bhutta *et al.* (2019) studied correlation and path analysis using 20 diverse rice genotypes. Plant height and yield attributes such as panicle length, grains per panicle, grain weight per panicle, tillers per plant and test weight were positively correlated in all genotypes. Grain weight per panicle showed highest positive effect on yield per plant and followed by spikelet fertility.

Chhangte *et al.* (2019) conducted an experiment to study the nature and degree of association between yield and its component characters. The characters like no. of grains per plant, no. of panicles per plant, 1000 grains weight, panicle length and plant height showed high significant positive correlation with grain yield per plant.

Dhavaleshvar *et al.* (2019) carried out an investigation to determine the degree of association between grain yield and yield attributing characters and their direct, indirect effects on grain yield in 27 advanced breeding lines of rice with four checks. Straw yield and harvest index showed significant positive correlation with grain yield per hectare. Therefore, the improvement of these traits through selection will automatically result in increased grain yield.

Singh *et al.* (2019) studied genetic parameters, correlation coefficients among yield and yield components in 101 rice genotypes for seven quantitative traits. Analysis of variance revealed that there was high significant difference for all characters among genotypes. GCV and PCV values were high for number of filled grains per panicle, grain yield per plant and ear bearing tillers. Broad sense heritability was high for plant height followed by grain yield per plant and days to flowering. Genetic advance was high for number of filled grains per panicle and grain yield per plant. Significant positive association of grain yield with number of panicles and test weight was observed.

Sreedhar and Reddy, (2019) studied association among seven traits in 40 rice genotypes. Genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients suggesting strong genetic association among the yield and yield components. Correlation coefficient analysis showed that number of productive tillers per m² and test weight exhibited significant positive correlation with yield at both genotypic and phenotypic levels. Significant negative correlation was observed between number of filled grains per panicle and yield.

Tiwari *et al.* (2019) conducted an experiment to estimate the correlation among different quantitative traits in seven rice genotypes. Positive and highly significant correlations were found both in genotypic and phenotypic levels between days to heading and days to maturity, days to heading and grain yield and days to maturity and grain yield. Negative and highly significant genetic correlation was observed between plant height and test weight.

Bhargava *et al.* (2020) conducted correlation studies among eight yield-related traits in segregating the F₂ population, which indicated that plant yield was associated positively with the height of the plant, productive tiller number, length of panicle, and grain number per panicle. It also showed that the number of productive tillers per hill, grain per panicle and plant height had a positive direct effect on plant yield.

Singh *et al.* (2020) investigated 33 coloured and white rice genotypes to study character associations for yield and quality parameters. The results on character associations revealed positive and significant association of grain yield with panicle length, grains per panicle and test weight; and the quality traits, namely, alkali spreading value, protein content, total antioxidant activity, zinc and iron content, indicating scope for simultaneous improvement of yield and quality traits through selection.

Soujanya *et al.* (2020) evaluated 51 rice genotypes for character association for grain yield per plant and various yield component characters. Grain yield per plant showed a significant positive association with number of productive tillers per plant and number of filled grains per panicle. This indicated that these characters are essential for yield improvement. Days to 50 per cent flowering, plant height, panicle length and grain yield per plant exhibited no correlation.

Swapnil *et al.* (2020) carried out an experiment comprising of 371 F₂ segregating progenies of the cross (Sahbhagidhan and BPT-5204), which were evaluated to study correlation among yield and yield components. The correlation studies revealed that seed yield per plant was positively and significantly correlated with number of tillers per plant, number of panicles per plant, number of spikelets per plant, number of grains per plant, number of spikelets per panicle, number of grains per panicle, fertility per cent and panicle length in F₂ generation.

Chamar *et al.* (2021) conducted an experiment to estimate the correlation coefficient among yield and its contributing traits in rice germplasm. For this they evaluated 72 germplasm accessions. The grain yield per plant had significant positive correlation with biological yield per plant followed by harvest index, panicle length, number of tillers per plant, number of productive tillers per plant, seed index and number of grains per panicle.

Fentie *et al.* (2021) registered positive and highly significant phenotypic and genotypic correlations of grain yield per ha with filled grains per panicle, panicle weight, biomass yield and harvest index, but it had negative genotypic and phenotypic correlation with unfilled grains per panicle and 1000 grain weight; only the phenotypic correlations being significant. Biomass yield, harvest index and the number of filled grains per panicle and panicle per plant exerted the highest positive direct effect on grain yield. These traits can be used as selection indices for the grain yield of lowland rice.

Lohiteswararao *et al.* (2021) studied associations between yield and yield attributing characters. Results revealed that grain yield per hill exhibited highly significant positive phenotypic association with traits viz., number of filled spikelets per panicle, number of spikelets per panicle, percentage of filled grain per panicle, days to 50 per cent flowering, 1000-grain weight, straw yield per hill and starch content indicating that direct selection for these characters will be rewarding.

Nath and Kole (2021) studied the correlation of different quantitative characters on seed yield in 26 diverse rice genotypes. Genotypic and phenotypic correlations of seed yield with plant height, flag leaf area, days to flowering, the number of primary and secondary branches per panicle, the number of spikelets and filled grains per panicle, spikelet fertility (per cent) and test weight were significant and positive.

Noatia *et al.* (2021) carried out an experiment to study the extent of character association in 53 breeding lines for 12 quantitative and 10 quality parameters. Grain yield per plant exhibited positive significant correlation with harvest index, effective tillers per plant, 1000 seed weight, spikelet fertility per cent, days to maturity and days to 50 per cent flowering indicating their importance in rice breeding programmes.

Faysal *et al.* (2022) carried out field experiment with 20 rice genotypes of rice for trait association of grain yield and different yield contributing agronomic characters. Correlation study revealed that selection based on plant height, number of effective tillers per hill, number of filled spikelets per panicle, flag leaf length, spikelet sterility, and harvest index (HI) would be effective for increasing the grain yield of rice.

Kumar (2022) undertook an experiment to ascertain association using 68 rice breeding lines for yield and its component traits. Estimates of association revealed that grain yield was found to have significant and positive association with test weight and grain length indicating that these traits are suitable for indirect selection.

Mathew *et al.* (2022) conducted an experiment to evaluate 34 rice genotypes for correlation analysis for yield and yield attributing traits. Data for 13 quantitative characters were recorded. Grain yield per hill showed positive significance with flag leaf length, number of spikelets per panicle, biological yield, harvest index, number of

tillers per hill and biological yield. Hence, direct selection for these characters is helpful.

Reddy *et al.* (2022) evaluated 23 rice genotypes including one check variety to study correlation for 13 quantitative characters. Correlation analysis revealed that grain yield indicated significant positive correlation with plant height followed by tillers per hill, panicles per hill, biological yield and harvest index in terms of phenotypic correlation coefficient whereas in terms of genotypic coefficient it showed positive and significant correlation.

Surjaye *et al.* (2022) evaluated 80 NPT lines of rice for 28 morphological and quality traits. These genotypes were planted in RCBD with three replications. Correlation and path coefficient analysis revealed that hulling index, panicle index and panicle weight per plant showed positive correlation with grain yield per plant and at the same time exhibited high positive direct effect towards yield.

Katkani *et al.* (2023) conducted an experiment with 32 advanced breeding lines of rice and represented the nature of association among the characters. Grain yield per plant showed positive and significant relationship with harvest index followed by biological yield per plant, number of productive tillers per plant, plant height, number of tillers per plant, number of grains per panicle, flag leaf angle and test weight in E I, showed significant positive correlation with harvest index, biological yield per plant and length of panicle in E II and harvest index, no. of grains per panicle, biological yield per plant, test weight and panicle length in E III.

2.3 To study the genetic divergence in advanced breeding lines of rice

For designing effective breeding programmes, the knowledge of greater genetic variation in germplasm and its relationships is necessary. Characterization of population was earlier done using morphological and biochemical markers, but now molecular markers are used which brought a revolution in characterization as they are easy to use as well as economical. As of now majorly genetic diversity is being analysed by D^2 statistics and molecular markers.

Bose and Pradhan (2005) estimated the nature and magnitude of genetic divergence in 35 rice genotypes using Mahalanobis's D^2 – statistics. The genotypes were grouped onto 10 clusters showing fair degree of relationship between geographic distribution and genetic divergence. Cluster IV showed maximum intra cluster divergence while inter cluster divergence was maximum between clusters IX and X. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. Traits like plant yield, days to 50 per cent flowering, and plant height were the major contributors to genetic divergence.

Dushyanthakumar (2008) conducted an experiment to study genetic diversity among 71 red rice genotypes using Mahalanobis D^2 statistics. On the basis of genetic distance, these genotypes were grouped into 10 clusters. Cluster X was the largest consisting of 20 genotypes, while clusters I, II, III, IV and IX contained two genotype each. Among the different characters studied, plant height, panicle length and grain yield contributed significantly to the genetic diversity. The maximum inter- cluster distance (38.09) was highest between Cluster II and Cluster V. The genotypes from these clusters may be used as a potential donor for future hybridization programme to develop higher grain yield with red kernel type.

Khalequzzaman *et al.* (2008) studied genetic diversity of 40 rice genotypes through Mahalanobis D^2 statistics for grain yield and yield contributing characters. The genotypes were grouped into six clusters. The inter cluster distances were higher than the intra cluster distances indicating wider genetic diversity among the genotypes of different clusters. The intra cluster distances were lower reflecting the homogeneity of the genotypes within the clusters. The cluster VI contained the highest number of genotypes (12) and the cluster IV contained the lowest (2). The highest intra cluster distance was noticed for the cluster VI and the lowest for cluster IV. The highest inter cluster distance was observed between cluster III and IV and the lowest between clusters II and VI. The genotypes from cluster IV could be hybridized with the genotypes of any of the four clusters for producing transgressive segregants. Days to flowering, duration and spikelets per panicle were mainly responsible for genetic divergence while considering mean values.

Pandey *et al.* (2009) evaluated 40 rice genotypes for their genetic diversity by studying 12 quantitative characters using cluster analysis. The genotypes were grouped into seven clusters based on Mahalanobis D^2 statistics. Out of total diversity 86.16 per cent of the divergence was contributed by the plant height, biological yield and test weight.

Banumathy *et al.* (2010) evaluated genetic diversity in 53 rice genotypes for eight yield and yield attributing characters using D^2 analysis. Based on the analysis, the genotypes were grouped into 11 clusters. Maximum number of 16 and 15 genotypes were grouped under cluster XI and I respectively. The maximum inter cluster D^2 value was between clusters I and X. The intra cluster distance was maximum in cluster VII, followed by cluster XI. Among the eight traits studied, maximum contribution was made by grain yield followed by days to 50 per cent flowering, total grains per panicle and plant height. Therefore, these characters may be given importance during the hybridization programme.

Dushyanthakumar and Anand (2010) conducted an experiment to study genetic diversity among 39 local rice genotypes using the Mahalanobis D^2 statistic. On the

basis of genetic distance, these genotypes were grouped into eight clusters. Cluster VI was the largest consisting of 21 genotypes, while clusters I, II, III, IV and V contained two genotype each and cluster VI and VIII contained four genotype each. The high degree of divergence was recorded between cluster IV and VIII. Based on the mean performance of traits studied, genotypes from cluster IV and II may be used as parents in future breeding programme to achieve desirable segregants.

Ovung *et al.* (2012) estimated the nature and magnitude of genetic divergence in 70 rice genotypes by considering 13 quantitative characters. Mahalanobis D^2 analysis revealed considerable amount of diversity in the material. The genotypes were grouped into nine clusters. Cluster I and cluster III constituted maximum number of genotypes (12 each). The genotypes falling in cluster VII had the maximum divergence, which was closely followed by cluster V and cluster I. The inter cluster distance was maximum between cluster VI and VII followed by cluster III and IX, suggesting that the genotypes in these clusters may be used as parents for future hybridization programme. Traits like spikelets per panicle, plant height and biological yield were the major contributors to genetic divergence.

Rani *et al.* (2013) screened 64 rice genotypes under submergence conditions to study the diversity pattern. The genotypes were grouped into eight clusters. Maximum of 22 genotypes were grouped into cluster I followed by cluster II consisting of 14 genotypes. Clusters IV and VI were with single genotype indicating the highest heterogeneity among the genotypes. Maximum inter-cluster distances were observed between clusters IV and VIII and V and VIII. The maximum contribution to total divergence was observed from traits viz., test weight, relative shoot elongation, grain yield per plant and days to 50 per cent flowering. Hybridization between clusters IV and VIII may result in desirable segregants with high yield, minimal shoot elongation and fast recovery after de-submergence.

Kodihalli *et al.* (2014) studied genetic diversity among 49 local rice genotypes using the Mahalanobis D^2 statistic under submergence. On the basis of genetic distance, these genotypes were grouped into six clusters. Cluster I was the largest, consisting of 20 genotypes. The maximum inter cluster distance was between cluster III and cluster V. Harvest index, straw yield per plant (g) and grain yield per plant (g) contributed significantly for the genetic diversity. Cluster II was characterized by the maximum mean value for the majority of these characters. Genotypes of cluster III and cluster V may be intercrossed to achieve wider segregation under submergence.

Rashid *et al.* (2014) studied 20 diverse cultivars of rice for their diversity. Cluster analysis revealed that maximum genetic diversity was present between cluster I and cluster VI. Minimum genetic diversity was found between cluster III and cluster

IV. They concluded that cultivars like IRRI-3, IRRI-4, KSK-133, SR-57, IRR15, SRS-64 can be used for hybridization and improve programs for developing new varieties.

Venkatesan *et al.* (2016) studied genetic divergence for 26 rice genotypes in both normal and submergence conditions based on Mahalanobis D^2 statistics and grouping of clusters by Toucher's method. The analysis of variance revealed the presence of variability among genotypes for all characters both under normal and submergence conditions. In D^2 the 26 genotypes were grouped into three different clusters in normal and five in submergence. Maximum intra cluster distance was observed between cluster III and I in normal, and cluster III and V in submergence.

Lahari, (2017) carried out an investigation for 49 rice genotypes to evaluate genetic divergence for 13 traits. Using Mahalanobis D^2 , 49 genotypes were grouped into eight clusters. The maximum inter cluster distance was observed between cluster VII and cluster VIII. Among all the characters, absolute growth rate had maximum contribution towards genetic divergence.

Prasad *et al.* (2018) evaluated 37 rice genotypes for genetic diversity with regard to grain yield, yield components and quality traits. The genotypes were classified into 18 clusters, based on Mahalanobis D^2 statistics. Milling percentage, days to 50 per cent flowering, number of grains per panicle, 1000-seed weight and head rice recovery percentage, together accounted for 89.79 per cent of the total genetic divergence, indicating their importance in selecting them as parents for hybridization programmes.

Ranjith *et al.* (2018) studied the nature and magnitude of genetic divergence in 30 rice genotypes. Mahalanobis D^2 analysis revealed a considerable amount of diversity in the material. The genotypes were grouped into six clusters. Cluster I-constituted a maximum number of genotypes (19). The genotypes falling in cluster-II had the maximum divergence. The inter-cluster distance was maximum between cluster III and V (228.14) followed by cluster III and V (214.44) suggesting that the genotypes constituted in these clusters may be used as parents for future hybridization programmes.

Samudin and Labalado (2019) analyzed 22 rice varieties for genetic diversity. The genetic diversity coefficient ranged from 7.81 to 54.29, while the phenotypic diversity coefficient ranged from 7.01 to 52.44. It was found that the coefficient of genetic diversity was greater than the coefficient of phenotype diversity in all observed traits except for panicle length.

Francis and Packiaraj, (2020) conducted experiment utilizing thirty-two elite rice varieties. The contribution of characters to divergence and clustering of varieties

were estimated using Mahalanobis' D^2 statistics and PCA analysis. Time to maturity, single plant yield and days to 50 per cent flowering contributed maximum to the genetic diversity as given by the per cent contribution to divergence. The varieties were grouped into seven diverse clusters. The study shows that the genetic diversity is being preserved in different varieties indirectly in breeding for different consumer preferences, ecosystems and climatic conditions.

Mishra *et al.* (2020) studied 21 different F_5 families derived from eight different crosses for genetic diversity on the basis of yield and its attributing characters. Based on D^2 analysis, the 21 families were grouped into eight clusters. Cluster I consisted maximum of six families followed by Cluster II with four families. The clusters VII and VIII were mono-familial although there was a common parent. The maximum inter-cluster distance was found between cluster III and IV. Relative contribution of 100-grain weight to the total divergence was highest, followed by plant height, days to 50 per cent flowering and straw yield.

2.4 Phenotypic evaluation of advanced breeding lines of rice for submergence tolerance

Among all the abiotic stresses, submergence is the third most important stress pertaining to rice. Though there are numerous varieties suitable for rainfed lowlands and deep-water ecosystems, they do not have considerable amount of tolerance to submergence and yield low under such conditions. As there is a possibility of finding submergence tolerance in advanced breeding lines, screening of the rice genotypes for their tolerance to submerged conditions can be useful. In this regard, similar works related to screening and evaluation of rice genotypes for submergence tolerance have been reviewed and presented below.

Mallik *et al.* (1988) screened rice germplasm and reported that FR13A and FR43B of India, Kurkaruppan of Srilanka and Goda heenati of Indonesia are excellent sources of flood tolerant rice cultivars. FR13A is good source of submergence tolerance at young seedling stage (10 days). CN 540 is found to be more resistant than FR13A at older stage (40 days) while FR43B remains resistant at all the growth stages.

Das *et al.* (2005) investigated various implications of flood water affecting seedling survival after submergence using rice genotypes with varied tolerance for submergence. They found that warm flood water decreases plant survival and turbid water augments plant mortality. Plants survived better in cool water, and survival decreased by eight per cent per unit increase in water temperature above 26 °C. Even the most tolerant rice cultivar, FR13A, experienced higher mortality with turbid floodwater. Correlation studies revealed that cultivars with the capacity to maintain higher biomass, higher chlorophyll, and non-structural carbohydrate concentrations after submergence had higher survival.

