ASSESSMENT OF GENETIC VARIABILITY IN ADVANCED BREEDING LINES OF RICE (*Oryza sativa* L.) AND THEIR COMPARATIVE STUDY UNDER SUBMERGENCE

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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 THEIR CAMPARATIVE STUDY UNDER SUBMERGENCE’** 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 **AKSHATA JADAR, ID. No. MA1TBA0457** (akshatajadar5@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
October, 2023

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A.V. Jadar

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Assessment of Genetic Variability in Advanced Breeding Lines of Rice (*Oryza sativa* L.) and their Comparative Study under Submergence

(AKSHATA JADAR)

ABSTRACT

The present investigation was conducted during *Kharif* 2022. Forty five advanced breeding lines of rice of cross RNR-15048 × Tunga, along with five checks were studied under randomised complete block design for genetic variability, genetic diversity and character association under non- submergence condition at AHRS, Kathalagere. Same advanced breeding lines of rice along with four checks were screened for submergence tolerance under the 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, panicle length, number of spikelets per panicle, number of filled grains per panicle, test weight, grain length breadth ratio and grain yield. Correlation study revealed a significant positive association of the 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 grain length breadth ratio with grain yield. Mahalanobis D^2 statistics grouped 45 advanced breeding lines of rice along with checks into seven clusters. Maximum inter-cluster distance was observed between cluster VI and VII. Among advanced breeding lines of rice screened under submerged condition, the highest survival percentage was observed for R×T-8-9-25, R×T-8-9-17, R×T-8-9-14, R×T-5-9-5, R×T-2-4-5. Genetic variability revealed high PCV, GCV, heritability and genetic advance for survival percentage and stem elongation percentage. Phenotypic correlation for physiological traits revealed significant positive correlation of survival percentage with grain yield. Advanced breeding lines R×T-8-9-25, R×T-8-9-17, R×T-8-9-14, R×T-5-9-5, R×T-2-4-5 could be proposed for further screening in different locations of hill zones of Karnataka.

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ಭತ್ತದ ಸುಧಾರಿತ ಪ್ರಜನನ ಸಾಲುಗಳಲ್ಲಿ ಅನುವಂಶೀಯ ಭಿನ್ನತೆ ಹಾಗೂ ಮುಳುಗುವಿಕೆಯ ಅಡಿಯಲ್ಲಿ ಅವುಗಳ ತುಲನಾತ್ಮಕ ಅಧ್ಯಯನ

(ಅಕ್ಷತಾ ಜಾಡರ)

ಸಾರಾಂಶ

ಪ್ರಸ್ತುತ ಅಧ್ಯಯನವನ್ನು ೨೦೨೨ ರ ಮುಂಗಾರಿನಲ್ಲಿ ಕೈಗೊಳ್ಳಲಾಯಿತು. ನಲವತ್ತೈದು ಭತ್ತದ ಸಂಯೋಜಿತ ಆರ್.ಎನ್.ಆರ್–೧೫೦೪೮ x ತುಂಗಾದ ಸುಧಾರಿತ ಪ್ರಜನನ ಸಾಲುಗಳು ಮತ್ತು ಐದು ಚೆಕ್‌ಗಳನ್ನು ಯಾದೃಚ್ಛಿಕ ಸಂಪೂರ್ಣ ಬ್ಲಾಕ್ ವಿನ್ಯಾಸದ ಪರಿಸ್ಥಿತಿಯಲ್ಲಿ ಅನುವಂಶಿಕ ವ್ಯತ್ಯಾಸ, ಗುಣಲಕ್ಷಣಗಳ ಪರಸ್ಪರ ಸಂಬಂಧ ಮತ್ತು ಅನುವಂಶಿಕ ವೈವಿಧ್ಯತೆಗಾಗಿ ಮುಳುಗಿಸದ ಸ್ಥಿತಿಯಲ್ಲಿ ಕೃ.ತೋ.ಸಂ.ಕೇ., ಕತ್ತಲಗೆರೆಯಲ್ಲಿ ಅಧ್ಯಯನಮಾಡಲಾಗಿದೆ. ವ.ಕೃ.ತೋ.ಸಂ.ಕೇ., ನವಿಲೆ, ಶಿವಮೊಗ್ಗದಲ್ಲಿ ಮುಳುಗಿದ ಸ್ಥಿತಿಯಲ್ಲಿ ಮುಳುಗುವಿಕೆ ಸಹಿಷ್ಣುತೆಗಾಗಿ ಅದೇ ಸುಧಾರಿತ ಪ್ರಜನನ ಸಾಲುಗಳು ಮತ್ತು ನಾಲ್ಕು ಚೆಕ್‌ಗಳನ್ನು 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, ತೆನೆಯ ಉದ್ದ, ಪ್ರತಿ ತೆನೆಗೆ ಧಾನ್ಯಗಳ ಸಂಖ್ಯೆ, ಪ್ರತಿ ತೆನೆಗೆ ತುಂಬಿದ ಧಾನ್ಯಗಳ ಸಂಖ್ಯೆ, ೧೦೦೦ ಧಾನ್ಯಗಳ ತೂಕ, ಧಾನ್ಯದ ಉದ್ದ ಮತ್ತು ಅಗಲ ಮತ್ತು ಪ್ರತಿ ಗಿಡದ ಧಾನ್ಯದ ಇಳುವರಿ ಮಧ್ಯಮದಿಂದ ಹೆಚ್ಚಿನ ವಿಭಿನ್ನಾರ್ಥದ ಗುಣಾಂಕ (ಪಿ.ಸಿ.ವಿ), ವ್ಯತ್ಯಾಸದ ವಂಶವಾಹಿ ಬಗೆ ಗುಣಾಂಕ (ಜಿ.ಸಿ.ವಿ), ಹೆಚ್ಚಿನ ಅನುವಂಶೀಯತೆ ಮತ್ತು ಸರಾಸರಿ ಶೇಕಡಾವಾರು ಅನುವಂಶೀಯ ಮುಂಗಡವನ್ನು ಹೊಂದಿದೆ. ಪರಸ್ಪರ ಸಂಬಂಧದ ಅಧ್ಯಯನದಲ್ಲಿ ಪ್ರತಿ ಗಿಡದಲ್ಲಿನ ತೆಂಡೆಗಳ ಸಂಖ್ಯೆ, ಪ್ರತಿ ಗಿಡದಲ್ಲಿನ ಉತ್ಪಾದಕ ತೆಂಡೆಗಳ ಸಂಖ್ಯೆ, ಪ್ರತಿ ತೆನೆಗೆ ಧಾನ್ಯಗಳ ಸಂಖ್ಯೆ, ಪ್ರತಿ ತೆನೆಗೆ ತುಂಬಿದ ಧಾನ್ಯಗಳ ಸಂಖ್ಯೆ, ತೆನೆಯ ಉದ್ದ, ತೆನೆಯ ಫಲವತ್ತತೆ, ೧೦೦೦ ಧಾನ್ಯಗಳ ತೂಕ, ಧಾನ್ಯದ ಉದ್ದ ಮತ್ತು ಅಗಲ, ಪ್ರತಿ ಗಿಡದ ಧಾನ್ಯದ ಇಳುವರಿಗೆ ಗಮನಾರ್ಹ ಸಕಾರಾತ್ಮಕ ಸಂಬಂಧ ಕಂಡುಬಂದಿದೆ. ಮಹಲನೋಬಿಸ್ ಡಿ^{೨} ಅಂಕಿ ಅಂಶಗಳ ಅನುಸಾರ ೪೫ ಭತ್ತದ ಸುಧಾರಿತ ಪ್ರಜನನ ಸಾಲುಗಳು ಮತ್ತು ೫ ಚೆಕ್‌ಗಳನ್ನು ೭ ಗುಂಪುಗಳಾಗಿ ವರ್ಗೀಕರಿಸಿದೆ. ಗುಂಪು ೬ ಹಾಗೂ ೭ ರ ನಡುವೆ ಗರಿಷ್ಠ ಅಂತರ ಕಂಡು ಬಂದಿದೆ. ಮುಳುಗಿಸಿದ ಸ್ಥಿತಿಯಲ್ಲಿ ತಳಿ ಆರ್ x ಟಿ–೮–೯–೨೫, ಆರ್ x ಟಿ–೮–೯–೧೭, ಆರ್. x ಟಿ–೫–೭–೫ ಮತ್ತು ಆರ್ x ಟಿ–೨–೪–೫ ಹೆಚ್ಚು ನೀರು ಮುಳುಗುವಿಕೆ ಸಹಿಷ್ಣುತೆ ತೋರಿದೆ. ಅನುವಂಶೀಯ ವ್ಯತ್ಯಾಸ ಅಧ್ಯಯನದಲ್ಲಿ ನೀರು ಮುಳುಗಡೆಯ ಸಹಿಷ್ಣುತೆ, ಕಾಂಡ ಉದ್ದವಾಗುವ ಸಾಮರ್ಥ್ಯವು ಹೆಚ್ಚಿನ ಪಿ.ಸಿ.ವಿ ಮತ್ತು ಜಿ.ಸಿ.ವಿ ಹೊಂದಿರುತ್ತದೆ. ನೀರು ಮುಳುಗಡೆಯ ಸಹಿಷ್ಣುತೆ, ಪ್ರತಿ ಗಿಡದ ಇಳುವರಿಗೆ ಗಮನಾರ್ಹ ಸಕಾರಾತ್ಮಕ ಸಂಬಂಧವನ್ನು ತೋರಿಸಿದೆ. ಆರ್ x ಟಿ–೮–೯–೨೫, ಆರ್. x ಟಿ–೮–೯–೧೭, ಆರ್ x ಟಿ–೮–೯–೧೪, ಆರ್ x ಟಿ–5–೯–೫ ಮತ್ತು ಆರ್ x ಟಿ–೨–೪–೫ ತಳಿಗಳನ್ನು ಕರ್ನಾಟಕದ ಗುಡ್ಡಗಾಡು ವಲಯದ ವಿವಿಧ ಸ್ಥಳಗಳಲ್ಲಿ ನೀರು ಮುಳುಗುವಿಕೆಯ ಸಹಿಷ್ಣುತೆಗಾಗಿ ಪ್ರಸ್ಥಾಪಿಸಬಹುದಾಗಿದೆ.