Sarkar *et al.* (2009) conducted an experiment during *kharif* 2005–07 under rainfed lowlands and controlled submergence. Under flash-flooding, genotypes with *Sub1* survived complete submergence stress with turbid water for up to 12 days, whereas genotypes without *Sub1* did not survive. Swarnan *sub1* gave higher grain yield than ‘Swarna’ with a yield advantage of up to 1.65 tonnes per ha. The results suggest that rice genotypes with *Sub1* have great potential for improving the productivity of rainfed lowland rice prone to flash flooding.

Sarkar and Bhattacharjee (2011) identified submergence tolerant landraces and evaluated them for survival percentage under submergence along with *SUB1* introgressed cultivars. 20 days submergence caused greater damage than 14 days of submergence in *Sub1* introgressed cultivars. Survival percentage reduced when plants were submerged for more period. Survival percentage of land races was more compared to *Sub1* introgressed cultivars.

Akinwale *et al.* (2012) evaluated submergence tolerance of 20 rainfed lowland rice cultivars with flood water depth of 1.5m for a period of 14 days in a randomized complete block design with three replicates. Thirty day old seedlings were submerged for 14 days under 100cm of water followed by normal condition. Data was collected on plants for stem elongation, date at 50 per cent flowering, plant height, number of tillers at maturity, number of panicles at maturity and grain weight. Plant survival recorded 10 days after de-submergence showed large cultivar differences. Percentage survival varied from 3.2 to 97.5 per cent. Plant elongation during submergence was found to be negatively correlated with survival ($r = -0.80$), indicating the importance of reduced elongation growth during submergence.

Niroula *et al.* (2012) screened 109 *Oryza* genotypes belonging to different rice genome groups for flooding tolerance. The response to survival rate varied between the cultivars and wild accessions belonging to different groups as well as within the group. Flooding-tolerant wild accessions of *Oryza rhizomatis* and *Oryza eichingeri*, belonging to the C-genome group exhibited high survival rate of 100 per cent similar to tolerant indica variety FR13A.

Linh *et al.* (2013) evaluated twelve rice varieties under complete submergence of 13-15 days. Due to the absence of *Sub1* loci Vietnamese elite varieties such as Khangdan 18, Bacthom 7 and OM6976 as well as IR42 (sensitive check) were completely destroyed after 13-15 days of complete submergence. Imported rice varieties such as IR49830-7 and BR11-*Sub1* (carrying QTL/*Sub1*) exhibited regeneration, growth and development after de-submergence and showed higher survival rate in 10 to 14 days of complete submergence with the survival rate of 25.4 per cent and 37.2 per cent respectively.

Nugraha *et al.* (2013) evaluated the response of 18 rice genotypes to various flooding conditions. The results showed that *Sub1* introgression rice lines had higher survival compared to non-*Sub1* and did not much elongate their shoots during submergence. In sensitive genotypes, submergence decreased the panicle number, grain number per panicle and panicle fertility. Consequently, the yield declined. The *Sub1* introgression lines had higher chlorophyll concentration and less depletion in soluble sugar and starch after submergence. Introgression of the *Sub1* into high-yielding varieties improved submergence tolerance without affecting yield potential. The study indicates that introgression of the *Sub1* into taller type rice varieties should be done to compensate the effect of suppressed elongation.

Ranawake *et al.* (2014) screened 25 rice cultivars for submergence tolerance at seedling and vegetative stages. At seedling stage, germinated seedlings were grown for two weeks and five days, nine days and 14 days complete submergence stresses were given in separate experiments. The experiment was repeated using six-week-old plants for vegetative stage. Survival rate and plant height were recorded. At five days, nine days and 14 days submergence periods 100 per cent, 32 per cent and 24 per cent of rice cultivars survived respectively at the seedling stage while 64 per cent, 28 per cent and 16 per cent of rice cultivars survived respectively at vegetative stage. At 14-day complete submergence, Bg 379/2 had highest survival rate at both seedling (20 per cent) and vegetative stage (17.5 per cent). All survived rice cultivars elongated (100 per cent) under 14-day submergence stress at both seedling and vegetative stages. There was a correlation between elongation and survival percentage of rice cultivars.

Singh *et al.* (2015) evaluated 144 rice cultivars to screen submergence tolerant rice cultivars. The survival percentage ranged from 0.00 per cent to 100 per cent. 26 cultivars showed more than 40 per cent survivability. Twelve cultivars showed survival percentage of 80 to 100 per cent. Five cultivars showed more than 70 per cent survival.

Goswami *et al.* (2017) conducted detailed physiological and genotyping studies of 27 rice genotypes and one wild rice relative, with a focus on submergence tolerance traits and *Sub1* loci. Detailed allelic diversity study of *Sub1A* loci suggested that rice varieties IR42, Panibhasha, Khoda and Kalaputia share a common allele that is different from FR13A, Keralasundari, Bhashakalmi, Kumrogore. Two other genotypes Meghi and Khoda shares both alleles of *Sub1A* loci (present in IR42 and FR13A groups) in addition to a new variant. Three rice genotypes (Meghi, Bhashakalmi and Keralasundari) showed beneficial properties in relation to induced submergence stress and can be considered valuable to utilize in breeding program for submergence tolerance.

Nishanth *et al.* (2017) studied 525 germplasm lines and screened for survival percentage under submergence. They were scored from one to nine using IRRI standard method. Among all the lines none of them scored one with 100 per cent survival, second

lines (Jaladhi and IET 21465) scored three with 96 per cent survival, 68 lines scored five with 75 to 94 per cent survival rate, 230 lines scored seven with survival rate between 50 to 74 per cent and 225 lines scored nine with less than 49 per cent survival rate. Among the checks FR13A showed the highest survival rate of 96 per cent and Jyothi showed the least survival rate of eight per cent.

Gautam *et al.* (2018) conducted phenotypic screening for submergence tolerance during *kharif* 2015. Out of 35 genotypes 32 were *Sub1* introgressed BC₂F₃ lines with three parents *i.e.*, Ranjit, Bahadur and Swarna sub1. The phenotypic screening of genotypes showed that all *Sub1* introgressed lines had significantly higher survival rates and less change in plant height compared to original recipient parents. The *Sub1* introgressed lines showed less elongation during submergence as compared to the parents and the susceptible check IR42.

Barik *et al.* (2019) evaluated submergence responses in 88 lowland indigenous rice (*Oryza sativa* L.) landraces from Koraput, India, in pot experiment to identify submergence-tolerant rice genotypes. Five rice landraces Samudrabali, Basnamundi, Gadaba, Surudaka and Dokarakuji were the most tolerant to submergence when submerged for up to 14 days. Samudrabali, Basnamundi and Godoba were notable for having greater survival rates, more vigorous with greater biomass than a standard submergence tolerant variety FR13A.

Kumari *et al.* (2019) carried out experiment with 240 mutant lines derived from FR13A, FR13B and Labella along with three untreated checks (FR13A, FR13B and Labella). These were evaluated for their survival percentage under submerged condition and yield potential. High magnitude of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) and genetic advance as percentage of mean were observed for number of tillers per plant, number of fertile tillers per plant, relative shoot elongation and survival percentage, indicating that these traits could be used as selection indices for yield improvement and submergence tolerance.

Wening *et al.* (2019) evaluated 95 lines and four checks of rice for submergence tolerance in Indonesia Centre of Rice Research in different environmental conditions using augmented design with five blocks in 1) submergence condition conducted in submergence pool and 2) optimal conditions in irrigated field. The selection methods carried out were 1) selection based on survival rate and vigour, 2) selection based on productivity under submergence and sensitivity index on productivity characters 3) selection based on weighted selection index using sensitivity index variables of agronomic and morphological characters. Cluster gram analysis was done to separate tolerant and sensitive lines. Among all the lines evaluated 18 lines were found to be tolerant and can be further used for breeding programme.

MATERIAL AND METHODS

III MATERIAL AND METHODS

The present investigation was conducted at Agricultural and Horticultural Research Station, Kathalagere and Zonal Agricultural and Horticultural Research Station, Navile, Shivamogga under artificially created submergence conditions and the details of material used and methods adopted during the course of investigation on “Assessment of Genetic Variability in Advanced Breeding Lines of Rice (*Oryza sativa* L.) and Screening for Submergence Tolerance” are furnished below.

3.1 Experiment I: Genetic variability, diversity and character association studies among advanced breeding lines of rice with regard to yield and yield attributing traits under non-submergence condition

3.1.1 Experimental material

Thirty two F₅ advanced breeding lines of rice cross RNR-15048 × KPR-1 along with five check varieties viz., RNR-15048, KPR-1, BPT-5204, JGL-1798, KHP-11, were collected from the Department of Genetics and Plant Breeding, College of Agriculture, Shivamogga to study genetic variability, diversity and character association for yield and yield attributing traits under non submergence (Table 3.1.1). The investigation was carried out during *kharif* 2022 at AHRS, Kathalagere. The advanced lines included in the study are listed in Table 3.1.1.

3.1.2 Experimental methods

3.1.2.1 Experimental layout and cultural operations

The experiment was laid out in Randomised Complete Block Design (RCBD) with two replications for testing 32 advanced breeding lines of rice with five checks. The seeds of 32 advanced breeding lines were sown to raise nursery bed during *Kharif* 2022 at AHRS, Kathalagere. Twenty one days old seedlings were transplanted manually to the main field at the rate of one seedling per hill in RCBD with two replications by following spacing of 20 cm row to row and 15 cm plant to plant. The recommended package of practices was followed to maintain a healthy and good crop stand.

3.1.2.2 Method of sampling and recording observations

Five plants were randomly selected from each line and labelled for recording the observations in each treatment. Mean of the observations recorded on these five plants was subjected for statistical analysis. The characters for which observations were recorded are described below.

3.1.2.2.1 Days to 50 per cent flowering

Total number of days taken by each rice genotypes from the date of sowing to the opening of the first flower in fifty per cent of the plants was observed and recorded.

Table 3.1.1 List of rice genotypes used in the present experiment

Line no.	Genotype	Line no.	Genotype
1	R×K-1-4-3	22	R×K-7-2-11
2	R×K-7-2-1	23	R×K-2-2-14
3	R×K-1-4-4	24	R×K-7-2-12
4	R×K-7-2-2	25	R×K-1-4-15
5	R×K-1-4-5	26	R×K-4-2-13
6	R×K-8-2-3	27	R×K-1-4-16
7	R×K-1-4-6	28	R×K-3-2-14
8	R×K-5-2-4	29	R×K-1-4-17
9	R×K-1-4-7	30	R×K-6-2-15
10	R×K-7-2-5	31	R×K-1-4-18
11	R×K-1-4-8	32	R×K-7-2-16
12	R×K-12-2-6	33	RNR-15048 (Check I)
13	R×K-1-4-9	34	KPR-1 (Check I)
14	R×K-7-2-7	35	BPT-5204 (Check I)
15	R×K-1-6-10	36	JGL-1798 (Check I)
16	R×K-14-2-8	37	KHP 11 (Check I)
17	R×K-4-4-11	38	FR13A (Check II)
18	R×K-7-2-9	39	Swarna sub-1(Check II)
19	R×K-1-4-12	40	Jyothi (Check II)
20	R×K-8-2-10	41	BPT-5204 (Check II)
21	R×K-1-4-13		

NOTE: 1. Rice genotypes from 33 to 37 were used as checks for experiment I.
2. Rice genotypes from 37 to 41 were used as checks for experiment II.



Plate 1: Nursery operations at ZAHRS, Navile, Shivamogga



Plate 2: Overview of experimental plot during submergence



Plate 3: Overview of experimental plot after de-submergence



Plate 4: Over view of experimental field under non submergence condition at AHRS, Kathalagere

3.1.2.2.2 Days to maturity

The total number of days taken by each rice genotypes from sowing to physiological maturity was observed and recorded.

3.1.2.2.3 Plant height (cm)

Height of the plant from the base of plant to the tip (flag leaf) excluding awn was measured at morphological maturity of the plant using a metal scale. It is expressed in terms of centimeter (cm).

3.1.2.2.4 Number of tillers per plant

The number of tillers per plant was recorded by counting both the productive and unproductive tillers in a hill.

3.1.2.2.5 Number of productive tillers per plant

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

3.1.2.2.6 Panicle length (cm)

Length of the panicle was measured from flag leaf node to the tip of the panicle excluding awns if any and recorded using metal scale. It is expressed in terms of centimetre (cm).

3.1.2.2.7 Number of spikelet per panicle

Number of spikelets (filled and chaffy) were counted in a randomly selected five panicles and number of spikelets per panicle or number of grains per panicle was recorded by taking the average of five plants.

3.1.2.2.8 Number of filled grains per panicle

Five panicles were taken from the sampled plants and the number of filled grains were counted and averaged to obtain number of filled grains per panicle.

3.1.2.2.9 Spikelet fertility (%)

Number of filled grains were counted in a randomly selected five panicles and averaged to obtain number of filled grains per panicle. Spikelet fertility per panicle was estimated by the ratio average number of filled grains of five panicles to the average number of spikelets of five panicles and expressed in terms of percentage.

3.1.2.2.10 Test weight (g)

Weight of one thousand randomly selected filled grains using electronic balance and expressed in terms of grams (g).

3.1.2.2.11 Length Breadth (L/B) ratio

The length and breadth of five randomly selected grains was recorded using measuring scale and the ratio of length and breadth was determined by dividing the length of single grain with its corresponding breadth, averaged and recorded for each genotype.

3.1.2.2.12 Grain yield per plant (g)

Total weight of the grains from five plants from each advanced breeding line of rice was measured in grams and averaged to obtain the per plant yield.

3.2 Experiment II: Phenotypic evaluation of advanced breeding lines of rice for submergence tolerance

3.2.1 Experimental material

The material used under present study consisted of 32 advanced breeding lines with Swarna sub-1 and FR13A as tolerant checks at national level and Jyothi, BPT-5204 as local checks, these were issued for research purpose from the Department of Genetics and Plant Breeding, College of Agriculture, Navile, Shivamogga. The list of rice lines included in the study are presented in Table 3.1.1.

3.2.2 Experimental methods

3.2.2.1 Experimental layout and cultural operations

The experiment was laid out in Randomized Complete Block Design (RCBD) with two replications to evaluate submergence tolerance in advanced breeding lines of rice. Advanced breeding lines were sown during *kharif* 2022 for raising the nursery. Twenty one days old seedlings were transplanted manually into the main field with single seedling per hill in RCBD design with spacing of 20 cm row to row and 15 cm plant to plant.

3.2.2.2 Screening for submergence tolerance

The transplanted seedlings were allowed for proper establishment (one week) and were submerged in water with a depth of 50 to 60 cm for a period of 14 days. The crop was then de-submerged and the cultural operations as well as plant protection measures were taken up according to the recommended package of practices in order to establish a good and healthy crop stand.

The number of plants survived even after fifteen days of submergence were recorded to know the survival percentage. The number of seedlings before submergence and number of seedlings survived after submergence were noted and percentage of survival for each genotype was calculated.

3.2.2.2.1 Survival percentage

The survival percentage was calculated as with the formula based on Standard Evaluation System for Rice (SES) (Anonymous, 1988).

$$\text{Survival percentage} = \frac{\text{Number of survived hills at 15 days of re-emergence}}{\text{Number of hills before submergence}} \times 100$$

Score	Survival percentage (%)
1	100
3	95-99
5	75-94
7	50-74
9	0-49

3.2.2.2.2 Stem elongation (%)

Height of the plant was recorded during 15 days after submergence in submerged condition as well as the same in control (non-submerged) condition. Extent of elongation of the plant stem was determined by deducing plant height of control plants from the height of the plants of respective genotype after submergence and it is expressed as percentage of plant height compared to non-submerged condition (Sarkar and Bhattacharjee, 2011).

3.2.2.3 Per cent difference of various traits between submergence and non submergence condition

Among the morphological traits studied between submergence and non submergence of the same genotype, change in per cent mean was calculated. The characters for which change in per cent mean was recorded are described below.

3.2.2.3.1 Days to 50 per cent flowering

Total number of days taken by each rice genotypes from the date of sowing to the opening of the first flower in fifty per cent of the plants was observed and recorded.

3.2.2.3.2 Number of tillers per plant

The number of tillers per plant was recorded by counting both the productive and unproductive tillers in a hill.

3.2.2.3.3 Number of productive tillers per plant

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

3.2.2.3.4 Test weight (g)

Weight of one thousand randomly selected filled grains using electronic balance and expressed in terms of grams (g).

3.2.2.3.5 Grain yield per plant (g)

Total weight of the grains from five plants from each advanced breeding line of rice was measured in grams and averaged to obtain the per plant yield.

3.3 Statistical analysis

The mean values of five randomly selected plants for recording 12 different characters were used for statistical analysis. The experimental data on both growth and yield parameters were compiled and subjected to the following statistical analysis. Analysis was carried out by using R software.

3.3.1 Analysis of variance (ANOVA)

The data of mean value for all the characters were analysed for their variance following Randomized Complete Block Design outlined by Cochran and Cox (1957).

Analysis was done using software WINDOSTAT version 9.2 and R software present at Department of Genetics and Plant Breeding, CoA, 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)	SS _t		

Where,

r = number of replications

df = degrees of freedom

t = number of genotypes

SSr = replication sum of squares

MSSR= replication mean sum of squares

SSg = genotypic sum of squares

MSSG= genotype mean sum of squares

SSe = error sum of squares (SS_t-SSg-SSr)

The Sum of squares can be obtained as follows,

1. Total sum of squares (TSS) = Σ (No. of observations)² - CF

Where, CF= Correction factor

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

Where, n= Number of replications

$$3. \text{ Replication sum of squares (SSR)} = \Sigma (R_j)^2/s - CF$$

Where, s= Number of genotypes

$$4. \text{ Error sum of squares (SSE)} = TSS - SSG - SSR$$

3.3.1.1 Mean

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

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

Where,

X = observations

n = number of observations

3.3.1.2 Range

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

3.3.1.3 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.

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

3.3.1.4 Standard error difference between two means (SEd.m)

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

$$SEd.m = \sqrt{\frac{2MSSE}{r}}$$

Where,

r = number of replications

MSSE = error mean sum of squares

3.3.1.5 Critical difference (CD)

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

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

Where,

r = number of replications

MMSE = error mean sum of squares

t = table t value at 5 % or 1 % probability level for error degrees of freedom.

3.3.1.6 Coefficient of variation (CV)

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

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

3.3.1.7 Variance

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

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

3.3.2 Estimation of genetic parameters

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

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

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \text{MSS (error)}$$

3.3.3 Coefficient of variability

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

3.3.3.1 Phenotypic coefficient of variation (PCV)

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

3.3.3.2 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

Categorization of the range of variability as proposed by Sivasubramanian and Menon (1973) is as follows.

Scales	Value of GCV and PCV (%)
Low	Less than 10
Moderate	10 – 20
High	More than 20

3.3.4 Heritability and Genetic advance

3.3.4.1 Heritability

Heritability in broad sense as the ratio of genotypic variance to the total variance in the non-segregating populations. Heritability was calculated by the formula given by Lush (1949).

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

Where,

h_{bs}^2 = Heritability in broad sense

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

As suggested by Johnson *et al.* (1955), (h_{bs}^2) estimates were categorized as follows:

Scales	Values of heritability in broad sense (%)
Low	Less than 30
Moderate	30 – 60
High	More than 60

3.3.4.2 Genetic Advance (Predicted)

Genetic advance denotes the improvement in the genotypic value of the new population over the base population, and it is estimated by the following formula suggested by Johnson *et al.* (1955).

$$\text{Genetic Advance (Predicted)} = H \times \sqrt{\sigma_p^2} \times K$$

Where,

H = Heritability coefficient

$\sqrt{\sigma_p^2}$ = Phenotypic standard deviation

K = Selection differential at given intensity

3.3.4.3 Genetic advance as per cent of mean (GAM)

Genetic advance as per cent of mean was calculated by following formula.

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

Where,

GA = Expected genetic advance

$\bar{X}$ = General mean of the character in the population

The range of GAM was classified as suggested by Johnson *et al.* (1955).

Scales	Value of Genetic Advance (%)
Low	Less than 10
Moderate	10 – 20
High	More than 20

3.3.5 Correlation coefficient analysis

The correlation coefficients were calculated to determine the degree of association of the characters with yield and also among the different yield components. Genotypic and phenotypic coefficients of correlation between all pairs of characters were determined by using variance and covariance components as

suggested by Al Jibouri (1958). The analysis was done by using the WINDOSTAT version 9.2 software and R software.

$$r_g(xy) = \frac{\text{Cov}_g(xy)}{\sqrt{\sigma_g^2(x) \times \sigma_g^2(y)}}$$

$$r_p(xy) = \frac{\text{Cov}_p(xy)}{\sqrt{\sigma_p^2(x) \times \sigma_p^2(y)}}$$

Where,

$r_g(xy)$, $r_p(xy)$ are the genotypic and phenotypic correlation coefficients respectively.

Cov_g and Cov_p are the genotypic and phenotypic covariance respectively.

σ_g^2 and σ_p^2 are the genotypic and phenotypic variance respectively.

x and y are the two traits for which correlation coefficient is estimated.

The calculated value of r was compared with table r value with (n-2) degree of freedom at 5 and 1 per cent of significance.

3.3.6 Genetic diversity

3.3.6.1 Mahalanobis' D^2 analysis

Mahalanobis' (1936) D^2 statistics was used for assessing the genetic divergence between populations. D^2 analysis was done by using the WINDOSTAT version 9.2 software and R software installed at Department of Genetics and Plant Breeding, KSNUAHS, 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 correlated genotypes (Rao, 1952).

3.3.6.2 Clustering of D^2 values

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

3.3.6.2.1 Intra cluster distance

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

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

Where,

$\sum D_i^2$ is the sum of distance between all possible combinations of the $(n_i n_i)$ number of entries included in a cluster.

n_i = number of lines in cluster i.

n_j = number of lines in cluster j.

EXPERIMENTAL RESULTS

IV EXPERIMENTAL RESULTS

The current study aimed to determine the type and extent of genetic diversity, variability and character association with regard to grain yield and attributes that contribute to yield among 32 advanced breeding lines of rice and their tolerance to submergence. The following subheadings are used to present the experimental findings in this chapter.

- 4.1 Genetic variability study among advanced breeding lines of rice for grain yield and its attributing traits
- 4.2 Phenotypic correlation analysis for grain yield and its attributing traits
- 4.3 Genetic divergence among advanced breeding lines for grain yield and its attributing traits
- 4.4 Screening of advanced breeding lines of rice for submergence tolerance
- 4.5 Morphological and physiological characterization of advanced breeding lines of rice for submergence tolerance
- 4.6 Phenotypic correlation studies among morphological and physiological characters with grain yield
- 4.7 Per cent difference of various traits between submergence and non submergence condition

4.1 Genetic variability study among advanced breeding lines of rice for grain yield and its attributing traits

Advanced breeding lines of rice demonstrated considerable population variability under the non-submergence condition, according to the analysis of variance (ANOVA), which found significant differences for all characters examined. Table 4.1.1 shows the analysis of variances for each of the 12 traits.

Table 4.1.2 lists the genetic variability metrics for each of the 12 traits, including mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (in the broad sense) and genetic advance as per cent mean (GAM).

4.1.1 Days to 50 per cent flowering

Days to 50 per cent flowering was found to be ranging from 101.00 to 129.00 days with a mean of 116.78 days. KPR-1 was the earliest to flower at 101 days and R×K-4-4-11 was late to flower at 129 days. Low PCV and GCV of 4.94 and 4.76 per cent was recorded respectively with high heritability of 93.12 per cent and low genetic advance as per cent mean of 9.48.

Table 4.1.1 Analysis of variance for yield and its attributing characters in advanced breeding lines under non submergence

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	2.61	6.54	17.89	1.91	0.39	1.07
Genotype	36	63.34**	65.92**	767.22**	10.67**	11.54**	9.89**
Error	36	2.29	3.09	63.18	2.17	2.08	0.48
CD (5%)		3.07	3.57	16.12	2.99	2.93	1.41
CD (1%)		4.12	4.79	21.62	4.01	3.92	1.89
CV %		1.23	1.19	5.89	9.83	9.63	3.17

Source of variation	Degrees of freedom	Number of spikelets per panicle	Number of filled grains per panicle	Spikelet fertility (%)	Test weight (g)	Length breadth ratio	Grain yield per plant (g)
Replication	1	66.46	83.42	14.06	4.06	0.01	17.22
Genotype	36	3404.82**	2301.55**	27.20**	9.48**	0.19**	73.21**
Error	36	680.34	561.99	3.71	1.94	0.02	18.19
CD (5%)		52.90	48.08	3.91	2.83	0.28	8.65
CD (1%)		70.93	64.47	5.24	3.79	0.37	11.60
CV %		10.00	10.13	2.05	6.67	4.00	14.55

** - Significant at 1% level

Table 4.1.2 Genetic variability parameters for yield and yield related characters in advanced breeding lines under non submergence

Sl No.	Characters	Mean	Range		PCV (%)	GCV (%)	h ² (bs) (%)	GAM (%)
			Min	Max				
1	Days to 50 per cent flowering	116.78	101.00	129.00	4.94	4.76	93.12	9.48
2	Days to maturity	146.81	131.00	159.00	4.00	3.81	91.02	7.50
3	Plant height (cm)	134.9	90.00	164.80	15.10	13.90	84.78	26.37
4	Number of tillers per plant	14.98	10.20	23.00	16.92	13.78	66.28	23.11
5	Number of productive tillers per plant	14.97	9.50	23.00	17.42	14.52	69.44	26.37
6	Panicle length (cm)	21.89	13.20	25.30	10.39	9.89	90.70	19.42
7	Number of spikelets per panicle	260.81	175.80	392.00	17.32	14.15	66.69	23.80
8	Number of filled grains per panicle	233.98	144.00	337.62	16.17	12.60	60.74	20.23
9	Spikelet fertility (%)	93.98	81.13	98.50	4.18	3.65	75.97	6.55
10	Test weight (g)	20.93	15.60	29.50	11.42	9.27	65.97	15.52
11	Length breadth ratio	3.43	2.44	3.98	9.45	8.56	82.04	15.98
12	Grain yield per plant (g)	29.32	21.20	41.85	23.06	17.89	60.19	28.59

4.1.2 Days to maturity

Mean days to maturity was 146.81 days and found to be of range 131.00 to 159.00 days. KPR-1 was the earliest to mature at 131 days, while R×K-4-4-11 had late maturity at 159 days. The low PCV and GCV of 4.00 and 3.81 per cent was observed respectively. A high heritability estimates of 91.02 per cent with low GAM of 7.50 per cent was found.

4.1.3 Plant height (cm)

It was revealed that the plant height significantly differed among advanced breeding lines. Plant height had a range from 90.00 cm to 164.80 cm with the mean value of 134.90 cm. KPR-1 exhibited minimum height of 90 cm and R×K-7-2-5 recorded maximum height of 164 cm. The moderate PCV and GCV of 15.10 and 13.90 per cent was found respectively. This trait recorded high heritability of 84.78 per cent and high GAM of 26.37 per cent.

4.1.4 Number of tillers per plant

Number of tillers per plant significantly differed among advanced breeding lines with a range of 10.20 to 23.00 and a mean value of 14.98. The lowest number of tillers per plant, i.e., 10, were recorded by R×K-8-2-10 and the highest number of tillers was recorded by JGL-1798, with 23 tillers per plant. Phenotypic and genotypic coefficients of variability recorded were 17.42 and 14.52 per cent, respectively. High genetic advance as per cent mean of 23.11 and high heritability of 66.28 per cent were recorded.

4.1.5 Number of productive tillers per plant

Number of productive tillers per plant significantly differed among advanced breeding lines of rice with a range of 9.50 to 23.00 and a mean value of 14.97. The lowest number of tillers of nine per plant was recorded by R×K-8-2-10 and the highest number of tillers was recorded by JGL-1798 with 23 tillers per plant. Moderate phenotypic and genotypic coefficients of 17.42 and 14.52 per cent was observed respectively. High genetic advance as per cent mean of 26.37 and high heritability of 69.44 per cent was observed.

4.1.6 Panicle length (cm)

A wide range of variability was exhibited by the panicle length among advanced breeding lines. It was ranging from 13.20 to 25.30 cm with a mean value of 21.89 cm. R×K-1-4-16 exhibited the highest panicle length of 25.30 cm and lowest by R×K-7-2-12 (13.20). Moderate PCV of 10.39 and low GCV of 9.89 per cent respectively was exhibited by the trait coupled with high heritability of 90.70 per cent and moderate GAM of 19.42 per cent was recorded.

4.1.7 Number of spikelets per panicle

Number of spikelets per panicle had exhibited wide variability. Moderate PCV and GCV of 17.32 and 14.15 per cent respectively was recorded for the trait coupled with high heritability of 66.29 per cent and high GAM of 23.80 per cent. The mean value of 260.81 was recorded with the range of 175.80 to 392.00. The genotype R×K-4-4-11 exhibited a minimum number of 176 grains per panicle, whereas JGL-1798 had a maximum number of 392 grains per panicle.

4.1.8 Number of filled grains per panicle

Moderate PCV and GCV of 16.17 and 12.60 per cent respectively was observed for the trait number of filled grains per panicle coupled with high heritability of 60.74 per cent and high GAM of 20.23 per cent. Variability was found more with the mean value of 233.98 recorded and the range of 144.00 to 337.62. The genotype R×K-3-2-14 exhibited a minimum number of 144 filled grains per panicle, whereas JGL-1798 had a maximum number of 337 filled grains per panicle.

4.1.9 Spikelet fertility (%)

Spikelet fertility ranged from 81.13 to 98.50 per cent. The mean spikelet fertility value was found to be 93.98 per cent. The highest spikelet fertility was found to be 98.50, exhibited by R×K-8-2-3 and the lowest spikelet fertility of 81.13 was exhibited by R×K-1-4-8. Low PCV and GCV of 4.18 and 3.65, respectively were recorded by the trait spikelet fertility with a high heritability of 75.97 per cent. Low genetic advance as per cent mean of 6.55 was exhibited by the trait.

4.1.10 Test weight (g)

Test weight had a range from 15.60 to 29.50 grams, with a mean of 20.93 grams. R×K-6-2-15 had recorded the lowest test weight of 15.60 grams and KHP-11 recorded the highest test weight of 29.50 grams. Moderate PCV of 11.42 and low GCV of 9.27 with high heritability of 65.97 per cent and moderate GAM of 15.52 was found for this character.

4.1.11 Length breadth ratio

Length breadth ratio had a range of 2.44 to 3.98. The mean length breadth ratio was found to be 3.43. The highest length breadth ratio was exhibited by BPT-5204 (3.98) and the lowest was by R×K-7-2-11 (2.44). The trait exhibited low GCV and PCV 9.45 and 8.56, respectively, with a high heritability of 82.04 per cent. Moderate genetic advance as per cent mean of 15.98 was observed.

4.1.12 Grain yield per plant (g)

Grain yield per plant significantly varied, with the range of 21.20 grams to 41.85 grams with a mean of 29.32 grams. The lowest grain yield of 21.20 grams was recorded by R×K-1-4-12, and the highest grain yield of 41.85 grams was recorded by R×K-1-4-8. The trait showed a high PCV of 23.06 and a moderate GCV

of 17.89. Heritability was high, with a value of 60.19 per cent and a high GAM of 28.59 was obtained.

4.2 Phenotypic correlation analysis for grain yield and its attributing traits

To ascertain the type of relationship between grain yield and its corresponding traits under non-submergence conditions, phenotypic correlations among a total of 12 quantitative characters were determined and are shown in Table 4.2.1

4.2.1 Correlation of grain yield per plant with other characters

Grain yield per plant was found to have a significant and positive association with number of tillers per plant ($r = 0.60$), number of productive tillers per plant ($r = 0.63$), panicle length ($r = 0.66$), number of spikelets per panicle ($r = 0.70$), number of filled grains per panicle ($r = 0.72$), spikelet fertility ($r = 0.67$), test weight ($r = 0.45$) and length breadth ratio ($r = 0.36$). In contrast, a non-significant negative correlation was found for days to 50 per cent flowering ($r = -0.10$), days to maturity (-0.18) and plant height ($r = -0.12$).

4.2.2 Correlation among yield attributing characters

4.2.2.1 Days to 50 per cent flowering

A significant positive correlation was exhibited by days to 50 per cent flowering with days to maturity (0.82) and grain length breadth ratio (0.26). It revealed a non-significant positive correlation with spikelet fertility (0.14), panicle length (0.19) and test weight (0.18). It exhibited non-significant negative correlation with plant height (-0.16), number of tillers per plant (-0.19), number of productive tillers per plant (-0.17), number of filled grains per panicle (-0.14), number of spikelets per panicle (-0.15).

4.2.2.2 Days to maturity

Days to maturity had shown significant positive correlation with days to 50 per cent flowering (0.82). Non significant positive correlation was exhibited by panicle length (0.09) and test weight (0.07) and grain length breadth ratio (0.11). The number of tillers per plant (-0.33), number of productive tillers per plant (-0.26), number of filled grains per panicle (-0.25) and number of spikelets per panicle (-0.28) had shown significant negative correlation with the days to maturity. Negative non-significant correlation was observed with plant height (-0.08) and spikelet fertility (-0.06).

4.2.2.3 Plant height (cm)

Significant negative association was shown by plant height with number of tillers per plant (-0.48), number of productive tillers per plant (-0.55), number of spikelets per panicle (-0.23), number of filled grains per panicle (-0.30), panicle length

Table 4.2.1 Phenotypic correlation for grain yield and yield contributing traits in advanced breeding lines of rice under non submergence.

	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	1	0.82**	-0.16	-0.19	-0.17	0.19	-0.15	-0.14	0.14	0.18	0.26*	-0.10
X ₂		1	-0.08	-0.33**	-0.26*	0.09	-0.28*	-0.25*	-0.06	0.07	0.11	-0.18
X ₃			1	-0.48**	-0.55**	-0.57*	-0.23*	-0.30**	-0.24*	-0.35**	-0.14	-0.12
X ₄				1	0.93**	0.57**	0.67**	0.76**	0.45**	0.54**	0.30*	0.60**
X ₅					1	0.62**	0.62**	0.70**	0.49**	0.56**	0.35**	0.63**
X ₆						1	0.54**	0.58**	0.69**	0.59**	0.39**	0.66**
X ₇							1	0.81**	0.66**	0.42**	0.31**	0.70**
X ₈								1	0.52**	0.47**	0.25*	0.72**
X ₉									1	0.48**	0.42**	0.67**
X ₁₀										1	0.37**	0.45**
X ₁₁											1	0.36**
X ₁₂												1

*, ** Significant at 5% and 1% respectively.

Where,

X ₁ - Days to 50 per cent flowering	X ₅ - Number of productive tillers per plant	X ₉ - Spikelet fertility (%)
X ₂ - Days to maturity	X ₆ - Panicle length (cm)	X ₁₀ - Test weight (g)
X ₃ - Plant height (cm)	X ₇ - Number of spikelets per panicle	X ₁₁ - Length breadth ratio
X ₄ - Number of tillers per plant	X ₈ - Number of filled grains per panicle	X ₁₂ - Grain yield per plant (g)

(-0.57), test weight (-0.35). Non-significant negative correlation was found with days to 50 per cent flowering (-0.16), days to maturity (-0.08), spikelet fertility (-0.24) and grain length breadth ratio (-0.14).

4.2.2.4 Number of tillers per plant

Number of tillers per plant showed significant positive correlation with number of productive tillers per plant (0.93), panicle length (0.57), number of filled grains per panicle (0.76), number of spikelets per panicle (0.67), spikelet fertility (0.45), test weight (0.54) and grain length breadth ratio (0.30). Significant negative correlation was found with days to maturity (-0.33) and plant height (-0.48). Whereas, non-significant negative correlation with days to 50 per cent flowering (-0.19) was observed.