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ಅನುವಂಶೀಯತೆ ಮತ್ತು ಸಸ್ಯತಳಿ ಅಭಿವೃದ್ಧಿ ಶಾಸ್ತ್ರ ವಿಭಾಗ
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ಅಕ್ಟೋಬರ್, ೨೦೨೩

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INTRODUCTION

I INTRODUCTION

Rice (*Oryza sativa* L), is one of the leading cereal crops in the world, feeding nearly half of the world's population hence, it is referred to as **"Global Grain".** Rice plays an essential role in ensuring food security. To meet the demand of the increasing population and to combat food security in India, the present yield levels has to be increased up to 121 million tonnes by 2050 and the production of rice needs to be elevated by almost two million tons every year. (Buelah *et al.,* 2022).

Rice belongs to the family Poaceae (Graminae) with chromosome number 24. The genus includes 24 species, out of which 22 are wild and two *viz*., *Oryza sativa* and *Oryza glaberima* are cultivated**.** Rice was declared as the theme of the international year of rice 2004, indicating its enormous importance as an item of food and commerce.

Rice, besides being a good source of protein and also contains various vitamins such as thiamine and niacin and minerals such as zinc and phosphorus. (Bagchia *et al.,* 2016). Rice is widely grown in tropical and subtropical regions with a wide range of ecosystems under varying temperature and water regimes in more than 114 countries. Nearly 90% of the world's rice crop is produced in Asian countries. The leading producer of rice in the world is China followed by India and Indonesia. India ranks first, having the highest area of cultivation of rice in the world, followed by China. In India, West Bengal has the highest total rice production, followed by Uttar Pradesh. Other major rice producing states are Punjab, Andhra Pradesh, Tamil Nadu, Bihar, Chhattisgarh and Odisha. In the year 2021-22 the rice area, production and productivity in India was 46.38Mha, 130.29mt and 2.81 t/ha, respectively. (Anonymous, 2022).

Evaluation of genetic variability is crucial for any breeding program. The existence of genetic variability among traits is essential in selecting desirable genetic material for the production of high yielding varieties (Tiwari *et al.,* 2019), which is the ultimate tool in plant breeding. 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 gain is necessary for the successful genetic improvement of a genotype (Kishore *et al.,* 2015). Rice shows a bewildering wide range of genetic variability due to the genetic differences among individuals within a population which serves as a pre-requisite in identifying genetically divergent parents to create new genetic stocks. (Nath and Kole *et al.,* 2021). Hence, genetic variability among traits is essential for breeding and selecting desirable types (Awad-allah *et al.,* 2022).

Genetic diversity becomes a precondition for the plant breeder in order to choose the right type of parents for the hybridization programme. Information on genetic diversity in terms of nature and degree of divergence for grain yield, yield components and quality characters helps the plant breeder to select parents suitable for hybridization programmes and designing effective breeding strategies which ultimately aim at developing high yielding varieties with good grain quality. Mahalanobis D^2 statistics serve as a beneficial tool that helps the breeder to measure genetic diversity by quantifying the degree of diversification and detecting clustering patterns to establish a link between genetic and environmental divergence. It aids in identifying the traits that significantly add on to the genetic divergence.

The grain yield is the result of multiple interactions between various yield components and this impedes a thorough understanding of trait association and direct and indirect effects contributed by each character on grain yield before the initiation of any breeding programme. The correlation coefficient is a statistical measure of the degree (strength) and direction of the relationship between two or more variables under study. Correlation coefficient analysis helps to identify the mutual relationship between various plant characters and determines the component characters for which selection can be done resulting in genetic improvement in yield. (Buelah *et al.,* 2022). Thus, correlation studies help by providing information about the inter-relationship between yield and its attributes and estimating the magnitude of association among traits.

Rice production is severely affected by abiotic stresses due to frequent changes in climatic conditions such as drought, submergence, salinity, cold and mineral toxicity. Flash and stagnant flooding in lowland ecosystems affects plant stand detrimentally by causing anoxia based on the duration of submergence stress, which is the third most important constraint affecting high yield in India among all the other 42 biotic and abiotic stresses. A total of 22 million hectares of rice fields in the entire world are unfavourably submerged every year, which affects the livelihood of more than 100 million people (Singh *et al.,* 2015). Submergence can be classified as either complete or incomplete based on the depth of the flood water. If the water depth is more than 100cm, it is complete submergence, it may persevere for several months in deep water areas (Vergera *et al.,* 2014).

The majority of the present day cultivated rice varieties are not suitable to sustain the submerged conditions, so farmers tend to grow low yielding local landraces which results in poor quality produce. Characters desirable for complete submergence and prolonged partial submergence tolerance vary. So, the identification of tolerant sources with high survival rate associated with high yield in different submerged conditions is of utmost importance. Hence, keeping all these points under consideration, the current study entitled **"Assessment of Genetic Variability in Advanced Breeding Lines of Rice (*Oryza sativa* L.) and their Comparative Study under Submergence"** is carried out with the following objectives:

1) To assess the genetic variability in advanced breeding lines of rice
2) To assess the genetic diversity in advanced breeding lines of rice
3) To study character association for grain yield and its related traits
4) To screen advanced breeding lines of rice under submergence condition

REVIEW OF LITERATURE

II REVIEW OF LITERATURE

Rice is the second most 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 an 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. The germplasm collection provides immense scope for wide variability. Knowledge of the nature and degree of genetic divergence would help the plant breeder in choosing the right parents for the breeding programme (Vivekanandan and Giridharan,1998).