4.2.2.5 Number of productive tillers per plant

Number of productive tillers per plant exhibited significant positive correlation with number of tillers per plant (0.93), panicle length (0.62), number of filled grains per panicle (0.70), number of spikelets per panicle (0.62), spikelet fertility (0.49), test weight (0.56) and grain length breadth ratio (0.35). Whereas, with plant height (-0.55) and days to maturity (-0.26) significant negative correlation was found. Non-significant negative correlation was observed with days to 50 per cent flowering (-0.17).

4.2.2.6 Panicle length (cm)

Panicle length had a significant positive correlation with the traits like number of tillers per plant (0.57), number of productive tillers per plant (0.62), number of filled grains per panicle (0.58), number of spikelets per panicle (0.54), spikelet fertility (0.69), test weight (0.59) and grain length and breadth ratio (0.39). Non-significant positive correlation was observed with days to 50 per cent flowering (0.19), days to maturity (0.09). Significant negative correlation was observed with plant height (-0.57).

4.2.2.7 Number of spikelets per panicle

Number of spikelets per panicle exhibited significant positive correlation with number of tillers per plant (0.67), number of productive tillers per plant (0.62), panicle length (0.54), spikelet fertility (0.66), test weight (0.42), grain length breadth ratio (0.31) and number of filled grains per panicle (0.81). Significant negative correlation was seen with days to maturity (-0.28), plant height (-0.23). Non-significant negative correlation was observed with days to 50 per cent flowering (-0.15).

4.2.2.8 Number of filled grains per panicle

Number of filled grains per panicle exhibited significant positive correlation with number of tillers per plant (0.76), number of productive tillers per plant (0.70), panicle length (0.58), spikelet fertility (0.52), test weight (0.47), grain length breadth

ratio (0.25) and number of spikelets per panicle (0.81). Significant negative correlation was seen with days to maturity (-0.25), plant height (-0.30). Non-significant negative correlation was observed with days to 50 per cent flowering (-0.14).

4.2.2.9 Spikelet fertility (%)

Spikelet fertility had significant positive association with number of tillers per plant (0.45), number productive tillers per plant (0.49), panicle length (0.69), number of filled grains per panicle (0.52), number of spikelets per panicle (0.66), length and breadth ratio (0.42) and test weight (0.48). A non-significant positive association to spikelet fertility was exhibited by days to 50 per cent flowering (0.14). Non-significant negative correlation was observed with days to maturity (-0.06) and plant height (-0.24).

4.2.2.10 Test weight (g)

Test weight exhibited a significant positive correlation with number of tillers per plant (0.54), number of productive tillers per plant (0.56), panicle length (0.59), number of filled grains per panicle (0.47), number of spikelets per panicle (0.42), spikelet fertility (0.48) and grain length and breadth ratio (0.37). Whereas, a positive non-significant correlation was found with days to 50 per cent flowering (0.18), days to maturity (0.07). Significant negative correlation was seen with plant height (-0.35).

4.2.2.11 Length breadth ratio

Significant positive association with length breadth ratio was shown by days to 50 per cent flowering (0.26), number of tillers per plant (0.30), number of productive tillers per plant (0.35), panicle length (0.39), number of filled grains per panicle (0.25), number of spikelets per panicle (0.31), spikelet fertility (0.42) and test weight (0.37). A non-significant positive correlation was exhibited by days to maturity (0.11). Whereas, negative non-significant association was observed for plant height (-0.14).

4.3 Genetic divergence among advanced breeding lines for grain yield and its attributing traits

For assessing the genetic diversity in a large number of genotypes, D^2 statistics is useful which detects genetically divergent parents so they can be effectively utilized in hybridization programmes. Thirty two advanced breeding lines of rice and five checks were subjected to the Mahalanobis' D^2 analysis in the current investigation.

4.3.1 Clustering pattern of advanced breeding lines

Six clusters from 37 genotypes were obtained based on the D^2 statistics. The lines were formed into groups in such a way that within each cluster D^2 statistics value was smaller than those between the clusters. Table 4.3.1 represents the clustering patterns of all the 37 genotypes.

Table 4.3.1 Clustering pattern of advanced breeding lines based on D² values

Cluster No.	No. of genotypes	Genotypes
I	15	R×K-1-4-3, R×K-1-4-4, R×K-7-2-2, R×K-1-4-5, R×K-5-2-4, R×K-1-4-7, R×K-7-2-5, R×K-14-2-8, R×K-1-4-12, R×K-7-2-11, R×K-2-2-14, R×K-7-2-12, R×K-4-2-13, R×K-3-2-14, R×K-1-4-17
II	11	R×K-1-4-8, R×K-12-2-6, R×K-1-4-9, R×K-7-2-7, R×K-1-6-10, R×K-7-2-9, R×K-8-2-10, R×K-1-4-13, R×K-1-4-15, R×K-1-4-16, R×K-7-2-16
III	3	RNR-15048 (Check), BPT-5204 (Check), JGL-1798 (Check)
IV	4	R×K-4-4-11, R×K-6-2-15, R×K-1-4-18, KHP 11 (Check)
V	3	R×K-7-2-1, R×K-8-2-3, R×K-1-4-6
VI	1	KPR-1 (Check)

The clustering pattern obtained revealed that the biggest cluster formed was cluster I, which had fifteen lines within it. This was followed by cluster II with eleven lines present in the cluster; cluster III and cluster V was found to have three lines each and cluster IV had four lines. Cluster VI is the smallest one with one advanced breeding line.

4.3.2 Intra and inter clusters distance

The distance for the advanced breeding lines were assessed within the cluster and also between the two clusters.

As presented in Table 4.3.2, Cluster IV exhibited maximum intra cluster distance of 45.67 when compared with all the six clusters, which was followed by cluster V (37.92), cluster III (24.13), cluster II (15.96) and cluster I (13.35). The inter cluster distance was exhibited the highest between cluster IV and cluster VI (295.41), followed by cluster II and cluster VI (181.43), indicating that the genotypes within these clusters are highly diverse. The lowest inter cluster distance was between cluster I and cluster V (22.60), followed by cluster I and cluster III (42.40), indicating that the traits within the clusters were less diverse.

4.3.3 Cluster means analysis

Cluster means were calculated using Tocher's method, for all the 12 yield and its attributing traits. Cluster means recorded for yield and yield related traits from six clusters are presented in Table 4.3.3.

4.3.3.1 Days to 50 per cent flowering

Days to 50 per cent flowering was found to have the highest cluster mean value of 124.88 for cluster IV followed by cluster II (120.18). Lowest value of cluster mean was recorded for cluster VI (103.00) followed by cluster III (110.17).

4.3.3.2 Days to maturity

The cluster mean value was maximum for days to maturity for cluster IV (154.63) followed by cluster II (150.14). The cluster mean value was minimum for cluster VI (133.00) followed by cluster III (141.00).

4.3.3.3 Plant height (cm)

Plant height exhibited the maximum cluster mean value of 141.13 for cluster IV followed by cluster I (139.62). Whereas, the lowest cluster mean value was observed for cluster V (129.67) followed by cluster III (131.30).

4.3.3.4 Number of tillers per plant

The number of tillers per plant exhibited the highest cluster mean value in cluster III (20.77), followed by cluster VI (19.90) and the lowest cluster mean value was found for cluster I (15.63), followed by cluster V (15.83).

Table 4.3.2 Inter and intra cluster distance for yield and its component characters in advanced breeding lines

Clusters	I	II	III	IV	V	VI
I	13.35	45.65	42.40	121.35	22.60	85.15
II		15.96	78.34	46.76	48.12	181.43
III			24.13	148.62	58.25	46.42
IV				45.67	123.79	295.41
V					37.92	109.12
VI						0.00

- Diagonal values indicate intra cluster distances
- Above diagonal values indicate inter cluster distances

Table 4.3.3. Cluster means for yield and its component characters in advanced breeding lines

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
I	112.07	143.00	139.62	15.63	15.25	18.84	227.27	214.59	86.40	20.56	3.18	31.16
II	120.18	150.14	137.80	16.56	16.50	21.62	236.98	223.86	89.53	21.03	3.46	34.09
III	110.17	141.00	131.30	20.77	20.77	22.30	339.83	312.17	94.77	23.05	3.79	40.77
IV	124.88	154.63	141.13	17.17	17.04	21.40	292.69	254.33	89.16	22.64	3.42	34.28
V	112.17	145.00	129.67	15.83	15.68	22.11	213.47	207.33	85.50	20.60	3.19	31.70
VI	103.00	133.00	139.00	19.90	19.90	22.65	336.00	316.50	94.56	18.50	2.99	41.00

Where,

X ₁ - Days to 50 per cent flowering	X ₉ - Spikelet fertility (%)
X ₂ - Days to maturity	X ₁₀ - Test weight (g)
X ₃ - Plant height (cm)	X ₁₁ - Length breadth ratio
X ₄ - Number of tillers per plant	X ₁₂ - Grain yield per plant (g)

4.3.3.5 Number of productive tillers per plant

Maximum cluster mean value was found for the number of productive tillers per plant in cluster III (20.77) followed by cluster VI (19.90). Whereas, mean cluster value was the lowest for cluster I (15.25) followed by cluster V (15.68).

4.3.3.6. Panicle length (cm)

Panicle length exhibited the highest cluster mean value of 22.65 cm by the cluster VI followed by cluster III (22.30 cm). Cluster I (18.84 cm) followed by cluster IV (21.40 cm) exhibited the lowest cluster mean value.

4.3.3.7 Number of spikelets per panicle

The highest cluster mean value of 339.83 was recorded for the trait number of spikelets per panicle in cluster III followed by cluster VI (336.00). However, cluster mean value was the lowest for cluster V (213.47) followed by cluster I (227.27).

4.3.3.8 Number of filled grains per panicle

Number of filled grains per panicle exhibited the highest cluster mean value of 316.50 by cluster VI followed by cluster III (312.17). Also, the lowest cluster mean was observed for cluster V (207.33) followed by cluster I (214.59).

4.3.3.9 Spikelet fertility (%)

The maximum cluster mean value for spikelet fertility was exhibited by cluster III (94.77) followed by cluster VI (94.56). The lowest cluster mean value was observed for cluster V (85.50) followed by cluster I (86.40).

4.3.3.10 Test weight (g)

Test weight exhibited the highest cluster mean value of 23.05 g in cluster III, followed by cluster IV (22.64 g). Whereas, the lowest cluster mean value was seen in the cluster VI (18.50 g) followed by cluster I (20.56 g).

4.3.3.11 Length breadth ratio

Length breadth ratio recorded the highest cluster mean value for cluster III (3.79) followed by cluster II (3.46). However, the lowest cluster mean value was recorded by cluster VI (2.99) followed by cluster I (3.18).

4.3.3.12 Grain yield per plant (g)

Grain yield recorded the highest cluster mean value in cluster VI (41.00 g) followed by cluster III (40.77 g). Cluster mean value was observed to be the lowest for cluster I (31.16 g), followed by cluster V (31.70 g).

4.3.4 Contribution of different characters towards divergence

Contribution of the traits studied towards genetic divergence in percentage was recorded and represented in Table 4.3.4.

Among all the characters studied for yield and its attributing traits percentage contribution to total divergence was differed in different traits, days to 50 per cent flowering (41.8%) contributed the highest for diversity among the advanced breeding lines followed by number of filled grains per panicle (11.7%), days to maturity (10.3%), number of productive tillers per plant (8.4 %), number of spikelets per panicle (5.9 %), grain yield per plant (5.6 %), spikelet fertility (4.3%), grain length and breadth ratio (4.1%), panicle length (3.2%), plant height (3.0%), test weight (1.6%) and number of tillers per plant (0.2%).

4.4 Screening of advanced breeding lines of rice for submergence tolerance

Thirty two advanced breeding lines along with two susceptible local checks Jyothi, BPT-5204, and two tolerant national checks, FR13A and Swarna sub-1 were evaluated for survival percentage under submerged conditions. Evaluation was done by taking observation of number of plants survived 14 days after de-submergence and scored from 1 to 9 according to the Standard Evaluation Method recommended by International Rice Research Institute (IRRI), Philippines which is presented in Table 4.4.1 and Table 4.4.2.

The range of survival percentage among the evaluated advanced breeding lines of rice was from 5.56 to 96.00 per cent. None of the rice genotypes had 100 per cent survival with a score of 1, whereas the check Swarna sub-1 recorded the highest survival rate of 96.00 per cent with a score of 3. FR13A (85.00%) with a score of 5 followed by two lines scored 7 with survival percentage range of 50-74 per cent which includes R×K-1-4-5 (50.00%), R×K-1-4-17 (50.00%) and 32 genotypes scored 9 with survival percentage ranging from 0 to 49 which includes lines R×K-1-4-3, R×K-7-2-1, R×K-1-4-4, R×K-7-2-2, R×K-8-2-3, R×K-1-4-6, R×K-5-2-4, R×K-1-4-7, R×K-7-2-5, R×K-1-4-8, R×K-12-2-6, R×K-1-4-9, R×K-7-2-7, R×K-1-6-10, R×K-14-2-8, R×K-4-4-11, R×K-7-2-9, R×K-1-4-12, R×K-8-2-10, R×K-1-4-13, R×K-7-2-11, R×K-2-2-14, R×K-7-2-12, R×K-1-4-15, R×K-4-2-13, R×K-1-4-16, R×K-3-2-14, R×K-6-2-15, R×K-1-4-18, R×K-7-2-16, Jyothi and BPT-5204.

Among the national checks Swarna sub-1 had highest survival percentage of 96.00 per cent and FR13A had survival percentage of 85.00 per cent and checks Jyothi and BPT-5204 showed the survival percentage 30 per cent and 22.22 per cent respectively.

Out of 36 genotypes evaluated, most of the genotypes (32) scored 9 with survival per cent ranging from 0-49%. Highest survival percentage of 96.00 per cent

Table 4.3.4 Contribution of different traits towards total divergence

Sl No.	Character	Contribution %
1	Days to 50 per cent flowering	41.8
2	Number of filled grains per panicle	11.7
3	Days to maturity	10.3
4	Number of productive tillers per plant	8.4
5	Number of spikelets per panicle	5.9
6	Grain yield per plant (g)	5.6
7	Spikelet fertility (%)	4.3
8	Length breadth ratio	4.1
9	Others	8

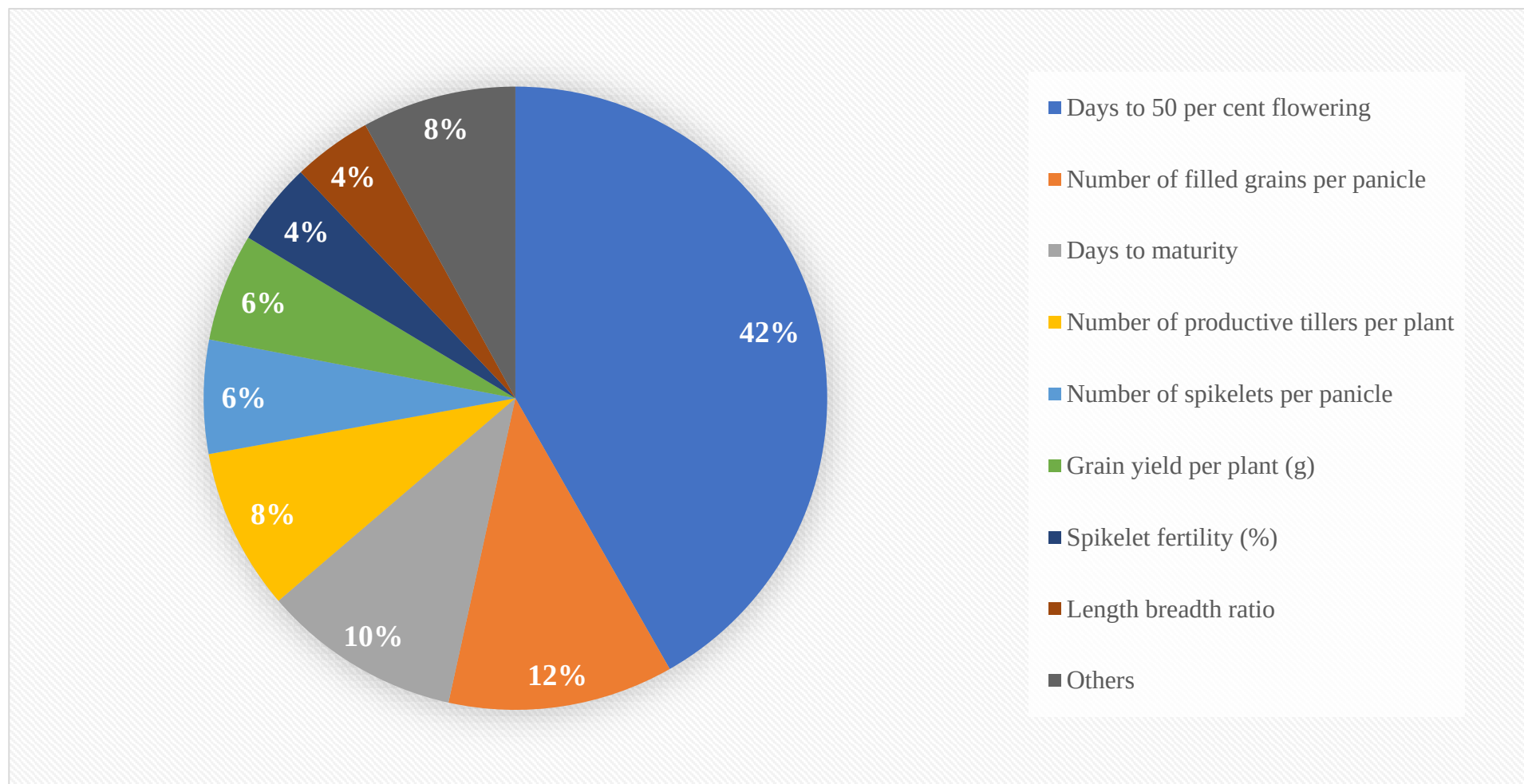


Fig 1: Per cent contribution of different traits towards total divergence

Table 4.4.1 List of advanced breeding lines of rice taken for the experiment with their respective survival percentage and IRRI Standard Evaluation System score