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

2.1 To assess genetic variability in advanced breeding lines of rice.

Genetic improvement of any crop depends on the amount of variability present in the germplasm and the heritability of the desirable traits. So, the magnitude of variability in the 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 programmes in crops like rice.

Vanaja and Babu (2007) evaluated the 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 the L/B ratio of grain, milling percentage, amylose content, water uptake, and volume expansion. All quality attributes exhibited a high broad sense heritability. 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, implying the potential of these parameters to be used in breeding programmes.

Pandey *et al.* (2009) evaluated 40 rice genotypes for genetic variability by studying 12 quantitative characters. Analysis of variance revealed the existence of a sufficient amount of variability in the gene pool for all traits. The higher 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 indicating that this character was highly influenced by the 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 the 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 a significant difference among the lines indicating the presence of high variability among them. A 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 (30.52 percent; 31.18 percent) and filled grain per panicle (26.05 percent; 26.86 percent) had high GCV and PCV. Almost all the characters showed a little variation between PCV and GCV revealing little influence of the environment in the expression of these traits. 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 indicating the existence of genetic variability for all the traits varying from lower to higher coefficients. 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. The moderate genotypic and phenotypic coefficients of variance were recorded for panicle length, grain breadth and L/B ratio. The days to 50 per cent flowering had recorded lower values of genotypic and phenotypic variance. 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 to obtain information on genetic variability using 44 diverse rice genotypes. The analysis of variance revealed significant differences among the genotypes for all the traits indicating the presence of sufficient variability among the genotypes for various traits. High estimates of genotypic and phenotypic coefficient of variation were observed for the 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 the number of grains per panicle, grain yield per plant, straw yield per plant, harvest index, 1000-grain weight, grain L/B ratio and amylose content indicating selection may be effective for these characters.

Pradhan *et al.* (2015) evaluated 30 rice cultivars under both normal and submerged situations to study the genetic basis of yield variations. Highly significant differences among the test genotypes were present for all characters except fertility percentage and grain yield per plant under normal conditions and except grain yield per plant under sub-merged condition. The majority of traits exhibited a 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 percent flowering, plant height, grain number and 100-grain weight indicate the presence of additive gene effects. Hence, selection based on phenotypic performance would be effective.

Devi *et al.* (2016) studied variability in 27 rice genotypes. Higher estimates of PCV and GCV were observed for yield per plant (42.04) and filled seeds per panicle (33.9) indicating the 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 a 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 with check variety Swarna Sub 1. 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 CO_2 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 understudies 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 the genotypic coefficient variation. The magnitude of PCV and GCV was high for the number of grains per panicle. High heritability coupled with high genetic advance as per cent of mean was observed for the number of grains per panicle, number of tillers per plant, 1000-grain weight, 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 study variability, heritability and genetic advance (GA) in 83 rice genotypes. Analysis of variance indicated significant differences among the genotypes for different morphological characters. High GCV and PCV were observed for grain yield per plant, panicle weight/plant, biological yield/plant, filled spikelets/plant, test weight, harvest index and number of tillers/plant, whereas moderate GCV and PCV were observed for plant height. High heritability coupled with high genetic advance as percent of mean was observed for grain yield per plant, panicle weight/plant, biological yield/plant, filled spikelets/plant, harvest index, test weight, number of tillers/plant, panicle length/plant, whereas high heritability coupled with moderate genetic advance as percent of mean for days to 50 percent flowering and days to maturity.

Lahari *et al.* (2017) carried out an investigation at the College of Agriculture, Shivamogga during summer 2016 to screen 107 rice genotypes including four checks (FR13A, Swarna Sub1, Hemavathi and Jyothi) for their survival ability under submergence. Among 107 genotypes, 49 genotypes with higher survival percentage were selected and laid out using a randomized complete block design with two replications under submergence during *Kharif* 2016 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 were recorded in the 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 an investigation with 50 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 indicating the additive type of gene action.

Ram *et al.* (2017) carried out an 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, indicating enough variability in the material. The characters *viz*., grain yield/plant and biological yield exhibited high Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV). Days to 50 per cent flowering, plant height, days to maturity, spikelet's fertility and harvest index recorded low estimates of PCV and GCV. Small differences between GCV and PCV were recorded for all the characters studied, indicating less influence of environment on these characters. 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, indicating that simple selection could be effective for improving these characters.

Rashid *et al.* (2017) conducted an experiment to estimate genetic variability in ten rice genotypes. Analysis of variance showed higher estimates of PCV and GCV were observed for the number of filled grains per panicle (27.53; 26.84), number of unfilled grains per panicle (26.76;25.28) and plant height (23.14; 23.00) indicating the possibility of genetic improvement through direct selection, while days to 50 per cent flowering, days to maturity, panicle length, number of effective tillers per plant, fertility (percent), test weight and yield per panicle showed low PCV and GCV values indicating the need for variability by hybridization or mutation followed by selection. High heritability values (>60 percent) along with high genetic advance and genetic advance as a 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 an investigation with 23 rice genotypes for 13 quantitative characters to study genetic variability, heritability and genetic advance. Analysis of variance showed significant difference for all the characters studied. 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. High estimates 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 the number of spikelets per panicle and plant height, indicating a predominance of additive gene effects and possibilities of effective selection for the improvement of these characters.

Anyaoha *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 an 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. Analysis of variance revealed 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 the 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 an additive gene effect.

Divya *et al.* (2018) conducted a present study with 33 genetically diverse rice genotypes in a randomized complete block design with two replications. Analysis of variance was found to be significant for all the traits. Moderate genotypic and phenotypic coefficients of variance were recorded for the 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 the number of productive tillers per plant, 1000 grain weight, number of grains per panicle and seed yield per plant.

Gautam *et al.* (2018) 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, panicle number per plant indicated that selection would be effective for these characters. Among all the traits, high heritability (>80) with high genetic advance (>20) as per cent of mean was recorded for leaf length, stem thickness, leaf width, test weight and grain width. The high estimates of heritability indicate considerable genetic variation and less influence of environment in the expression of these characters. High genetic advance coupled with high heritability indicates that these traits are controlled by additive genes and hence, 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. Analysis of variance revealed 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 suggesting their 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 land races showing wide variation among genotypes. PCV was more than GCV for all traits.

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.

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 ($p<0.05$) 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. The highest heritability was recorded for days to 50 per cent flowering and plant height followed by yield and panicles per meter square. High to medium heritability with high GCV and high genetic advance as percentage of means were exhibited for plant height, 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 the 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.

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

Chamar *et al.* (2021) conducted an experiment to study the morphological characters and to estimate genetic variability in rice germplasm. For this they evaluated 72 germplasm accessions. The analysis of variance revealed that highly significant variations were recorded among all the germplasm accessions for all the traits under study. It indicated that an adequate amount of genetic variability was present in all studied characters. High estimates of phenotypic coefficient of variations (PCV%), genotypic coefficient of variations (GCV%) and high heritability coupled with high genetic advance as percentage of mean was recorded for were recorded for number of tillers per plant, number of productive tillers per plant, number of grains per panicle, biological yield per plant and grain yield per plant.

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 the number of grains and low for spikelet fertility (per cent).

Demeke *et al.* (2022) conducted a study using 70 genotypes of upland rice (*Oryza sativa* L.) to evaluate the genetic variability, heritability, and genetic advance among morphological, yield-related and quality parameters. There was a highly significant difference ($P < 0.001$) and high diversity among the genotypes for both quantitative and qualitative parameters. The range of genotypic and phenotypic coefficient of variance was 6.1% to 44.51% and 6.5% to 45.81%, respectively. Broad sense heritability was high for all traits. Genetic advance as per cent of the mean ranged from 11.02% to 89.07%. This study indicated the existence of sufficient variability among the genotypes.

Niharika *et al.* (2022) carried out an investigation at ZAHRS, Shivamogga, by using multi-parent advanced breeding lines of the MF_6 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 the majority of yield attributing traits. The knowledge about the genetic variability of yield contributing characters, inter relationship among them and their relation with yield are necessary for an effective breeding programme.