Line no.	Genotype	Survival percentage (%)	Score
1	R×K-1-4-3	11.11	9
2	R×K-7-2-1	22.22	9
3	R×K-1-4-4	11.11	9
4	R×K-7-2-2	22.22	9
5	R×K-1-4-5	50.00	7
6	R×K-8-2-3	16.67	9
7	R×K-1-4-6	11.11	9
8	R×K-5-2-4	16.67	9
9	R×K-1-4-7	11.11	9
10	R×K-7-2-5	5.56	9
11	R×K-1-4-8	11.11	9
12	R×K-12-2-6	5.56	9
13	R×K-1-4-9	5.56	9
14	R×K-7-2-7	5.56	9
15	R×K-1-6-10	27.78	9
16	R×K-14-2-8	22.22	9
17	R×K-4-4-11	5.56	9
18	R×K-7-2-9	11.11	9
19	R×K-1-4-12	11.11	9
20	R×K-8-2-10	27.78	9
21	R×K-1-4-13	5.56	9
22	R×K-7-2-11	22.22	9
23	R×K-2-2-14	11.11	9
24	R×K-7-2-12	27.78	9
25	R×K-1-4-15	5.56	9
26	R×K-4-2-13	27.78	9
27	R×K-1-4-16	5.56	9
28	R×K-3-2-14	11.11	9
29	R×K-1-4-17	50.00	7
30	R×K-6-2-15	16.67	9
31	R×K-1-4-18	5.56	9
32	R×K-7-2-16	5.56	9
33	Jyothi	30.00	9
34	BPT-5204	22.22	9
35	FR13A	85.00	5
36	Swarna sub-1	96.00	3

Table 4.4.2 Classification of advanced breeding lines of rice based on survival percentage under submergence based on IRRI Standard Evaluation System

Survival percentage	No. of genotypes	Genotypes
100%	0	Nil
95-99%	1	Swarna sub-1
75-94%	1	FR13A
50-74%	2	R×K-1-4-5, R×K-1-4-17
0-49%	32	R×K-1-4-3, R×K-7-2-1, R×K-1-4-4, R×K-7-2-2, R×K-8-2-3, R×K-1-4-6, R×K-5-2-4, R×K-1-4-7, R×K-7-2-5, R×K-1-4-8, R×K-12-2-6, R×K-1-4-9, R×K-7-2-7, R×K-1-6-10, R×K-14-2-8, R×K-4-4-11, R×K-7-2-9, R×K-1-4-12, R×K-8-2-10, R×K-1-4-13, R×K-7-2-11, R×K-2-2-14, R×K-7-2-12, R×K-1-4-15, R×K-4-2-13, R×K-1-4-16, R×K-3-2-14, R×K-6-2-15, R×K-1-4-18, R×K-7-2-16, Jyothi, BPT-5204

was reported by national check variety Swarna sub-1. Among advanced breeding lines R×K-1-4-5, R×K-1-4-17 scored 7 with highest survival per cent of 50.00. The lowest survival percentage of 30 per cent was observed in check Jyothi and 22.22 per cent for check BPT-5204 with score 9. Among advanced breeding lines R×K-1-4-9, R×K-7-2-5, R×K-12-2-6, R×K-7-2-7, R×K-4-4-11, R×K-1-4-13, R×K-1-4-15, R×K-1-4-16, R×K-1-4-18, R×K-7-2-16 exhibited the lowest survival percentage of 5.56 per cent, lines R×K-1-4-3, R×K-1-4-4, R×K-1-4-6, R×K-1-4-7, R×K-1-4-8, R×K-7-2-9, R×K-1-4-12, R×K-2-2-14, R×K-3-2-14 had survival percentage of 11.11 per cent, lines R×K-8-2-3, R×K-5-2-4, R×K-6-2-15 showed survival percentage of 16.67 per cent, lines R×K-7-2-1, R×K-7-2-2, R×K-14-2-8, R×K-7-2-11 had survival percentage of 22.22 per cent, lines R×K-1-6-10, R×K-8-2-10, R×K-7-2-12, R×K-4-2-13 exhibited survival percentage of 27.78 % with score of 9. List of the genotypes evaluated for submergence, their survival percentage are presented in Table 4.4.1 and Table 4.4.2 respectively.

4.5 Morphological and physiological characterization of advanced breeding lines of rice for submergence tolerance

4.5.1 Genetic variability studies for physiological parameters

Among 32 advanced breeding lines of rice and four checks, stem elongation percentage and survival percentage were studied under submerged conditions and were subjected to variability analysis. A wide range of variability with a wide genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense), and genetic advance as per cent mean (GAM) was reported for these parameters presented in Table 4.5.1.

4.5.1.1 Survival percentage

The survival percentage exhibited a mean value of 27.34 per cent with a range of 5.56 per cent to 95.00 per cent. High GCV (55.94) and PCV (58.85) along with high heritability (90.37) was shown by survival percentage coupled with high genetic advance as per cent mean (109.55).

4.5.1.2 Stem elongation (%)

The mean stem elongation of 34.05 per cent with a range from 12.38 to 55.88 per cent was obtained. High GCV (28.99) and PCV (31.09) were recorded for stem elongation per cent. High heritability of 86.89 per cent for stem elongation was seen with high genetic advance as per cent mean value of 55.66.

4.6 Phenotypic correlation studies among morphological and physiological characters with grain yield

The phenotypic correlation studies of physiological traits like stem elongation percentage and survival percentage with grain yield per plant (g) were studied as a dependent trait and the details are presented in the Table 4.6.1.

Table 4.5.1 Genetic variability parameters for morphological and physiological traits in advanced breeding lines of rice under submergence

Sl No.	Characters	Mean	Range		PCV (%)	GCV (%)	h ² (bs) (%)	GAM (%)
			Min	Max				
1	Survival percentage	27.34	5.56	96.00	58.85	55.94	90.37	109.55
2	Stem elongation (%)	34.05	12.38	55.88	31.09	28.99	86.89	55.66

Where,

GCV = Genotypic coefficient of variation

PCV = Phenotypic coefficient of variation

h² (bs) = Heritability (broad sense)

GAM = Genetic advance as per cent mean

Table 4.6.1 Phenotypic correlation of grain yield with morphological and physiological traits in advanced breeding lines of rice under submergence

	Survival percentage	Stem elongation (%)	Grain yield per plant
Survival percentage	1	-0.26*	0.54**
Stem elongation (%)		1	-0.36**
Grain yield per plant			1

* **, Significant at 5% and 1% respectively.

4.6.1 Survival percentage

Survival percentage under stress condition showed a significant positive correlation with grain yield per plant (0.54) and a significant negative correlation was seen with stem elongation percentage (-0.26).

4.6.2 Stem elongation (%)

Significant negative correlation was exhibited by stem elongation percentage with survival percentage (-0.26) and grain yield per plant (-0.36).

4.7 Per cent difference of various traits between submergence and non submergence condition

4.7.1 Per cent difference of various traits

Among the morphological traits studied between submergence and non submergence of the same genotype, there was a change in per cent mean observed for four traits. The per cent difference for four traits between submergence and non submergence condition revealed that days to 50 per cent flowering showed an increased number of days for flowering in submerged condition than non submergence, while the rest of the traits (number of tillers per plant, the number of productive tillers per plant and test weight) exhibited decreased mean value under submergence stress than under non submergence condition. The comparison is represented through Table 4.7.1.

4.7.1.1 Days to 50 per cent flowering

The per cent difference in days to 50 per cent flowering among 32 advanced breeding lines was found to be the highest for R×K-1-4-12 (22.32%), followed by R×K-1-4-5 (18.06%) and the difference was found to be minimum for R×K-1-4-15 (3.70%) followed by R×K-7-2-16 (5.57%).

4.7.1.2 Number of tillers per plant

Maximum per cent difference to number of tillers by advanced breeding lines of rice on comparing under submergence with non submergence was found to be R×K-1-4-7 (53.90%) followed by R×K-8-2-3 (53.36%) while the minimum difference was exhibited by R×K-7-2-16 (6.60%) followed by R×K-14-2-8 (7.43%). Number of tillers per plant obtained was decreased under submergence condition than under non submergence condition due to stress impact.

4.7.1.3 Number of productive tillers per plant

Number of productive tillers per plant exhibited the highest per cent difference of 54.58% by R×K-1-4-7 followed by 53.36% of R×K-8-2-3. Whereas, minimum per cent difference was seen in R×K-14-2-8 (11.49%) followed by R×K-1-4-9 (11.76%). Number of productive tillers obtained was reduced under submergence condition than under non submergence condition due to stress impact.

Table 4.7.1 a. Estimates of per cent difference for days to 50 per cent flowering under submergence and non submergence condition

Sl No.	Genotypes	Days to 50 per cent flowering		
		Submergence	Non submergence	Change in % mean
1	R×K-1-4-3	126.00	110.50	14.03
2	R×K-7-2-1	128.00	114.00	12.28
3	R×K-1-4-4	131.00	115.00	13.91
4	R×K-7-2-2	123.00	116.00	6.03
5	R×K-1-4-5	134.00	113.50	18.06
6	R×K-8-2-3	129.00	121.50	6.17
7	R×K-1-4-6	133.00	122.50	8.57
8	R×K-5-2-4	131.00	123.00	6.50
9	R×K-1-4-7	129.00	111.50	15.70
10	R×K-7-2-5	129.00	114.50	12.66
11	R×K-1-4-8	135.00	120.50	12.03
12	R×K-12-2-6	132.00	119.50	10.46
13	R×K-1-4-9	140.00	123.50	13.36
14	R×K-7-2-7	137.00	122.00	12.30
15	R×K-1-6-10	128.00	117.00	9.40
16	R×K-14-2-8	130.00	113.50	14.54
17	R×K-4-4-11	141.00	129.00	9.30
18	R×K-7-2-9	132.00	119.50	10.46
19	R×K-1-4-12	137.00	112.00	22.32
20	R×K-8-2-10	128.50	120.50	6.64
21	R×K-1-4-13	134.00	117.50	14.04
22	R×K-7-2-11	136.50	116.00	17.67
23	R×K-2-2-14	128.00	115.50	10.82
24	R×K-7-2-12	123.00	114.00	7.89
25	R×K-1-4-15	126.00	121.50	3.70
26	R×K-4-2-13	127.00	112.00	13.39
27	R×K-1-4-16	137.00	121.50	12.76
28	R×K-3-2-14	124.00	112.50	10.22
29	R×K-1-4-17	125.00	109.50	14.16
30	R×K-6-2-15	141.00	125.50	12.35
31	R×K-1-4-18	137.00	120.50	13.69
32	R×K-7-2-16	127.00	120.30	5.57
33	Mean	131.22	117.67	11.59
34	BPT-5204 (Check)	127.00	111.50	12.20

Table 4.7.1 b. Estimates of per cent difference for number of tillers per plant under submergence and non submergence condition

Sl No.	Genotypes	Number of tillers per plant		
		Submergence	Non submergence	Change in % mean
1	R×K-1-4-3	9.00	13.75	34.55
2	R×K-7-2-1	10.00	13.90	28.06
3	R×K-1-4-4	9.00	13.50	33.33
4	R×K-7-2-2	8.30	13.40	38.06
5	R×K-1-4-5	9.30	15.60	40.38
6	R×K-8-2-3	5.90	12.65	53.36
7	R×K-1-4-6	7.80	12.45	37.35
8	R×K-5-2-4	8.80	13.75	36.00
9	R×K-1-4-7	6.80	14.75	53.90
10	R×K-7-2-5	6.80	13.85	50.90
11	R×K-1-4-8	9.30	15.80	41.14
12	R×K-12-2-6	7.40	15.65	52.72
13	R×K-1-4-9	12.10	13.60	11.03
14	R×K-7-2-7	8.50	14.60	41.78
15	R×K-1-6-10	8.50	11.58	26.57
16	R×K-14-2-8	13.70	14.80	7.43
17	R×K-4-4-11	9.20	12.50	26.40
18	R×K-7-2-9	10.50	13.25	20.75
19	R×K-1-4-12	9.70	17.05	43.11
20	R×K-8-2-10	7.60	9.85	22.84
21	R×K-1-4-13	10.90	14.70	25.85
22	R×K-7-2-11	10.10	13.10	22.90
23	R×K-2-2-14	10.10	13.20	23.48
24	R×K-7-2-12	11.00	16.70	34.13
25	R×K-1-4-15	10.80	15.60	30.77
26	R×K-4-2-13	14.30	16.35	12.54
27	R×K-1-4-16	12.70	15.20	16.45
28	R×K-3-2-14	9.90	17.05	41.94
29	R×K-1-4-17	11.40	13.66	16.54
30	R×K-6-2-15	11.30	14.67	22.96
31	R×K-1-4-18	9.80	13.80	28.99
32	R×K-7-2-16	10.80	17.40	6.60
33	Mean	9.73	14.30	30.71
34	BPT-5204 (Check)	8.80	17.90	50.83

Table 4.7.1 c. Estimates of per cent difference for number of productive tillers per plant under submergence and non submergence condition

Sl No.	Genotypes	Number of productive tillers per plant		
		Submergence	Non submergence	Change in % mean
1	R×K-1-4-3	9.00	13.60	33.82
2	R×K-7-2-1	10.00	13.90	28.06
3	R×K-1-4-4	9.00	13.50	33.33
4	R×K-7-2-2	8.20	13.40	38.81
5	R×K-1-4-5	9.20	15.40	40.26
6	R×K-8-2-3	5.90	12.65	53.36
7	R×K-1-4-6	7.80	12.30	36.59
8	R×K-5-2-4	8.80	13.75	36.00
9	R×K-1-4-7	6.70	14.75	54.58
10	R×K-7-2-5	6.80	13.85	50.90
11	R×K-1-4-8	9.20	15.55	40.84
12	R×K-12-2-6	7.30	15.65	53.35
13	R×K-1-4-9	12.00	13.60	11.76
14	R×K-7-2-7	8.50	14.60	41.78
15	R×K-1-6-10	8.40	11.58	27.43
16	R×K-14-2-8	13.10	14.80	11.49
17	R×K-4-4-11	9.20	12.50	26.40
18	R×K-7-2-9	10.50	13.25	20.75
19	R×K-1-4-12	9.70	17.05	43.11
20	R×K-8-2-10	7.60	12.10	37.19
21	R×K-1-4-13	10.80	14.20	23.94
22	R×K-7-2-11	10.10	13.10	22.90
23	R×K-2-2-14	10.00	13.20	24.24
24	R×K-7-2-12	11.00	16.70	34.13
25	R×K-1-4-15	10.80	15.60	30.77
26	R×K-4-2-13	14.20	16.35	13.15
27	R×K-1-4-16	12.70	15.20	16.45
28	R×K-3-2-14	9.90	17.05	41.94
29	R×K-1-4-17	10.80	13.10	17.62
30	R×K-6-2-15	11.30	14.66	22.96
31	R×K-1-4-18	9.80	13.80	28.99
32	R×K-7-2-16	10.80	17.30	37.57
33	Mean	9.66	14.31	32.33
34	BPT-5204 (Check)	8.80	17.35	49.27

Table 4.7.1 d. Estimates of per cent difference for test weight (g) under submergence and non submergence condition

Sl No.	Genotypes	Test weight (g)		
		Submergence	Non submergence	Change in % mean
1	R×K-1-4-3	17.90	21.50	16.74
2	R×K-7-2-1	17.70	20.00	11.50
3	R×K-1-4-4	17.40	18.50	5.95
4	R×K-7-2-2	15.20	20.90	27.27
5	R×K-1-4-5	19.75	23.20	14.87
6	R×K-8-2-3	19.10	21.20	9.91
7	R×K-1-4-6	17.90	20.05	10.72
8	R×K-5-2-4	13.80	21.00	34.29
9	R×K-1-4-7	16.50	19.80	16.67
10	R×K-7-2-5	15.50	20.45	24.21
11	R×K-1-4-8	19.40	21.15	8.27
12	R×K-12-2-6	18.70	19.05	1.84
13	R×K-1-4-9	19.00	21.75	12.64
14	R×K-7-2-7	17.40	19.00	8.42
15	R×K-1-6-10	20.50	23.00	10.87
16	R×K-14-2-8	15.60	19.55	20.20
17	R×K-4-4-11	18.70	21.70	13.82
18	R×K-7-2-9	20.90	23.55	11.25
19	R×K-1-4-12	17.60	21.00	16.19
20	R×K-8-2-10	17.80	22.20	19.82
21	R×K-1-4-13	19.80	21.90	9.59
22	R×K-7-2-11	16.90	21.00	19.52
23	R×K-2-2-14	18.00	21.70	17.05
24	R×K-7-2-12	18.80	22.35	15.88
25	R×K-1-4-15	20.60	23.50	12.34
26	R×K-4-2-13	19.70	20.56	4.18
27	R×K-1-4-16	15.50	18.85	17.77
28	R×K-3-2-14	18.70	22.93	18.45
29	R×K-1-4-17	19.60	22.70	13.66
30	R×K-6-2-15	19.80	24.10	17.84
31	R×K-1-4-18	17.40	21.25	18.12
32	R×K-7-2-16	17.20	18.65	7.78
33	Mean	18.07	21.19	14.61
34	BPT-5204 (Check)	17.70	24.90	28.90

Table 4.7.1 e. Estimates of per cent difference for grain yield per plant (g) under submergence and non submergence condition

Sl. No.	Genotypes	Grain yield per plant		
		Submergence	Control	Change in %
1	R×K-1-4-3	20.75	31.80	34.75
2	R×K-7-2-1	22.50	33.60	33.04
3	R×K-1-4-4	23.00	33.00	30.30
4	R×K-7-2-2	13.20	29.90	55.85
5	R×K-1-4-5	25.70	32.00	19.69
6	R×K-8-2-3	21.70	32.50	33.23
7	R×K-1-4-6	23.40	36.00	35.00
8	R×K-5-2-4	21.90	34.30	36.15
9	R×K-1-4-7	20.80	34.25	39.27
10	R×K-7-2-5	24.00	35.50	32.39
11	R×K-1-4-8	21.40	41.85	48.66
12	R×K-12-2-6	25.80	33.90	23.89
13	R×K-1-4-9	24.60	31.20	21.15
14	R×K-7-2-7	18.40	32.60	43.56
15	R×K-1-6-10	20.60	33.30	38.14
16	R×K-14-2-8	21.00	29.20	28.08
17	R×K-4-4-11	29.85	35.00	14.71
18	R×K-7-2-9	22.78	30.45	25.19
19	R×K-1-4-12	17.10	21.20	23.81
20	R×K-8-2-10	18.90	36.70	48.50
21	R×K-1-4-13	29.86	38.80	23.04
22	R×K-7-2-11	23.50	31.70	25.87
23	R×K-2-2-14	20.60	37.00	44.32
24	R×K-7-2-12	24.20	33.30	27.33
25	R×K-1-4-15	23.89	31.30	23.67
26	R×K-4-2-13	27.80	38.45	27.70
27	R×K-1-4-16	25.45	36.95	31.12
28	R×K-3-2-14	24.05	33.30	27.78
29	R×K-1-4-17	30.50	35.80	14.80
30	R×K-6-2-15	22.00	42.10	46.60
31	R×K-1-4-18	24.20	40.00	39.50
32	R×K-7-2-16	22.29	31.20	28.56
33	Mean	22.99	34.00	32.05
34	BPT-520 (Check)	23.75	40.60	41.50

4.7.1.4 Test weight (g)

Test weight per cent difference was found to be the lowest in R×K-12-2-6 (1.84%) followed by R×K-4-2-13 (4.18%). The highest per cent difference was found in R×K-5-2-4 (34.29%) followed by R×K-7-2-2 (27.27%). Test weight showed mean reduction under stress condition than under non submergence.