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

2.2 To assess the genetic diversity in advanced breeding lines of rice.

For designing effective breeding programmes, the knowledge of greater genetic variation in population 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 and economical. As of now majorly genetic diversity is being analysed by D^2 statistics and molecular markers.

Ni *et al.* (2002) evaluated the genetic diversity in thirty-eight rice cultivars and two wild species accessions (*O. rufipogon* and *O. nivara*) were evaluated using 111 microsatellite markers distributed over the whole rice genome. A total of 753 alleles were detected, and the number of alleles per marker ranged from 1 to 17, with an average of 6.8. Compared to *indica* cultivars, the *japonica* group showed significantly higher genetic diversity on chromosomes 6 and 7 and considerably lower diversity on chromosome 2. The results suggested that a relatively small number of microsatellite markers could be used for the estimation of genetic diversity and the identification of rice cultivars.

Bose and Pradhan (2005) estimated the nature and magnitude of genetic divergence in 35 rice genotypes using Mahalonobis's D^2 – statistics. The genotypes were grouped into 10 clusters showing a 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 genotypes each. There was no parallelism between genetic diversity and geographical distribution. 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.

Khalequzzaman *et al.* (2008) studied the 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 cluster VI contained the highest number of genotypes (12) and cluster IV contained the lowest (2). The highest intra cluster distance was noticed for 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. Cluster IV showed high genetic distance from all clusters except cluster II. The genotypes from cluster IV could be hybridized with the genotypes of any of the four clusters for producing transgressive segregants.

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.

Seetharam *et al.* (2009) characterized thirty rice genotypes by SSR markers and morphological characters in this study. Out of 35 primers of SSR markers, 28 were found to be polymorphic. The PIC value ranged from 0.064 (RM 274) to 0.72 (RM 580) with an average of 0.46. The Jaccard's similarity coefficient ranged from 0.42 to 0.90. At the genetic similarity of 56 per cent the genotypes were grouped into five clusters. PCA components explained 41.6 per cent of the variation. There was overlapping of tolerant genotypes and susceptible genotypes within the cluster. Morphological traits of each genotype were measured on five randomly chosen plants. The matrix of average taxonomic distance was estimated using Euclidian distance. The average taxonomic distance ranged from 1.5 to 7.78. At an Euclidean distance of 3.49, 30 genotypes were grouped into IV clusters. PCA components explained 38.4 per cent of the variation.

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, while clusters II, IV, V, VI, VIII, IX and X had only two genotypes each. The maximum inter cluster D^2 value was between cluster I and X (32.96) followed by cluster I and IV (32.90). Intra cluster distance was maximum in cluster VII (24.62) followed by cluster XI (22.15) indicating hybridization involving genotypes within the same clusters may result in good cross combinations. Among the eight traits studied, maximum contribution was made by grain yield (50.87 per cent) followed by days to 50 per cent flowering (15.02 per cent), total grains per panicle (10.52 per cent) and plant height (10.23 per cent).

Dushyanthakumar and Anand (2010) conducted an experiment to study genetic diversity among 39 local rice genotypes using Mahalanobis D^2 statistic. On the basis of genetic distance, these genotypes were grouped into eight clusters. ClusterVI was the largest consisting of 21 genotypes, while clusters I, II, III, IV and V contained two genotypes each and cluster VI and VIII contained four genotypes each. The high degree of divergence was recorded between cluster IV and VIII. Based on the mean performance of traits studied, two clusters (IV and II) which were having local rice genotypes may be used as parents in future breeding programmes to achieve desirable segregants for tall stature plants, number of panicles per plant, panicle length and high grain yield.

Upadhyay *et al.* (2012) conducted a study with the aim of developing molecular tags for rice lines. A set of 29 rice varieties were studied for diversity using SSR, a total of 87 alleles were produced that were 100 percent polymorphic. Twelve sets of SSR primers amplified specific alleles in 14 genotypes. The PIC value ranged from 0.57 to 0.98 with an average of 0.78 and average genetic similarity of 0.38 was observed among the popular varieties. A maximum similarity of 0.82 was observed between Jayshree and Sarjoo52 and a minimum similarity of 0.05 between Jaya and Pusa

Basmati 1. Out of 29 genotypes, 14 produced specific alleles, which can be used as molecular tags for particular genotypes when utilized along with the non-polymorphic markers.

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 a 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 (2907) had the maximum divergence, which was closely followed by cluster V (2027) and cluster I (1762). The inter cluster distance was maximum between cluster VI and VII (18054), followed by cluster III and IX (12520), suggesting that the genotypes in these clusters may be used as parents for future hybridization programmes. Traits like spikelets per panicle, plant height and biological yield were the major contributors to genetic divergence.

Rahman *et al.* (2012) conducted an experiment to assess genetic diversity and molecular characterization among 21 rice varieties using Thirty-four microsatellite markers. The number of alleles per locus ranged from 2 to 11, with an average of 4.18 alleles across 34 loci. A total of 57 rare alleles were detected at 24 loci, whereas 42 unique alleles were detected at 20 loci. The results revealed that 14 rice varieties produced unique alleles that could be used for identification, molecular characterization, and DNA fingerprinting of these varieties.

Rani *et al.* (2013) screened 64 rice genotypes under submergence conditions to study the diversity pattern for identifying and developing varieties suitable for flood prone areas. The genotypes were grouped into eight clusters. A maximum of 22 genotypes were found in 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 (3269.73) and V and VIII (3248.71). 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 indicating the importance of these characteristics for submergence tolerance. Hybridization between clusters IV and VIII may result in desirable segregants with high yield, minimal shoot elongation and fast recovery after de-submergence as these groups are extreme for traits associated with submergence tolerance.

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, while two genotypes were present in cluster II, eight in cluster III, twelve in cluster IV, four in cluster V and three in cluster VI. The maximum inter cluster distance was between Cluster III and cluster V. Among the different characters studied, harvest index, straw yield/ plant (g) and grain yield/ plant (g) contributed significantly for the genetic diversity. The cluster II was characterized by maximum mean value for the majority of these characters. Hence, Doddiga and Hasuli may be used as parents in future breeding programmes. 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, IRRI5, and SRS-64 could be used for hybridization and improve programs for developing new varieties.

Ashraf *et al.* (2016) used 24 SSR markers to estimate the genetic diversity in 16 rice genotypes. The level of polymorphism among the genotypes was evaluated from the number of alleles and PIC value for each of the 24 SSR loci. A total of 68 alleles were detected across the 16 genotypes by using these 24 SSR markers. The number of alleles per locus varied from 2 to 6. The PIC values varied from 0.36 to 0.86 with an average of 0.62 per locus. Based on the information generated, the genotypes were separated into six different clusters. Cluster 1 comprised of 4 genotypes separated from each other at a similarity value of 0.40. Cluster II comprised three landraces separated at a similarity value of 0.45. Cluster III comprised three genotypes separated at a similarity value of 0.46. Cluster IV had two landraces and was not sub clustered. Cluster V had three genotypes separated at a similarity value of 0.28. Cluster VI comprised a single variety with independent lineage.

Venkatesan *et al.* (2016) conducted an investigation to study the submergence tolerance of 26 rice genotypes. Genetic divergence was studied based on Mahalanobis D^2 statistics and grouping of clusters was done by Toucher's method. In D^2 analysis, genotypes were grouped into three different clusters in normal and five clusters in submergence. Genotypes Swarna Sub 1, AURL 41051, AURL 4135, AURL 4139 and AURL 4125 were predicted as best as per their performance in normal and submergence. The maximum intra cluster distance was observed in cluster IV in submergence. The maximum inter cluster distance was observed between clusters III and I in normal and clusters III and V in submergence.