4.7.1.5 Grain yield per plant (g)

Grain yield per plant was found to exhibit a large per cent difference under submergence compared to control. Maximum per cent difference was in R×K-7-2-2 (55.85%) followed by R×K-1-4-8 (48.66%). Whereas, the lowest per cent difference was observed in R×K-4-4-11 (14.71%) followed by R×K-1-4-17 (14.80%). Grain yield obtained will be decreased under submergence condition than under control condition commonly.

DISCUSSION

V DISCUSSION

Rice is an important cereal crop and more than half of the world's population consumes rice as a staple food. It is a primary source of income in many Asian nations. Crop improvement programmes have improved a number of rice cultivars to fulfil human requirements for higher yield potential, tolerance to stresses, improved quality and elevated nutritional content. Even though above mentioned improvements had incredible influence on rice production in the recent past, exponential population expansion and the loss in arable land available for the crop to expand on account of global warming cause demand for the rice crop to outpace its present production. It is unexpected to grow rice during the monsoon season and produce it under abiotic pressures such as seasonal flash flooding, which is most common, especially in South and Southeast Asia.

The National Rice Research Institute, Cuttack has discovered that the landrace FR13A, also known as "Dhalaputia" in Orissa, India, is a real submergence-tolerant genotype. This land race has been used to undertake considerable research on various submergence tolerance mechanisms. Similar activities have been carried out in the current investigation of screening of advanced breeding lines of rice for submergence tolerance. To screen for submergence tolerance, advanced breeding lines of rice should undergo phenotypic evaluation under water for at least 14 days or more, at a depth of 50 to 60 cm. Based on the information about the degree of variability and the character association present between them, the screened material mentioned above can be used further.

In the current experiment, 32 advanced breeding lines of rice along with four checks were further examined for morphological and physiological analyses after being evaluated for submergence tolerance along with four checks. And furthermore, genetic studies on variability and diversity, correlation analyses of various yield and yield related traits were also investigated with 32 advanced breeding lines and five checks.

The experimental results obtained are discussed under the following sub-headings

- 5.1 Genetic variability study among advanced breeding lines of rice for grain yield and its attributing traits
- 5.2 Phenotypic correlation analysis for grain yield and its attributing traits
- 5.3 Genetic divergence among advanced breeding lines for grain yield and its attributing traits
- 5.4 Screening of advanced breeding lines of rice for submergence tolerance
- 5.5 Morphological and physiological characterization of advanced breeding lines of rice for submergence tolerance

5.6 Phenotypic correlation studies among morphological and physiological characters with grain yield

5.7 Per cent difference of various traits between submergence and non submergence condition

5.1 Genetic variability study among advanced breeding lines of rice for grain yield and its attributing traits

One of the key targets of the rice breeding programme is yield improvement. For genetic improvement, it is crucial to have a thorough understanding of the types and degrees of genetic variation that affect quantitative heritable traits like yield and their corresponding attributes. Variability in the population is essential for any breeding programme and is vital for crop improvement for any desired character. Accordingly, determining level of diversity in the gene pool is perhaps the most crucial stage in every breeding effort. Critical evaluation of genetic variability measures including genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as a per cent of mean are prerequisites for any crop improvement effort in plant breeding.

5.1.1 Analysis of Variance for grain yield and its attributing characters

Significant difference was recorded among the advanced breeding lines for various traits that were genetically diverse and hence selection will be effective. Parallel results were quoted by Edukondalu *et al.* (2017), Manjunatha and Kumara (2019) and Katkani *et al.* (2023).

5.1.2 Genetic variability parameters for grain yield and yield attributing characters

In the current investigation, phenotypic and genotypic coefficients of variation were recorded low for days to 50 per cent flowering and days to maturity. Similar findings were reported for both the traits by Edukondalu *et al.* (2017), Gour *et al.* (2017), Tiwari *et al.* (2019) and Katkani *et al.* (2023). Sumanth *et al.* (2017) obtained similar results for days to 50 per cent flowering and on par results were obtained for days to maturity by Prasad *et al.* (2017). Occurrence of low estimate value of phenotypic and genotypic coefficients of variation indicates that selection of these characters for crop improvement program will be inappropriate.

Spikelet fertility was found to have low genotypic and phenotypic coefficient of variation. The results obtained were parallel to the findings of Sravan *et al.* (2012), Nath and Kole (2021) and Niharika *et al.* (2022). Panicle length exhibited moderate PCV similar to the outcomes of Dhanwani *et al.* (2013) and Sandeep *et al.* (2018), low GCV in accordance with Singh *et al.* (2021) and Katkani *et al.* (2023).

PCV and GCV obtained was moderate for plant height. The findings for plant height were in accordance with Edukondalu *et al.* (2017), Gour *et al.* (2017), Chamar *et al.* (2021) and Katkani *et al.* (2023).

Number of tillers per plant and number of productive tillers per plant were found to exhibit moderate PCV and GCV value and similar results were reported by Dhanwani *et al.* (2013), Devi *et al.* (2016), Srujana *et al.* (2017), Sumanth *et al.* (2017), Singh *et al.* (2021) and Katkani *et al.* (2023). Moderate estimates of GCV and PCV indicate that there is reasonable scope for enhancing crop yield through selection of these traits.

Grain length and breadth ratio was found to exhibit low PCV and GCV, similar results were reported by Edukondalu *et al.* (2017) and Bandi *et al.* (2018). Grain yield per plant found to exhibit high PCV in accordance with Edukondalu *et al.* (2017), Ram *et al.* (2017) and Katkani *et al.* (2023). Moderate GCV in accordance with Bandi *et al.* (2018) and Tiwari *et al.* (2019).

Results showed moderate PCV for test weight similar to results obtained from Singh *et al.* (2021) and Katkani *et al.* (2023). Low GCV for test weight were on par with the results Sravan *et al.* (2012).

The traits viz., number of spikelets per panicle and number of filled grains per panicle recorded moderate PCV and GCV. Identical results were observed by Niharika *et al.* (2022) and Katkani *et al.* (2023) for number of filled grains per panicle and number of spikelets per panicle.

For all the characters studied, it was found that the phenotypic coefficients of variation values were more than the corresponding genotypic coefficients of variation. Chamar *et al.* (2021), Singh *et al.* (2021), Niharika *et al.* (2022) and Katkani *et al.* (2023) have reported the higher PCV estimates than GCV estimates for all the characters evaluated. A narrow difference of PCV and GCV was observed indicating that environmental influence is less and genetic factors contribute the most for variability in these characters.

Although information on the variability and its extent present in the advanced breeding lines studied, together with the influence of environment, can be obtained from phenotypic and genotypic coefficients of variation, an appropriate estimate of the extent of inheritance of the traits cannot be furnished. As a result, the heritability of a trait will give plant breeders the chance to decide how much selection pressure needs to be applied in the crop improvement programme for a specific environmental condition. High heritability in the broad sense combined with high genetic advance as a per cent of mean serve as direct selection criteria because they provide estimates of the traits' heritability, which depicts the efficacy of selection in improvement of the characters (Johnson *et al.*, 1955).

5.1.3 Heritability and genetic advance

The measurement of genetic variability passed down from previous generations is called heritability (Lush, 1949). As a direct parameter for selection, heritability in the broad sense combined with high genetic advance as a per cent mean, serve to estimate the index of trait transmissibility. These variables are all primarily controlled by additive gene action, demonstrating the efficacy of selection for the improvement of the attribute (Johnson *et al.*, 1955).

Among the traits studied, high heritability was observed for the traits viz., days to 50 per cent flowering, days to maturity, plant height, number of tillers per plant, number of productive tillers per plant, panicle length, number of filled grains per panicle, number of spikelets per panicle, spikelet fertility, test weight, grain length breadth ratio and grain yield per plant. Similar results of high heritability were obtained by Edukondalu *et al.* (2017), Anyaoha *et al.* (2018) and Bandi *et al.* (2018) for days to 50 per cent flowering, days to maturity, plant height, number of tillers per plant, number of spikelets per panicle, test weight and grain length breadth ratio. Whereas, Edukondalu *et al.* (2017) and Divya *et al.* (2018) explained about high heritability for panicle length and number of productive tillers per panicle. For the trait like for spikelet fertility results were on par with Sravan *et al.* (2012) and Sandeep *et al.* (2018). Similar results of high heritability were obtained by Singh *et al.* (2021) and Katkani *et al.* (2023) for grain yield per plant.

Genetic advance as per cent of mean estimates the measure of genetic gain obtained under selection. Genetic advance as per cent mean was high for the traits viz., plant height, number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle, test weight and grain yield per plant. However, moderate genetic advance as per cent mean was noticed for grain length and breadth ratio and panicle length.

Low GAM was exhibited by the traits, days to 50 per cent flowering, days to maturity and spikelet fertility. Low genetic advance as per cent mean for days to 50 per cent flowering and days to maturity was reported. Similar results were recorded by Tiwari *et al.* (2019), Chamar *et al.* (2021) and Niharika *et al.* (2022). Low genetic advance as per cent mean for spikelet fertility was recorded. Results were recorded on par with Tiwari *et al.* (2019).

Moderate GAM for panicle length and grain length and breadth ratio were obtained. The results were similar to results obtained by Prasad *et al.* (2017), Chamar *et al.* (2021) and Katkani *et al.* (2023).

High GAM for plant height, number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle,

test weight and grain yield per plant was found to be in accordance with results obtained by Edukondalu *et al.* (2017), Prasad *et al.* (2017) and Katkani *et al.* (2023). Nandan *et al.* (2010) obtained similar results for number of spikelets per panicle, number of filled grains per panicle and test weight. Results of Divya *et al.* (2018) were on par for grain yield, days to 50 per cent flowering and plant height; Nath and Kole (2021) for plant height, test weight and number of filled grains per panicle. Biswajit *et al.* (2017) reported on par results for number of spikelets per panicle, plant height, test weight and grain yield per plant.

In current investigation, traits viz., plant height, number of tillers per plant, number of productive tillers per plant, number of grains per panicle, number of filled grains per panicle, test weight and grain yield per plant exhibited high genetic advance as per cent mean coupled with high heritability along with moderate to high GCV and PCV value indicating that, due to additive gene action the heritability is exhibited which can be employed in crop improvement program and can implement effective selection process.

5.2 Phenotypic correlation analysis for grain yield and its attributing traits

5.2.1 Correlation of grain yield with other characters

Grain yield per plant was found to have a significant and positive association with number of tillers per plant ($r = 0.60$), number of productive tillers per plant ($r = 0.63$), panicle length ($r = 0.66$), number of spikelets per panicle ($r = 0.70$), number of filled grains per panicle ($r = 0.72$), spikelet fertility ($r = 0.67$), test weight ($r = 0.45$) and length breadth ratio ($r = 0.36$). While, non-significant negative correlation was found for days to 50 per cent flowering ($r = -0.10$), days to maturity (-0.18) and plant height ($r = -0.12$).

The results obtained were found to be similar with the results of Niharika *et al.* (2022), which depicted a positive and significant association of number of tillers per plant, number of productive tillers per plant, panicle length, number of spikelets per panicle, and test weight with grain yield. Kumar (2022) recorded similar results for test weight. Singh *et al.* (2020) obtained similar results of positive significant association of panicle length with grain yield. Babu *et al.* (2012) showed the similar results of grain yield having significant positive association with number of spikelets per panicle respectively. Significant positive association of grain yield with number of filled grains per panicle and spikelet fertility was recorded by Lohiteswararao *et al.* (2021). Whereas, non-significant negative association of days to 50 per cent flowering, days to maturity and plant height with grain yield was reported by Reddy *et al.* (2022). Similar result for plant height was obtained by Dhavaleshvar *et al.* (2019).

5.2.2 Correlation among yield components

A significant positive correlation was exhibited by days to 50 per cent flowering with days to maturity and grain length breadth ratio. It exhibited non-significant positive correlation with spikelet fertility, panicle length and test weight. It exhibited non-significant negative correlation with plant height, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle and number of spikelets per panicle. The results obtained were in accordance with Dhavaleshvar *et al.* (2019) for significant positive association of days to 50 per cent flowering with days to maturity. Positive association of days to 50 per cent flowering with spikelet fertility and with panicle length and test weight were similar to that of results obtained by Singh *et al.* (2018) and Niharika *et al.* (2022), respectively. Negative association of days to 50 per cent flowering with plant height were similar to that of results obtained by Niharika *et al.* (2022). Reddy *et al.* (2022) obtained negative association with number of tillers per plant and number of productive tillers per plant. Results for negative association for number of filled grains per panicle was reported similarly by Faysal *et al.* (2022). Negative association of number of spikelets per panicle with days to 50 per cent flowering was reported by Dhavaleshvar *et al.* (2019).

Days to maturity has shown significant positive correlation with days to 50 per cent flowering. Non-significant positive correlation was exhibited by panicle length, test weight, grain length breadth ratio, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, number of spikelets per panicle, has shown significant negative correlation with the days to maturity. Negative non-significant correlation was observed with plant height and panicle fertility. Results obtained were in accordance with trait days to 50 per cent flowering, as reported by Kumar (2022). Positive association with panicle length, test weight, number of tillers per plant, number of productive tillers per plant and number of filled grains per panicle was reported by Niharika *et al.* (2022). Dhavaleshvar *et al.* (2019) reported similar results for number of spikelets per panicle. Identical results for plant height and spikelet fertility showing non-significant negative association were reported by Niharika *et al.* (2022).

Significant negative association was shown by plant height with number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle, panicle length and test weight. Non-significant negative correlation was found with days to 50 per cent flowering, days to maturity, spikelet fertility and grain length breadth ratio. Significant negative association was shown by plant height with panicle length which was similar to results of Soujanya *et al.* (2020). Number of tillers per plant and number of productive tillers per plant was significantly negatively associated with plant height and were on par with results reported by Dhavaleshvar *et al.* (2019). For number of filled grains per panicle and

number of spikelets per panicle, similar results were reported by Dhavaleshvar *et al.* (2019) and Lohiteswararao *et al.* (2021). Results for test weight were in accordance with Reddy *et al.* (2022). Whereas, days to 50 per cent flowering and days to maturity showed non-significant negative association with plant height, similar to outcomes of Reddy *et al.* (2022). Results for test weight were in accordance with Reddy *et al.* (2022). Spikelet fertility was non- significantly negative correlated with plant height and similar results were quoted by Dhavaleshvar *et al.* (2019).

Number of tillers per plant showed significant positive correlation with number of productive tillers per plant, panicle length, number of filled grains per panicle, number of spikelets per panicle, spikelet fertility, test weight and grain length breadth ratio. Significant negative correlation was found with days to maturity and plant height. Whereas, non-significant negative correlation with days to 50 per cent flowering. Number of tillers per plant showed significant positive correlation with number of productive tillers per plant, panicle length, number of filled grains per panicle, number of spikelets per panicle and test weight, these results were similar to that of Niharika *et al.* (2022). Similar results for number of productive tillers per plant were quoted by Dhavaleshvar *et al.* (2019). Results for number of tillers per plant were similar to the outcome recorded by Kumar (2022). Association for spikelet fertility was similar to outcome of Dhavaleshvar *et al.* (2019). Significant negative association was found to be similar as reported by Dhavaleshvar *et al.* (2019) for days to maturity and plant height. Negative association for days to 50 per cent flowering was found to be reported in accordance to Reddy *et al.* (2022).

Number of productive tillers per plant exhibited significant positive correlation with number of tillers per plant, panicle length, number of filled grains per panicle, number of spikelets per panicle, spikelet fertility, test weight and grain length breadth ratio. Whereas, with plant height and days to maturity significant negative correlation was found. Non-significant negative correlation was observed with days to 50 per cent flowering. Significant positive association was reported by Niharika *et al.* (2022) for number of productive tillers per plant exhibited significant positive correlation with number of tillers per plant, panicle length, number of filled grains per panicle, number of spikelets per panicle and test weight. Spikelet fertility exhibited significant positive association similar to the results reported by Dhavaleshvar *et al.* (2019). Days to maturity showed significant negative correlation parallel to the findings of Dhavaleshvar *et al.* (2019). Plant height was found to have significant negative correlation comparable to the results by Reddy *et al.* (2022). Katkani *et al.* (2023) recorded results accordingly for negative association of days to 50 per cent flowering.