Vu *et al.* (2016) studied genetic diversity in a set of 40 rice varieties using 30 SSR markers covering all rice chromosomes. A total of 111 alleles were detected, with a mean of 3.7 alleles per locus. The number of polymorphic alleles detected by each SSR marker ranged from 2 to 6. The fragment size of a given SSR locus varied between 85 and 650 bp and the frequency of a major allele at each locus ranged from 32.5 per cent to 76.9 per cent. PIC value varied from 0.355 to 0.774 with an average of 0.594. The genetic similarity ranged from 0.03 to 0.97 with an average of 0.27. According to a constructed dendrogram of unweighted pair group method with arithmetic mean based on the SSR marker analysis, the tested rice varieties were clustered into two major groups consisting of five subgroups. Significant correlations existed between the mean genetic similarity and the mean seedling vigour estimated by shoot length under submergence among the tested varieties.

Ashok *et al.* (2017) assessed genetic divergence among 64 rice genotypes with 17 characters using Mahalanobis's D^2 analysis. The 64 rice genotypes were grouped in to nine clusters. Out of nine clusters, a maximum number of 30 genotypes are in cluster I. Cluster III is the second largest with 11 genotypes followed by cluster II and V each with nine genotypes. Cluster IV, VI, VII, VIII and IX possess one genotype each. Characters like head rice recovery, test weight, volume expansion ratio, milling percentage, number of grains per panicle, and protein percent together contributed 80% towards total divergence which should be taken into consideration while selecting parents for hybridization.

Devi *et al.* (2017) used microsatellite (SSR) markers to determine the allelic diversity and relationship among 30 genotypes of Basmati rice. A total of 50 alleles were found for 20 SSR loci with an average of 2.5 per locus, revealing all the tested primers showed different levels of polymorphism among the genotypes indicating the robust nature of SSR markers. Polymorphic information content (PIC value) ranged from 0.556 to 0.995. Clustering analysis based on UPGMA grouped the genotypes into three main clusters I, II and III comprised of 9, 7 and 14 genotypes, respectively.

Lahari *et al.* (2017) carried out the present investigation at the College of Agriculture, Shivamogga during summer of 2016 to screen 107 rice genotypes including four checks for their survival ability under submergence. Among 107 genotypes, 49 genotypes with higher survival percentage were selected and laid out using randomized complete block design with two replications under submergence during Kharif 2016 for evaluating genetic divergence for thirteen 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, the absolute growth rate had the maximum contribution towards genetic divergence.

Dhama *et al.* (2018) studied genetic diversity in rice using SSR markers in RCBD design for 20 rice cultivars. Total genomic DNA was isolated from each replication using the CTAB method and its quality was determined by UV-VIS spectrophotometer and integrity was confirmed using agarose gel electrophoresis. PCR amplification was done using 10 SSR markers and then electrophoresed which showed a total of 159 bands out of which 30 bands were polymorphic and 129 were monomorphic. The least genetic similarity was found between kalanamak and IR77734-93-2-3-2.

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 betweencluster 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.

Suwansa *et al*. (2018) studied genetic divergence in 22 upland rice varieties. Based on the D^2 analysis, the varieties were grouped into three clusters. Group I consisted of nine genotypes, group II consisted of five genotypes, and group III contained six genotypes. Group I exhibited the highest mean values for traits, such as plant height (163.20), days to 50 per cent flowering (83.20), flag leaf width (24.3), and 1000 grains weight (33.51). Group II showed the highest mean values for traits like days to maturity (116.20), flag leaf length (56.59 cm), panicle length (30.53) and the number of panicles per plant (75.98). Group Ill showed the highest mean values for the number of tillers per hill (5.48), yield per plant (59.67) and the number of panicles per plant (4.35). The genotypes of group II and group III had the best key agronomic traits *viz.*, 1000 grains weight, flag leaf length and days to 50 per cent flowering.

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.

Manjunatha (2020) studied the nature and magnitude of genetic divergence in 23 rice genotypes in six environments using Mahalanobis' D^2 by considering 13 quantitative traits. The genotypes were grouped into six clusters. Cluster-I constituted a maximum number of genotypes (16). The inter-cluster distance was maximum between cluster-I and IV (10.34), followed by cluster-III and V (9.82). Traits like days to maturity, plant height (cm), number of grains per panicle, test weight (g), harvest index (%), days to 50 per cent flowering and panicle length (cm) were the major contributor to genetic divergence.

Mishra *et al.* (2020) studied twenty-one 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 of a 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. The 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.

Singh *et al*. (2020) analysed the genetic divergence of 22 lowland genotypes with the help of Mahalanobis' D^2 statistics. The genotypes of rice were grouped into six clusters using Tocher's method. Cluster-I consists of a maximum number of genotypes forming the largest cluster, followed by cluster-VI with three genotypes. The intracluster distance ranged from 0.00 to 84.45. The inter-cluster distance ranged from 52 to 282.49. The highest intra-cluster distance was observed in cluster-VI (84.85), followed by cluster-I (67.75). The maximum inter-cluster distance was observed between cluster III and cluster IV, followed by cluster III and cluster IV. Due to the maximum inter-cluster distance between them, the genotype in cluster III and cluster IV exhibited a high degree of genetic diversity.

Tripathi *et al.* (2020) conducted a study to assess the genetic diversity among 27 rice cultivars with 12 SSR markers. The results revealed a total of 40 alleles were detected across 27 rice cultivars tested. PIC values varied widely among SSR loci tested and it ranged from 0.38 to 0.65, with an average of 0.56 per marker. The 27 rice cultivars were grouped into two major clusters i.e., cluster I and II with similarity coefficient of 0.13. Cluster I was subdivided into two minor sub-groups IA and IB having five and eight genotypes, respectively. These subgroups were further subdivided into minor groups. In a similar way, the second main cluster i.e., Cluster II was also sub divided into two minor sub-groups that is IIA and IIB having five and nine genotypes, respectively.

Barhate *et al*. (2021) studied genetic divergence for 45 genotypes of aromatic rice. The observation was recorded on 13 quantitative and three cooking quality characters. All the characters showed highly significant differences among the genotypes for all the characters, indicating that an appreciable amount of diversity was present among the genotypes. The 45 genotypes were grouped into 10 clusters, and the clusters I, II, IV, V, and VI contained 21, 4, 2, 8, and 5 genotypes, respectively. In contrast, clusters III, VII, VIII, IX, and X were mono-genotypic. D^2 analysis revealed that there was a wide diversity between the genotypes.

Sai *et al.* (2022) studied 60 rice genotypes to evaluate the genetic divergence for 15 yield and yield attributing characters. Based on Mahalanobis D^2 statistics, the 60 genotypes were grouped into nine clusters. On the basis of genetic distance and cluster means, clusters IV and IX, VI and IX, I and IX, were identified as clusters with high inter-cluster distance. Genotypes of these clusters could be used as parents in crop improvement programmes for the generation of promising segregants.

2.3. To study character association for grain yield and its related traits.

The main aspect of any breeding programme is to increase the yield, so there is 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 a correlation coefficient analysis for yield, yield components and grain quality characteristics in 14 genotypes of basmati rice. Plant height had a negative correlation with yield indicating 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 a negative correlation with these traits. Grain length had a 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 the 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. A direct effect of total biomass and harvest index was also high on grain yield. Thus, these traits contribute to 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 a negative association of plant survival percent with total shoot elongation and relative shoot elongation, where a 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 a significantly positive association of grain yield per plant with the 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 these traits can improve yield.

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

Sravan *et al.* (2012) studied the interrelationship of grain yield and its component traits using 36 exotic breeding lines. Grain yield per plant had a 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. For maximizing the grain yield per plant emphasis should be given to a selection of characters such as high biological yield, harvest index and number of spikelets per panicle for further crop improvement programmes.

Patel *et al.* (2014) conducted a study to obtain information on inter-relationship of grain yield and associated characters using 44 diverse rice genotypes. The results of correlation studies indicated that genotypic correlation coefficients were higher in magnitude than the phenotypic correlation coefficients for most of the traits. Grain yield per plant was found to be 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.

Rashid *et al.* (2014) studied 20 diverse cultivars of rice for correlation. Among the traits, days to heading, days to maturity, the number of productive tillers, and 1000-grain weight showed highly significant positive correlation with grain yield per plant whereas, flag leaf area, plant height and panicle length showed a highly significant negative correlation with grain yield per plant. The number of grains per panicle was non-significant and positively 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 conditions whereas it was only positively correlated with harvest index under submerged conditions. Both plot yield and grain yield per plant show a positive association with panicle number, fertile grain number and fertility percentage, whereas grain yield per plant exhibited a positive association with harvest index under both the conditions.

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 the importance of these characters for yield improvement, while head rice recovery was found to be significantly and positively correlated with milling percent and hulling percent.

Biswajit *et al.* (2017) evaluated 50 diverse rice genotypes in low land submerged field conditions at two locations to study the association between yield and yield components under submerged conditions with more than 50 cm of water depth for two weeks at the 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 correlations coefficient from data collected on 83 rice genotypes. Grain yield per plant showed a positive association with panicle weight/plant, biological yield/plant, number of tillers/plant and harvest index, while, a negative association with plant height. Hence, biological yield per plant, harvest index and number of seeds per plant are identified as crucial traits for developing high yielding genotypes of rice for future breeding programmes.

Lahari *et al.* (2017) carried out an investigation with 49 genotypes laid out using a randomized complete block design with two replications under submergence during *Kharif* 2016 for evaluating character association and path analysis. Correlation studies revealed a 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 an investigation to establish the nature of the 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 the realization of high yield in rice.

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

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

Dhavaleshvar *et al.* (2019), carried out an experiment to determine the degree of association between grain yield and yield attributing characters in 27 advanced breeding lines of rice with four checks. The experiment was conducted in a randomised complete block design (RCBD) with three replications. The result from the study revealed that straw yield and harvest index showed a significant positive correlation with grain yield per hectare. Hence, the improvement of these traits through selection will automatically result in increased grain yield.

Sreedhar and Reddy (2019) studied the 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 m^2 and test weight exhibited a significant positive correlation with yield at both genotypic and phenotypic levels. A significant negative correlation was observed between number of filled grains per panicle and yield.

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

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. A 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 F_2 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.

Chamar *et al.* (2021) conducted an experiment to study the morphological characters and to estimate the correlation coefficient among yield and its contributing traits in rice germplasm. For this they evaluated 72 germplasm accessions along with three local checks. The grain yield per plant had a 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. The grain yield also showed negative correlation with plant height, days to 50 per cent flowering and days to maturity.

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 the 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, grain yield per plant exhibited non-significant but positive association.

Fentie *et al*. (2021) registered positive and highly significant phenotypic and genotypic correlations of grain yield ha^{-1} with filled grains per panicle, panicle weight, biomass yield and harvest index, but it had negative genotypic and phenotypic correlations 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, while days to flowering exerted a negative direct effect on grain yield at both genotypic and phenotypic levels. 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 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.

Mushtaq *et al.* (2021) carried out an experiment to determine the association between grain yield and yield attributing components among advanced breeding lines of rice. Association studies indicated that characters *viz*., Plant height, total number of tillers per plant, number of effective tillers per plant, panicle length, 1000 grain weight and grain yield per plant had a significant positive relationship with grain yield per plot indicating their role in breeding rice varieties for higher grain yield.

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 analysis in 53 breeding lines for 12 quantitative and ten quality parameters. Grain yield per plant exhibited a 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) conducted a field experiment with 20 rice genotypes of rice for trait association of grain yield and different yield-contributing agronomic characters. A 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 among rice breeding lines for yield and its component traits among 68 rice breeding lines. Estimates of association revealed that grain yield was found to have a 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. An experiment was conducted in a randomised block design with three replications with a check. Data for 13 quantitative characters were recorded. For character association, 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 because it helps in determining the nature and extent of the relationship existing between the yield and its contributing components and their association.

Niharika *et al.* (2022) carried out an investigation by using multi-parent advanced breeding lines of the MF_6 generation developed by crossing eight diverse varieties having desirable traits. The correlation studies on yield and its contributing traits revealed that the majority of the traits were positively associated with yield. A significant positive association was found between grain yield with number of tillers per plant, the number of productive tillers per plant, panicle length, the number of filled grains per panicle, total number of spikelets per panicle, test weight.

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 a 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 a positive and significant correlation.

Katkani *et al.* (2023) conducted an experiment for 32 advanced breeding lines of rice and represented the nature of association among the characters. Grain yield/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 EI, showed significant positive correlation with harvest index, biological yield/plant and length of panicle in E II and harvest index, number of grains per panicle, biological yield/plant, test weight and panicle length in E III.

2.4. To screen advanced breeding lines of rice under submergence condition.

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 a considerable amount of tolerance to submergence and yield low under such conditions. As there is a possibility of finding submergence tolerance in advanced lines, screening of advanced breeding lines of rice for their tolerance to submerged conditions can be helpful. In this regard, similar works related to the screening and evaluating advanced breeding lines of rice 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 a good source of submergence tolerance at the young seedling stage (10 days). CN 540 is found to be more resistant than FR13A at the 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 an 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, 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. SwarnanSub1 gave a higher grain yield than 'Swarna' with a yield advantage of up to 1.65 tonnes/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. Twenty days of submergence caused greater damage than 14 days of submergence in *Sub1* introgressed cultivars. Survival percentage reduced when plants were submerged for more period. The survival percentage of landraces was higher compared to *Sub1* introgressed cultivars.

Akinwale *et al.* (2012) evaluated the submergence tolerance of 20 rainfed lowland rice cultivars with a flood water depth of 1.5m for 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 conditions. 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 ten 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 a 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 re-generation, growth and development after de-submergence and showed a higher survival rate in 10 to 14 days of complete submergence with a 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 in Los Banos, Philippines, in the wet season 2009. 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.

Kato *et al.* (2014) screened 80 elite genotypes for tolerance under stagnant flooding stress in the lowland rice fields in the wet and dry seasons. Elite genotypes carrying *Sub1* showed 49 per cent lower yield than those without *Sub1* under stagnant flooding, with no differences under shallow water conditions. Few high-yielding *Sub1* genotypes tolerated stagnant flooding and had intermediate stature with more shoot elongation in response to rising water than a moderately tolerant *Sub1* reference variety, resulting in greater canopy expansion and higher yield.

Ranawake *et al.* (2014) screened 25 rice cultivars for submergence tolerance at seedling and vegetative stages. At the seedling stage, germinated seedlings were grown for two weeks and five days, nine days and fourteen days complete submergence stresses were given in separate experiments. Survival rate and plant height were recorded. At five days, nine days and fourteen 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 the vegetative stage. At 14-day complete submergence, Bg 379/2 had the 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 compared to that of control plants. 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. Twenty-six cultivars showed more than 40 per cent survivability. Twelve cultivars showed a 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, focusing on submergence tolerance traits and *Sub1* loci. Detailed allelic diversity study of *Sub1A* loci suggests 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 share both alleles of *Sub1A* loci (present in IR42 and FR13A groups) in addition to a new variant. Three rice genotypes 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 the IRRI standard method. Among all the lines none of them scored one with 100 per cent survival, two 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 a 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 lowest 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 BC_2F_3 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 than the parents and the susceptible check IR42.

Kumari *et al.* (2019) carried out an 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 conditions and yield potential. Higher 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 the 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 rice checks for submergence tolerance in the Indonesia Centre of Rice Research in different environmental conditions using an augmented design with five blocks in 1) Submergence condition conducted in submergence pool and 2) optimal conditions in the 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 the breeding programme.