Panicle length was noticed to have a significant positive correlation with the traits like number of tillers per plant, number of productive tillers per plant, number of

filled grains per panicle, number of spikelets per panicle, spikelet fertility, test weight and grain length breadth ratio. Non-significant positive correlation was observed with days to 50 per cent flowering, days to maturity. Significant negative correlation was observed with plant height. Katkani *et al.* (2023) displayed a significant positive correlation with the traits, number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle. Findings for association of number of filled grains per panicle were on par with Niharika *et al.* (2022). Singh *et al.* (2020) quoted similar results for the trait grain length and breadth ratio. Results for correlation of test weight was on par with Dhavaleshvar *et al.* (2019). Niharika *et al.* (2022) found the results in accordance to that reported in the experiment for days to maturity. Singh *et al.* (2020) found positive association with days to 50 per cent flowering. Dhavaleshvar *et al.* (2019) reported negative significant association for number of tillers and number of productive tillers per plant. Dhavaleshvar *et al.* (2019) recorded on par results for plant height.

Number of spikelets per panicle exhibited significant positive correlation with number of tillers per plant, number of productive tillers per plant, panicle length, spikelet fertility, test weight, grain length breadth ratio and number of filled grains per panicle. Significant negative correlation was seen with days to maturity, plant height. Non-significant negative correlation was observed with days to 50 per cent flowering. Niharika *et al.* (2022) reported similar findings for number of tillers per plant, number of productive tillers per plant, panicle length, test weight and number of filled grains per panicle. Similar reports were found for panicle length by Dhavaleshvar *et al.* (2019). Significant negative association of number of spikelets per panicle with days to maturity and plant height were obtained by Katkani *et al.* (2023). Results for association for days to 50 per cent flowering were found in accordance with Dhavaleshvar *et al.* (2019).

Number filled of grains per panicle exhibited significant positive correlation with number of tillers per plant, number of productive tillers per plant, panicle length, spikelet fertility, test weight, grain length breadth ratio and number of spikelets per panicle. Significant negative correlation was seen with days to maturity and plant height. Non-significant negative correlation was seen with days to 50 per cent flowering. Niharika *et al.* (2022) reported similar findings for number of tillers per plant, number of productive tillers per plant, panicle length, test weight, number of spikelets per panicle and spikelet fertility. Katkani *et al.* (2023) reported identical association for days to maturity and plant height. Noatia *et al.* (2021) found similar results for plant height.

Spikelet fertility had significant positive association with number of tillers per plant, number productive tillers per plant, panicle length, number of filled grains per

panicle, number of spikelets per panicle, grain length breadth ratio and test weight. A non-significant positive association to spikelet fertility was exhibited by days to 50 per cent flowering. Non-significant negative correlation was observed with days to maturity and plant height. Dhavaleshvar *et al.* (2019) reported on par results for number of tillers and productive tillers per plant. The results obtained were found in harmony with the findings of Singh *et al.* (2018) for number of filled grains per panicle, number of spikelets per panicle and test weight. Similar results were obtained by Niharika *et al.* (2022) for number of filled grains per panicle and plant height. Jangala *et al.* (2022) found the results similar to that of current investigation studies for traits like days to 50 per cent flowering. Days to maturity showed negative association with spikelet fertility as quoted by Dhavaleshvar *et al.* (2019).

Test weight exhibited a significant positive correlation with number of tillers per plant, number of productive tillers per plant, panicle length, number of filled grains per panicle, number of spikelets per panicle, spikelet fertility and grain length breadth ratio. Whereas, a positive non-significant correlation was found with days to 50 per cent flowering and days to maturity. Significant negative correlation was seen with plant height. For number of tillers per plant, number of productive tillers per plant, panicle length, number of spikelets per panicle and number of filled grains per panicle significant positive association is quoted by Niharika *et al.* (2022). Similar results were obtained by Kumar (2022) for panicle length. Grain length breadth ratio recorded significant positive association with test weight, similarly quoted by Kumar (2022). Niharika *et al.* (2022) reported identical association for days to maturity and days to 50 per cent flowering. The results obtained were found in harmony with the findings of Kumar (2022) for plant height.

Significant positive association with length breadth ratio was shown by days to 50 per cent flowering, number of tillers per plant, number of productive tillers per plant, panicle length, number of filled grains per panicle, number of spikelets per panicle, spikelet fertility and test weight. A non-significant positive correlation was exhibited by days to maturity, Whereas, negative non-significant association was observed for plant height. Significant positive association was observed for days to 50 per cent flowering by Singh *et al.* (2018). For panicle length and test weight significant positive association was recorded by Kumar (2022). A significant positive correlation was exhibited by number of spikelets per panicle, number of productive tillers per plant and panicle length similar to the reports of Singh *et al.* (2020). Non-significant positive association was observed for days to maturity by Surjaye *et al.* (2022). Singh *et al.* (2020) reported identical association for plant height with grain length breadth ratio. Singh *et al.* (2018) reported comparable findings for plant height.

According to the results obtained grain yield per plant had significant and positive association with number of tillers per plant, number of productive tillers per

plant, panicle length, number of filled grains per panicle, number of spikelets per panicle, spikelet fertility, test weight and grain length breadth ratio, indicating that, all the above-mentioned traits should be given importance during crop improvement and selection of plants.

5.3 Genetic divergence among advanced breeding lines for grain yield and its attributing traits

Thirty seven genotypes including 32 advanced breeding lines and five checks were grouped into six clusters based on D^2 statistics. The groups formed were of such a way that within each cluster, genotypes had smaller value of D^2 statistics compared to those existing between the clusters. Clustering pattern obtained revealed that the biggest cluster formed was cluster I which had 15 genotypes carrying within it followed by cluster II with 11 genotypes, cluster IV had four lines, cluster III and cluster V had three lines. Cluster VI was the smallest with one genotype in the cluster. The results were in accordance with Khalequzzaman *et al.* (2008), Kodihalli and Dushyanthakumar (2014), Rashid *et al.* (2014) and Mith *et al.* (2018).

5.3.1 Average intra and inter cluster distance

Cluster IV exhibited the maximum intra cluster distance (45.67) followed by cluster V (37.92). Because of the greater amount of diversity existing among themselves the advanced breeding lines present within these two groups could be utilized better for hybridization program. Hence, hybridization is effectively utilized by selecting the genotypes of cluster IV and cluster V followed by cluster II and cluster VI.

Cluster IV with four genotypes (R×K-4-4-11, R×K-6-2-15, R×K-1-4-18 and KHP 11) and cluster VI with 1 genotype (KPR-1) were found to be the most divergent because of maximum inter cluster distance existing between them followed by cluster II (R×K-1-4-8, R×K-12-2-6, R×K-1-4-9, R×K-7-2-7, R×K-1-6-10, R×K-7-2-9, R×K-8-2-10, R×K-1-4-13, R×K-1-4-15, R×K-1-4-16 and R×K-7-2-16) with cluster VI (KPR-1). Clusters with the highest inter cluster distance are having more genetic diversity and such genotypes belonging to the clusters will be utilized for hybridisation program.

Meanwhile, those clusters with minimum inter cluster distance are found to have narrow genetic diversity and hybridisation between them will not be exhibiting better heterosis. Therefore, it is better to select those advanced lines having clusters with more inter cluster distance than with low inter cluster distance. Cluster I (R×K-1-4-3, R×K-1-4-4, R×K-7-2-2, R×K-1-4-5, R×K-5-2-4, R×K-1-4-7, R×K-7-2-5, R×K-14-2-8, R×K-1-4-12, R×K-7-2-11, R×K-2-2-14, R×K-7-2-12, R×K-4-2-13, R×K-3-2-14 and R×K-1-4-17) and cluster V (R×K-7-2-1, R×K-8-2-3 and R×K-1-4-6) recorded

the minimum inter cluster distance between them followed by cluster I (R×K-1-4-3, R×K-1-4-4, R×K-7-2-2, R×K-1-4-5, R×K-5-2-4, R×K-1-4-7, R×K-7-2-5, R×K-14-2-8, R×K-1-4-12, R×K-7-2-11, R×K-2-2-14, R×K-7-2-12, R×K-4-2-13, R×K-3-2-14 and R×K-1-4-17) and cluster III (RNR-15048, BPT-5204 and JGL-1798).

Existence of higher genetic diversity between the clusters with more inter cluster distance could be better utilised for developing the high yielding varieties or hybrids than selecting genotypes with minimum inter cluster distance for hybrid development.

5.3.2 Cluster means analysis

Cluster III (RNR-15048, BPT-5204 and JGL-1798) exhibited highest mean value for most of the traits like number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, spikelet fertility, test weight, grain length breadth ratio. It indicates that lines selected from this cluster could be directly selected and utilised in crop improvement program. Whereas, cluster IV (R×K-4-4-11, R×K-6-2-15, R×K-1-4-18 and KHP 11) was found to have maximum cluster mean value for days to 50 per cent flowering, days to maturity and plant height. Cluster VI (KPR-1) showed highest cluster mean value number of filled grains per panicle, panicle length and grain yield per plant.

The results obtained were similar as Ovung *et al.* (2012), Rani *et al.* (2013) and Lahari (2017). They inferred that, for hybridisation program selection of parents should be done from the two clusters which have high inter cluster distance so that maximum variability should be obtained in the segregating generations and for transgressive segregants to be generated.

5.3.3 Contribution of different characters towards divergence

Among all the characters studied for yield and its attributing traits, percentage contribution to total divergence was differed in different traits, days to 50 per cent flowering, number of filled grains per panicle, days to maturity, number of productive tillers per plant, number of spikelets per panicle, grain yield, spikelet fertility, grain length breadth ratio and panicle length all together contributed for 95.3 per cent towards total divergence. Ranjith *et al.* (2018) and Venkatesan *et al.* (2016) reported the higher contribution of days to 50 per cent flowering, test weight and grain yield per plant towards total divergence. Therefore, these traits should be considered for selecting the more diverse parents in programs of hybridisation.

Genotypes which belong to the cluster IV and VI, II and VI showed more inter cluster distance and the traits like days to 50 per cent flowering, days to maturity, spikelet fertility, test weight, number of filled grains per panicle and grain yield should be given more importance for the best parents selection in hybridisation program.

5.4 Screening of advanced breeding lines of rice for submergence tolerance

Advanced breeding lines of rice that are superior and tolerant for submergence conditions can be chosen by screening them during submergence. Thirty two advanced breeding lines of rice along with four checks were evaluated and the best lines identified will thrive better when they are subjected to stressful situation. The assessment of survival percentage of rice genotypes revealed that Swarna sub-1 (check), FR13A (check), R×K-1-4-5 and R×K-1-4-17, had the highest survival per cent. Whereas, Jyothi (check), BPT-5204 (check), R×K-1-4-9, R×K-7-2-5, R×K-12-2-6, R×K-7-2-7, R×K-4-4-11, R×K-1-4-13, R×K-1-4-15, R×K-1-4-16, R×K-1-4-18 and R×K-7-2-16 had the least mean survival percentage.

Sarkar *et al.* (2009), Linh *et al.* (2013), Nugraha *et al.* (2013), Nishanth *et al.* (2017) and Gautam *et al.* (2018) had reported in accordance with the obtained results for submergence screening. Swarna sub-1 and FR13A performed the highest survival rate with the highest survival percentage followed by better performance under severe submerged condition. All the 32 advanced breeding lines of rice revealed significant variation and wide range of survival percentage and survival ability.

5.5 Morphological and physiological characterization of advanced breeding lines of rice for submergence tolerance

Any genotype must have a high survival rate and good re-emergence after undergoing a limited time period of submergence in order to be tolerant to submergence conditions. The study conducted on survival percentage of rice genotypes revealed that Swarna sub-1 (check), FR13A (check), R×K-1-4-5 and R×K-1-4-17 had the highest survival per cent whereas Jyothi (check), BPT-5204 (check), R×K-1-4-9, R×K-7-2-5, R×K-12-2-6, R×K-7-2-7, R×K-4-4-11, R×K-1-4-13, R×K-1-4-15, R×K-1-4-16, R×K-1-4-18 and R×K-7-2-16 had the least mean survival percentage revealed their susceptibility to submergence condition. Similar findings were reported by Sarkar *et al.* (2009), Nugraha *et al.* (2013), Linh *et al.* (2013), Nishanth *et al.* (2017) and Gautam *et al.* (2018).

The stem elongation was recorded to be the highest for R×K-8-2-3 followed by R×K-1-4-7 than Jyothi (check) and the lowest percentage of stem elongation was seen in FR13A and Swarna sub-1 followed by R×K-1-4-15 and R×K-1-4-16. In the current investigation, the genotypes having high stem elongation will have better survival under submerged condition. However, rice genotypes with high stem elongation will have lesser yield because of more utilization of all the non-structural carbohydrates required for their survival as well as to obtain oxygen in such submerged condition through stem elongation. From the present study, moderate tolerant rice genotypes were found to have better survival percentage, moderate stem elongation and had given better yield even after subjected to stress condition. Das *et al.* (2005), Sarkar *et al.*

(2011), Singh *et al.* (2015) and Oladosu *et al.* (2020) achieved the similar results where the study of rice genotypes under submerged condition was carried out. Their outcomes obtained revealed that most of the rice genotypes having submergence tolerance had the capacity of moderate stem elongation with more survival percentage.

PCV and GCV obtained was higher for stem elongation percentage and survival percentage. Also, there was high heritability coupled with high genetic advance for these two traits under submergence. Adilakshmi and Rani (2012) and Kumari *et al.* (2019) revealed the similar results *i.e.*, high PCV and GCV coupled with high heritability and high genetic advance for survival percentage and stem elongation. However, Nishanth *et al.* (2017) noticed low PCV and GCV, with high heritability and moderate genetic advance as per cent mean for the same traits.

5.6 Phenotypic correlation studies among morphological and physiological characters with grain yield

Under submergence condition, survival per cent showed significant positive correlation with grain yield, whereas it showed significant negative correlation with stem elongation per cent.

Survival percentage exhibited significant positive correlation with grain yield per plant under submergence condition. However, a negative significant correlation for grain yield per plant was found with stem elongation percentage. Adilakshmi and Rani (2012), Vergara *et al.* (2014) and Kumari *et al.* (2019) obtained the similar findings. In contrast, Panda and Sarkar (2013) reported that increased stem elongation was found to be positively correlated with survival percentage.

Significant negative correlation was shown by stem elongation with grain yield per plant. The reports obtained were in agreement with the results obtained by Kawano *et al.* (2009) and Adilakshmi and Rani (2012). However, Kato *et al.* (2014) reported the positive relation of stem elongation at moderate level with grain yield.

From the current investigations, it was revealed that the traits like stem elongation percentage and survival percentage were found to be the important contributors to grain yield per plant under submergence condition. Hence, more importance should be given for developing the cultivars which are submergence tolerant.

5.7 Per cent difference in various traits between submergence and non submergence condition

The mean per cent difference for various traits revealed that the number of days to 50 per cent flowering showed an increase value under submergence condition when compared to non submergence condition, but the rest of the features (number of tillers

per plant, number of productive tillers per plant and test weight) indicated a mean value that was lower under stress than under non submergence.

The per cent difference in days to 50 per cent flowering among 32 advanced breeding lines was found to be the highest for R×K-1-4-12 followed by R×K-1-4-5 and the difference was found to be minimum for R×K-1-4-15 followed by R×K-7-2-16.

Maximum per cent difference for number of tillers per plant by advanced breeding lines of rice on comparing under submergence with non submergence was found to be R×K-1-4-7 followed by R×K-8-2-3 while the minimum difference was exhibited by R×K-7-2-16 followed by R×K-14-2-8.

Number of productive tillers per plant exhibited the highest per cent difference by R×K-1-4-7 followed by R×K-8-2-3. Whereas, minimum per cent difference was shown by R×K-14-2-8 followed by R×K-1-4-9.

Test weight per cent difference was noticed to be the lowest in R×K-12-2-6 followed by R×K-4-2-13. The highest per cent difference was found in R×K-5-2-4 followed by R×K-7-2-2. Test weight also showed mean reduction under stress condition than under non submergence condition.

Grain yield per plant per cent difference was maximum in R×K-7-2-2 followed by R×K-1-4-8. Whereas, the lowest per cent difference was observed in R×K-4-4-11 followed by R×K-1-4-17. Grain yield obtained will be decreased under submergence condition than under control condition commonly.

The per cent difference value for the common check in submergence and non submergence conditions lied between highest and lowest value for all the five characters studied.

The results were in harmony with the reports obtained by Nishanth *et al.* (2017), for the difference in mean per cent value for the traits like number of tillers per plant, number of productive tillers per plant and test weight, all these traits were found to have lesser value than under non submergence condition.

Conclusion

- ✓ Thirty two advanced breeding lines of rice cross RNR-15048 × KPR-1 were studied for genetic variability, diversity and characters associated with yield and its attributing traits under non submergence and screening for submergence tolerance was performed for the same 32 advanced breeding lines.
- ✓ Analysis of variance reported the presence of significant variation for all the yield and yield contributing traits analyzed among the 32 advanced breeding lines.
- ✓ Genetic variability studies revealed moderate to high PCV and GCV along with high heritability and high genetic advance as per cent mean for the majority of the characters, including plant height, number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle and grain yield per plant. The underlying basis of high heritability and genetic advance as per cent of mean is additive gene action, which suggests that selection will be successful.
- ✓ Correlation study reported that significant positive correlation of grain yield per plant was noticed with a number of traits like number of tillers per plant, number of productive tillers per plant, panicle length, number of spikelets per panicle, number of filled grains per panicle, spikelet fertility, test weight and grain length breadth ratio.
- ✓ D² analysis reported that the inter cluster distance was found to be maximum for cluster IV and cluster VI followed by the cluster II and cluster VI. Hence, the rice genotypes which belongs to these cluster will have maximum genetic diversity and hence the highest heterosis can be exploited by crossing genotypes which belongs to these clusters.
- ✓ Screening of the advanced breeding lines for submergence tolerance revealed that among the 32 advanced breeding lines evaluated, R×K-1-4-5 and R×K-1-4-17 reported the highest survival percentage of 50 per cent apart from checks.
- ✓ Hence the above advanced breeding lines can be proposed for further multilocation trials in hill zone (low lands) of Karnataka.