Singh *et al.* (2022) conducted an experiment on the morphological and physiological basis of submergence tolerance in Rice with 18 rice genotypes both tolerant and susceptible. Sub1 rice varieties like Swarna, Sambha Mahsuri and BR-11 showed more than 80 per cent survival when 60 days old plants were subjected to 14 days of complete submergence in clear water and stagnant conditions. After 14 days of complete submergence reduction in plant height, dry weight, carbohydrate and chlorophyll content was observed more in susceptible genotypes than the tolerant ones like Swarna Sub-1, IR-64 Sub-1.

MATERIAL AND METHODS

III MATERIAL AND METHODS

The present investigation was conducted at AHRS, Kathalagere and ZAHRS, Navile, KSNUAHS, Shivamogga under artificially created submergence conditions and the details of material used and methods adopted during the investigation on "Assessment of Genetic Variability in Advanced Breeding Lines of Rice (*Oryza sativa* L.) and their Comparative Study under Submergence” 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 its attributing traits under non-submergence.

3.1.1 Experimental material

Forty five advanced breeding lines of cross RNR-15048 × TUNGA including check varieties *viz*., Tunga, RNR-15048, 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 breeding lines of rice 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 experimental layout was laid out in Randomised Complete Block Design (RCBD) with checks with two replications for testing 45 advanced breeding lines of rice. The seeds of 45 advanced breeding lines of rice were sown to raise the 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 labeled for recording the observations in each treatment. The mean of the observations recorded on these five plants was subjected to statistical analysis. The characters for which observations were recorded are described below.

3.1.2.2.1 Days to 50 per cent flowering

The total number of days taken by each rice genotype from the date of sowing to the opening of the first flower in 50 per cent of the plants was observed and recorded.

Table 3.1.1 List of rice genotypes used in the present experiment

Line no.	Genotypes	Line no.	Genotypes
1	R×T-7-4-2	28	R×T-9-1-11
2	R×T-6-4-5	29	R×T-8-9-19
3	R×T-2-4-5	30	R×T-9-1-12
4	R×T-3-6-7	31	R×T-8-9-20
5	R×T-4-5-1	32	R×T-9-1-13
6	R×T-5-9-5	33	R×T-8-9-21
7	R×T-3-4-2	34	R×T-9-1-14
8	R×T-2-7-8	35	R×T-8-9-22
9	R×T-8-9-9	36	R×T-4-1-15
10	R×T-9-1-2	37	R×T-8-9-23
11	R×T-8-9-10	38	R×T-6-1-16
12	R×T-9-1-3	39	R×T-8-9-5
13	R×T-8-9-11	40	R×T-9-1-17
14	R×T-9-1-4	41	R×T-8-9-25
15	R×T-8-9-12	42	R×T-9-1-18
16	R×T-9-1-5	43	R×T-8-9-26
17	R×T-8-9-13	44	R×T-9-1-19
18	R×T-9-1-6	45	R×T-8-9-27
19	R×T-8-9-14	46	RNR-15048 (Check I)
20	R×T-9-1-7	47	Tunga (Check I)
21	R×T-8-9-15	48	BPT-5204 (Check I)
22	R×T-9-1-8	49	JGL-1798 (Check I)
23	R×T-8-9-16	50	KHP 11 (Check I)
24	R×T-9-1-9	51	FR13A (Check II)
25	R×T-8-9-17	52	Swarna sub-1(Check II)
26	R×T-9-1-10	53	Jyothi (Check II)
27	R×T-8-9-18	54	BPT-5204 (Check II)

NOTE: 1. Rice genotypes from 46 to 50 were used as checks for experiment I.
2. Rice genotypes from 51 to 54 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 genotype from sowing to physiological maturity was observed and recorded.

3.1.2.2.3 Plant height (cm)

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

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

3.1.2.2.7 Number of spikelets per panicle

The number of spikelets (filled and chaffy) were counted in randomly selected five panicles and number of spikelets per panicle or the 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 the number of filled grains per panicle.

3.1.2.2.9 Spikelet fertility (%)

The number of filled grains were counted in randomly selected five panicles and averaged to obtain the number of filled grains per panicle. Spikelet fertility per panicle was estimated by the ratio of the 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 grams (g).

3.1.2.2.11 Length Breadth (L/B) ratio

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

3.1.2.2.12 Grain yield per plant(g)

The total weight of the grains from five plants from each rice genotype 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 in the present study consisted of 45 advanced breeding lines of rice with Swarna sub-1 and FR13A as tolerant checks at the 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 advanced breeding lines of rice included in the study is 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 the advanced breeding lines of rice for submergence tolerance. Forty five advanced breeding lines of rice were sown during *Kharif* 2022 for raising the nursery. Twenty-one days old seedlings were transplanted manually into the main field with a single seedling per hill in RCBD design with a 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 at depth of 50 to 60 cm for a period of 15 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 that survived after fifteen days of submergence was recorded to know the survival percentage. The number of seedlings before submergence and number of seedlings that survived after submergence were noted and the survival percentage for each genotype was calculated.

3.2.2.2.1 Survival percentage

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

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

3.2.2.2.2 Stem elongation (%)

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

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

3.3 Statistical analysis

The mean values of five randomly selected plants for recording twelve different characters were used for statistical analysis. The experimental data on 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 mean value data 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 the Department of Genetics and Plant Breeding, KSNUAHS, Shivamogga.

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

Where,

r = number of replications
t = number of genotypes
MSSR= replication mean sum of squares
MSSG= genotype mean sum of squares
MSSE= error mean sum of squares

df = degrees of freedom
SSr = replication sum of squares
SSg = genotypic sum of squares
SSe = error sum of squares (SSt-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. Genotype sum of squares (SSG) = $\Sigma\ (Ti)^2/\text{n} - \text{CF}$

   Where, n= Number of replications

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

   Where, s= Number of genotypes

4. 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).

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

Where,

x_i = ith observation of a population

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 estimated by dividing the standard deviation (SD) by the square root of a number of observations (n) in the sample and is denoted by SE.

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

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

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

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

Where,

r= number of replications

MSSE= error mean sum of square

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 square

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 the 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).

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

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

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)

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

3.3.3.2 Genotypic coefficient of variation (GCV)

$$\text{GCV} = \frac{\sigma_g}{\overline{\overline{X}}} \times 100$$

Where,

$\overline{X}$= grand mean of the character

σ_p= phenotypic standard deviation

σ_g= genotypic standard deviation

Categorization of the range of variability as proposed by Shivasubramanian 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, is the ratio of genotypic variance to the total variance in the non-segregating populations. Heritability was calculated by the formula given by Lush (1949).

$$h^2_{bs} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

h^2_{bs} = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

As suggested by Johnson *et al.* (1955), (h^2_{bs}) 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).

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

Where,

H = Heritability coefficient

$\sqrt{\sigma^2_p}$ = Phenotypic standard deviation

K = Selection differential at a given intensity

3.3.4.3 Genetic advance as percent of the mean (GAM)

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

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

Where,

GA = Expected genetic advance

$\overline{X}$ = 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 Genetic diversity

3.3.5.1 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 the Department of Genetics and Plant Breeding, KSNUAHS, Shivamogga. The generalized distance between any two populations is given by formula,

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

Where,

D^2 = square of generalized distance

λ_{ij}= reciprocal of the common dispersal matrixσ_{ai}= (μ_{i1}-μ_{i2})

σ_{aj}= (μ_{j1}-μ_{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 byRao (1952).

3.3.5.2.1 Intra cluster distance

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

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

Where,

ΣD_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.

3.3.6 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. Both 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.

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

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

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.

$\sigma_g^2$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.

EXPERIMENTAL RESULTS

IV EXPERIMENTAL RESULTS

The aim of the current study was to examine the kind and extent of genetic diversity and variability with regard to yield and features that contribute to yield in 45 advanced breeding lines of rice in relation to 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 Genetic divergence among advanced breeding lines of rice for grain yield and its attributing traits

4.3 Phenotypic correlation analysis for 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 per plant

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

Analysis of variance (ANOVA) results for advanced breeding lines of rice under the non-submergence condition showed substantial differences for all traits examined, showing that those advanced breeding lines had enough population variability. Table 4.1.1 shows the variance analysis for each of the 12 attributes.