Future line of work

Based on the results obtained from the current investigation, the future line of work that could be proposed as follows:

- ✓ The presence of more genetic diversity among the advanced breeding lines for majority of the traits which indicates that they could be used for hybridization programmes.
- ✓ Under submergence condition, lines R×K-1-4-5 and R×K-1-4-17 showed better survival than other advanced breeding lines of rice evaluated and hence could be proposed for further screening in different locations of hill zone of Karnataka.

SUMMARY

VI SUMMARY

Rice stands as a significant cereal crop of global prominence, cultivated extensively across various regions of the world. It frequently faces a range of challenges from both biotic and abiotic factors. Among these challenges, submergence emerges as a major obstacle in regions characterized by substantial precipitation and lowland areas. The escalating impact of climate change on a global scale contributes to a continuous rise in water levels, exacerbating the situation in these areas with abundant rainfall and lowland geography. Consequently, it becomes imperative to create strains of rice that possess a degree of resilience to submergence, encompassing both hybrids and variants. These newly developed or identified genotypes require thorough evaluation in terms of their diversity, variability and correlation with respect to yield and the associated traits that contribute to it.

Taking into account all the aforementioned considerations, the current study titled “Assessment of Genetic Variability in Advanced Breeding Lines of Rice (*Oryza sativa* L.) and Screening for Submergence Tolerance” was carried out during the *kharif* season of 2022 at ZAHRS, Navile and AHRS, Kathalagere. This investigation focused on the evaluation of genetic variability, genetic diversity, and the interrelationship of traits among 32 advanced breeding lines resulting from the cross RNR-15048 × KPR-1 with the objective of selecting diverse advanced breeding lines suitable for hybridization, the assessment of variation within the population and the determination of associations between yield and its constituent characters.

Thirty two advanced breeding lines along with five checks (KPR-1, RNR-15048, BPT-5204, JGL-1798, KHP-11) were assessed for genetic variability, diversity and character association study during *kharif* 2022 under non-submergence condition in Randomised Complete Block Design with two replications. Within each replication, five plants were randomly chosen for each advanced breeding line. Various traits, including days to 50 per cent flowering, days to maturity, plant height, number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle, panicle length, spikelet fertility, test weight, grain length breadth ratio and grain yield per plant were observed and recorded.

Analysis of variance revealed the presence of significant difference among the advanced breeding lines for all the traits studied. The study of genetic variability revealed that genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were found to be moderate for most of the traits viz., plant height, number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle, panicle length, test weight and grain yield per plant. Low PCV and GCV were obtained for traits like days to 50 per cent

flowering, days to maturity, spikelet fertility and grain length breadth ratio. All the traits under study recorded high heritability. Genetic advance as per cent mean was found to be high for plant height, number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle, test weight and grain yield per plant. Moderate GAM was exhibited by the traits like panicle length, grain length breadth ratio and the traits days to 50 per cent flowering, days to maturity and spikelet fertility exhibited low GAM.

Correlation study reported the significant positive association of grain yield per plant with number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle, panicle length, spikelet fertility, test weight and grain length breadth ratio. Non significant negative association of grain yield per plant exhibited by days to 50 per cent flowering, days to maturity and plant height.

Thirty seven genotypes including 32 advanced breeding lines and five checks were grouped into six clusters based on D^2 statistics. Cluster I was found to be the largest with 15 genotypes, followed by cluster II with 11 genotypes, cluster IV with four genotypes, cluster III and cluster V with three genotypes each and Cluster VI was the solitary cluster. Cluster IV exhibited the maximum intra cluster distance followed by cluster V, cluster III, cluster II and cluster I. The highest inter cluster distance was exhibited between cluster IV and cluster VI followed by cluster II and cluster VI indicating that the genotypes within these clusters were highly diverse. The lowest inter cluster distance was noticed between cluster I and cluster V followed by cluster I and cluster III indicating that the traits within the clusters were less diverse.

Cluster III was exhibited the highest mean value for most of the traits viz., number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, spikelet fertility, test weight and grain length breadth ratio. It indicates that genotypes from this cluster could be directly selected and utilized in crop improvement programme. Whereas, cluster IV was found to have maximum cluster mean value for days to 50 per cent flowering, days to maturity and plant height. Cluster VI revealed the higher cluster mean value for number of filled grains per panicle, panicle length and grain yield per plant.

Thirty two rice advanced breeding lines along with four checks were screened for submergence tolerance during *khari* 2022 based on stem elongation and survival percentage.

Maximum survival percentage was exhibited by R×K-1-4-5 and R×K-1-4-17 when compared to other advanced breeding lines. Whereas, R×K-1-4-9 recorded the least survival percentage. Among checks, Swarna sub-1 exhibited the highest survival percentage and Jyothi exhibited the lowest survival percentage.

The stem elongation was recorded to be highest for R×K-8-2-3 followed by R×K-1-4-7 and the lowest percentage of stem elongation was seen in R×K-1-4-15 and R×K-1-4-16. Among check varieties, Jyothi was seen to have the highest stem elongation and FR13A, Swarna sub-1 recorded the least stem elongation percentage.

Analysis of variance under submergence revealed that there was significant difference among the rice genotypes for the physiological traits studied. The genetic variability studies revealed that there was high GCV and PCV for stem elongation and survival percentage. There was high genetic advance coupled with high heritability for the traits.

Under submergence condition, the examination of phenotypic correlations among physiological traits uncovered notable findings. A significant positive correlation was identified between the survival percentage and grain yield per plant. Conversely, a significant negative correlation was observed in relation to stem elongation.

R×K-1-4-5 and R×K-1-4-17 among the advanced breeding lines evaluated showed the highest survival percentage under submergence condition and performed consistently under both submergence and non submergence condition.

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APPENDICES

VIII APPENDIX

Appendix I: Rainfall data of AHRS Kathalagere for the year 2022

Month	Rainfall(mm)	No. of Rainy days	Normal RF	Temperature (°C)			Humidity (%)			Wind Speed(km/hr)		
				Min	Max	Avg	Min	Max	Avg	Min	Max	Avg
January	-	-	0.40	14	32	23	14	91	65	7	11	9
February	44.2	3	-	17	33	25	6	90	57	6	8	7
March	-	-	-	19	36	27	2	91	57	7	15	11
April	73.7	7	49.4	20	36	28	12	91	70	6	15	10
May	239.33	7	126.8	19	35	26	34	91	78	11	20	15
June	130.6	7	84.8	20	34	25	36	97	77	15	17	16
July	228.9	18	93.0	20	32	24	48	95	83	15	17	16
August	215.2	17	71.0	20	30	24	56	94	82	6	11	8
September	44.2	3	116.5	19	30	24	38	95	80	7	11	9
October	132.5	8	28.5	15	30	24	22	93	76	7	17	12
November	8.0	1	129.0	14	31	23	19	91	73	6	11	8
December	25.3	2	-	13	30	23	22	95	74	6	15	11
Total	1141.93	73	701.5									

Appendix II: Monthly meteorological data for the year 2022 recorded at the meteorological observatory, Zonal Agricultural and Horticultural Research Station, Navile, Shivamogga, Karnataka

	Total rainfall of month (mm)			Mean monthly maximum temperature (°C)			Mean monthly Minimum temperature (°C)			Mean monthly Sunshine hours			Mean monthly maximum Relative humidity (%)		
	N	A	D	N	A	D	N	A	D	N	A	D	N	A	D
July	221.20	378.70	157.50	27.70	27.49	-0.21	21.20	21.41	0.21	2.50	2.12	-0.38	84.00	93.48	9.48
August	197.90	364.10	166.20	27.70	28.05	0.35	22.10	21.34	-0.76	4.00	2.95	-1.05	84.00	94.32	10.32
September	112.00	90.80	-21.20	29.30	28.89	-0.41	21.90	20.93	-0.97	4.80	4.20	-0.60	80.00	92.03	12.03
October	179.40	119.40	-60.00	30.20	29.50	-0.70	21.60	19.85	-1.75	6.30	5.71	-0.59	77.00	86.80	9.80
November	45.80	12.40	-33.40	30.00	29.50	-0.46	19.20	18.26	-0.94	7.10	6.58	-0.52	70.00	83.29	13.29
Total	756.30	965.40	-	144.90	143.47	-	106.0	101.79	-	24.70	21.57	-	395.00	449.93	-

Note:

N- Normal meteorological data (mean of 1986-2021)

A - Actual meteorological data (2022)

D - Deviation from the normal (A-N)

Appendix III: Mean performance of advanced breeding lines of rice for twelve traits under non submergence condition

Genotype	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂
R×K-1-4-3	110.50	140.50	125.50	13.75	13.60	21.90	229.90	228.95	96.67	21.50	3.03	31.80
R×K-7-2-1	114.00	141.50	127.75	13.90	13.90	19.10	259.00	240.00	95.75	20.00	3.07	33.60
R×K-1-4-4	114.50	144.50	129.50	13.50	13.50	24.00	301.50	231.70	91.09	18.50	3.72	33.00
R×K-7-2-2	116.00	146.00	131.00	13.40	13.40	21.70	251.40	229.30	94.45	20.90	3.73	29.90
R×K-1-4-5	113.50	147.50	130.50	15.60	15.40	22.40	300.20	237.50	95.05	23.20	3.77	32.00
R×K-8-2-3	121.50	151.50	136.50	12.65	12.65	23.04	267.20	249.15	98.50	21.20	3.79	32.50
R×K-1-4-6	122.50	152.50	137.50	12.45	12.30	21.75	250.00	226.10	97.92	20.05	3.42	36.00
R×K-5-2-4	123.00	152.50	137.75	13.75	13.75	21.75	240.80	213.10	95.10	21.00	3.65	34.30
R×K-1-4-7	111.50	141.50	126.50	14.75	14.75	19.75	222.30	229.70	95.25	19.80	3.27	34.25
R×K-7-2-5	114.50	144.50	129.50	13.85	13.85	22.20	222.50	227.75	96.61	20.45	3.29	35.50
R×K-1-4-8	120.50	150.50	135.50	15.80	15.55	23.05	259.10	215.30	81.13	21.15	3.46	41.85
R×K-12-2-6	119.50	151.50	135.50	15.65	15.65	23.85	206.30	223.20	96.28	19.05	3.74	33.90
R×K-1-4-9	123.50	153.50	138.50	13.60	13.60	21.70	282.00	215.10	91.60	21.75	3.37	31.20
R×K-7-2-7	122.00	152.00	137.00	14.60	14.60	21.60	238.00	218.10	94.20	19.00	3.45	32.60
R×K-1-6-10	117.50	147.50	132.50	11.58	11.58	24.35	229.00	221.75	96.82	23.00	3.39	33.30
R×K-14-2-8	113.50	143.50	128.50	14.80	14.80	21.86	262.57	236.35	94.35	19.55	3.44	29.20
R×K-4-4-11	129.00	159.00	144.00	12.50	12.50	23.30	188.40	237.50	95.48	21.70	3.09	35.00
R×K-7-2-9	119.50	149.50	134.50	13.25	13.25	20.15	275.85	253.60	96.14	23.55	3.04	30.45
R×K-1-4-12	112.00	142.00	127.00	17.05	17.05	18.35	227.00	204.60	96.41	21.00	3.72	21.20
R×K-8-2-10	120.50	150.50	135.50	10.20	9.50	21.75	236.95	217.30	93.96	22.20	3.43	36.70
R×K-1-4-13	117.50	147.50	132.50	14.70	14.20	23.10	231.40	201.00	88.20	21.90	3.39	38.80
R×K-7-2-11	118.50	148.50	133.50	13.10	13.10	24.35	220.10	219.70	96.70	21.00	2.60	31.70
R×K-2-2-14	115.50	145.50	130.50	13.20	13.20	22.80	253.70	218.15	96.96	21.70	3.65	37.00
R×K-7-2-12	114.00	143.00	128.50	16.70	16.70	14.10	254.50	260.90	89.29	22.35	3.67	33.30
R×K-1-4-15	121.50	151.50	136.50	15.60	15.60	24.90	214.60	194.60	97.60	23.50	2.89	31.30
R×K-4-2-13	112.00	142.00	127.00	16.35	16.35	20.60	311.50	165.00	96.25	20.56	3.42	38.45
R×K-1-4-16	121.50	151.50	136.50	15.20	15.20	25.10	292.75	277.90	96.44	18.85	3.78	36.95
R×K-3-2-14	112.50	142.50	127.50	17.05	17.05	23.15	233.00	154.80	97.01	22.93	3.27	33.30
R×K-1-4-17	109.50	139.50	124.50	13.66	13.10	22.45	278.50	235.90	90.50	22.70	3.04	35.80
R×K-6-2-15	125.50	155.50	140.50	14.67	14.66	24.05	247.75	213.20	90.32	24.10	3.65	42.10
R×K-1-4-18	120.50	150.50	135.50	13.80	13.80	16.25	365.50	316.40	96.71	21.25	3.48	40.00
R×K-7-2-16	120.30	148.00	134.15	17.40	17.30	21.85	319.50	275.30	93.25	18.65	3.73	31.20
RNR-15048	114.00	144.00	117.50	19.00	17.50	21.10	261.00	249.60	90.35	17.45	3.86	38.60
KPR-1	101.00	131.00	94.50	18.40	17.45	22.65	312.00	292.75	92.56	18.50	2.99	39.90
BPT-5204	111.50	143.00	111.00	17.90	17.35	21.55	282.50	266.25	96.09	24.90	3.92	40.60
JGL-1798	105.00	136.00	97.00	23.00	21.00	22.65	379.00	319.31	87.60	20.30	3.60	37.60
KHP 11	124.50	155.50	119.35	18.50	17.95	22.05	242.80	240.50	88.71	29.13	3.28	40.30
Mean	116.78	146.81	134.9	14.98	14.97	21.89	260.81	233.98	93.98	20.93	3.43	29.32
CD (5%)	3.07	3.57	16.12	2.99	2.93	1.41	52.90	48.08	3.91	0.28	2.83	8.65
CV	1.23	1.19	5.89	9.83	9.63	3.17	10.00	10.13	2.05	4.00	6.67	14.55

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- Number of spikelets per panicle
X₈- Number of filled grains per panicle

X₉- Spikelet fertility (%)
X₁₀- Test weight (g)
X₁₁- Length breadth ratio
X₁₂- Grain yield per plant (g)

Appendix IV: Mean performance of advanced breeding lines of rice for the following traits under submergence condition

Genotype	X₁	X₂	X₃	X₄	X₅	X₆	X₇
R×K-1-4-3	43.00	11.11	126.00	9.00	9.00	17.90	20.75
R×K-7-2-1	49.70	22.22	128.00	10.00	10.00	17.70	22.50
R×K-1-4-4	31.00	11.11	131.00	9.00	9.00	17.40	23.00
R×K-7-2-2	37.54	22.22	123.00	8.30	8.20	15.20	13.20
R×K-1-4-5	33.50	33.33	134.00	9.30	9.20	19.75	25.70
R×K-8-2-3	55.88	16.67	129.00	5.90	5.90	19.10	21.70
R×K-1-4-6	26.80	11.11	133.00	7.80	7.80	17.90	23.40
R×K-5-2-4	40.79	16.67	131.00	8.80	8.80	13.80	21.90
R×K-1-4-7	52.87	11.11	129.00	6.80	6.70	16.50	20.80
R×K-7-2-5	37.67	5.56	129.00	6.80	6.80	15.50	24.00
R×K-1-4-8	34.14	11.11	135.00	9.30	9.20	19.40	21.40
R×K-12-2-6	28.00	5.56	132.00	7.40	7.30	18.70	25.80
R×K-1-4-9	22.25	5.56	140.00	12.10	12.00	19.00	24.60
R×K-7-2-7	32.91	5.56	137.00	8.50	8.50	17.40	18.40
R×K-1-6-10	24.87	27.78	128.00	8.50	8.40	20.50	20.60
R×K-14-2-8	38.93	22.22	130.00	13.70	13.10	15.60	21.00
R×K-4-4-11	38.07	5.56	141.00	9.20	9.20	18.70	29.85
R×K-7-2-9	22.00	11.11	132.00	10.50	10.50	20.90	22.78
R×K-1-4-12	31.28	11.11	137.00	9.70	9.70	17.60	17.10
R×K-8-2-10	37.65	27.78	128.50	7.60	7.60	17.80	18.90
R×K-1-4-13	29.00	5.56	134.00	10.90	10.80	19.80	29.86
R×K-7-2-11	40.50	22.22	136.50	10.10	10.10	16.90	23.50
R×K-2-2-14	32.55	11.11	128.00	10.10	10.00	18.00	20.60
R×K-7-2-12	30.15	27.78	123.00	11.00	11.00	18.80	24.20
R×K-1-4-15	12.38	5.56	126.00	10.80	10.80	20.60	23.89
R×K-4-2-13	23.20	27.78	127.00	14.30	14.20	19.70	27.80
R×K-1-4-16	13.95	5.56	137.00	12.70	12.70	15.50	25.45
R×K-3-2-14	40.44	11.11	124.00	9.90	9.90	18.70	24.05
R×K-1-4-17	30.07	38.89	125.00	11.40	10.80	19.60	30.50
R×K-6-2-15	27.17	16.67	141.00	11.30	11.30	19.80	22.00
R×K-1-4-18	51.15	5.56	137.00	9.80	9.80	17.40	24.20
R×K-7-2-16	39.18	5.56	127.00	10.80	10.80	17.20	22.29
Jyothi	46.95	30.00	125.00	8.60	8.50	18.50	21.9
BPT-5204	33.95	22.22	127.00	6.80	6.80	17.70	20.75
FR13A	33.95	85.00	126.00	11.20	11.20	16.00	23.38
Swarna sub-1	22.20	96.00	124.50	10.80	10.80	19.90	24.98
Mean	34.05	27.34	130.60	9.69	9.62	18.07	22.96

Where,

- X₁- Stem elongation (%)
- X₂- Survival percentage
- X₃- Days to 50 per cent flowering
- X₄- Numbers of tillers per plant
- X₅- Number of productive tillers per plant
- X₆- Test weight (g)
- X₇- Grain yield per plant (g)