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 (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 were seen to vary between 87.00 and 124.50 days, with a mean of 102.59 days. The earliest to flower was R×T-8-9-22 at 87 days, while the latest was KHP-11 at 124 days. High heritability of 94.72 per cent and moderate genetic progress as per cent mean of 14.95 were observed along with low PCV and GCV of 7.66 and 7.46 per cent respectively.

Table 4.1.1 Analysis of variance for yield and its attributing characters in advanced breeding lines of rice 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	3.61	3.61	14.59	2.07	0.89	0.3249
Genotypes	49	120.38^{**}	120.38^{**}	728.89^{**}	11.98^{**}	12.10^{**}	9.09^{**}
Error	49	3.26	3.26	64.57	2.07	2.21	0.74
CD (5%)		3.63	3.63	16.11	2.09	2.99	1.73
CD (1%)		4.84	4.84	21.49	3.86	3.98	2.30
CV		1.76	1.36	5.04	9.90	10.30	4.04

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 (cm)	Grain yield per plant (g)
Replication	1	8.01	0.90	5.18	6.90	0.08	4.08
Genotypes	49	4683.86^{**}	3998.93^{**}	13.72^{**}	23.22^{**}	0.30^{**}	129.98^{**}
Error	49	890.11	886.03	2.57	3.56	0.03	28.85
CD (5%)		59.96	59.82	3.22	3.79	0.37	10.79
CD (1%)		79.96	79.77	4.30	5.06	0.49	14.39
CV		11.22	12.27	1.66	7.36	5.44	13.96

**- significance at 1% level of significance

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

SL NO.	Character	Mean	Range		GCV (%)	PCV (%)	h^2_{bs} (%)	GAM (%)
			Minimum	Maximum				
1	Days to 50 per cent flowering	102.59	87.00	124.50	7.46	7.66	94.72	14.95
2	Days to maturity	132.59	117.00	154.50	5.77	5.93	94.72	4.57
3	Plant height (cm)	158.98	98.50	181.50	11.47	12.53	83.79	21.62
4	Number of tillers per plant	14.54	9.90	22.50	15.30	18.23	70.51	26.47
5	Number of productive tillers per plant	14.43	10.10	21.35	15.41	18.54	69.11	26.39
6	Panicle length(cm)	21.31	16.55	24.15	9.59	10.40	84.96	18.21
7	Number of spikelets per panicle	265.79	176.50	370.15	16.39	19.86	68.06	27.85
8	Number of filled grains per panicle	242.65	142.20	332.80	16.26	20.37	63.72	26.74
9	Spikelet fertility (%)	96.44	86.75	98.42	2.15	2.96	68.40	4.17
10	Length Breadth ratio (cm)	3.37	2.64	4.56	10.90	12.18	80.06	20.09
11	Test weight(g)	25.64	12.25	33.50	12.23	14.27	73.43	21.59
12	Grain yield per plant (g)	38.48	25.15	45.80	18.48	23.16	63.67	30.38

4.1.2 Days to maturity

The range of the mean days to maturity was determined to be between 117 and 154.59 days. The earliest to mature was R×T-8-9-22 at 117 days, and the latest to mature was KHP-11 at 154 days. Low PCV and GCV of 5.93 and 5.77 per cent, respectively were noted. High heritability estimate of 94.72 per cent and a moderate GAM of 11.57 per cent was recorded for the trait.

4.1.3 Plant height (cm)

It was discovered that the advanced breeding lines of rice had different plant heights. Plant height ranged from 98.50 cm to 181.50 cm, with mean value of 158.98 cm. JGL-1798 measured a maximum height of 181.50 cm, whereas R×T-8-9-9 showed a minimum height of 98.50 cm. Moderate PCV and GCV of 12.53 and 11.47 per cent, respectively were recorded. A high heritability of 83.79 per cent and a high GAM of 21.62 per cent were found for this variable.

4.1.4 Number of tillers per plant

The number of tillers per plant varied significantly among advanced breeding lines of rice with a range of 9.90 to 22.50 and a mean value of 14.54. The lowest number of tillers per plant was 16 for R×T-9-1-12 and the highest number was 24 for JGL-1798. The moderate genotypic and phenotypic coefficients of variation were measured at 18.23 and 15.30 per cent, respectively. High genetic advancement as per cent mean of 26.47 and high heritability of 70 per cent was noted.

4.1.5 Number of productive tillers per plant

The number of productive tillers per plant significantly differed among advanced breeding lines of rice with a range of 10.10 to 21.35 and a mean value of 14.43. The lowest number of tillers of 16 per plant was recorded by R×T-9-1-12 and highest number of tillers was recorded by JGL-1798 with 21 tillers per plant. Moderate phenotypic and genotypic coefficients of variability of 18.54 and 15.41 per cent were observed, respectively. Moderate genetic advance as per cent mean of 26.39 and high heritability of 69.11 per cent were noticed.

4.1.6 Panicle length (cm)

A wide range of variability was exhibited by the panicle length among advanced breeding lines of rice. It was ranging from 16.55 to 24.15 cm with a mean value of 21.31 cm. JGL-1798 exhibited highest panicle length of 24.15 cm and lowest by R×T-8-9-18 of 16.55 cm. Moderate PCV and low GCV value of 9.59 and 10.40 per cent, respectively, exhibited by the trait coupled with a high heritability of 84.96 per cent and moderate GAM of 18.21 per cent was recorded.

4.1.7 Number of spikelets per panicle

Wide variations in number of spikelets per panicle were visible. The trait has a moderate PCV and GCV of 19.86 and 16.39 per cent, respectively, along with a high heritability of 68.06 per cent and a high GAM of 27.85 per cent. With a range of 176.50 to 370.15 a mean value of 265.79 was noted. The minimum number of spikelets per panicle for R×T 9-1-9 was 176, while the maximum number of spikelets per panicle for R×T 8-9-23 was 370.

4.1.8 Number of filled grains per panicle

High PCV and moderate GCV of 20.37 and 16.26 per cent, respectively were noticed for the trait number of filled grains per panicle coupled with a high heritability of 63.72 per cent and high GAM of 26.74 per cent. Variability was found more with the mean value of 242.65 recorded and the range of 142.20 to 332.80. R×T 9-1-9 exhibited a minimum number of 142 filled grains per panicle whereas R×T 8-9-23 had a maximum number of 332 filled grains per panicle.

4.1.9 Spikelet fertility

The percentage of spikelet fertility varied from 86.75 to 98.42. It was discovered that the mean spikelet fertility value was 96.44 per cent. R×T-9-1-7 had highest spikelet fertility which was found to be 98.42 and JGL-1798 had lowest spikelet fertility which was 86.75. The trait spikelet fertility demonstrated low PCV and GCV of 2.96 and 2.15, respectively with a high heritability of 68.40 per cent. The characteristic showed low genetic advance with a mean of 4.17 per cent.

4.1.10 Test weight (g)

Test weight had a range from 12.25 to 33.50 grams with a mean of 33.50 grams. RNR-15048 has recorded lowest test weight of 12.25 grams and Tunga recorded highest test weight of 33.50 grams. Moderate PCV and GCVwere found 14.27 and 12.23 per cent, respectively with a high heritability of 73.43 per cent and high GAM of 21.59 per cent recorded.

4.1.11 Length breadth ratio

Length breadth ratio had a range of 2.64 to 4.56. The mean length and breadth ratio was found to be 3.37. Highest length breadth ratio was exhibited by R×T-9-1-19 of value 4.56 and lowest was by R×T-9-1-7 value of 2.64. Low GCV and PCV of 10.90 and 12.18, respectively exhibited by the trait with a high heritability of 80.06 per cent. Moderate genetic advance as per cent mean of 20.09 was observed.

4.1.12 Grain yield per plant (g)

The range of the grain yield per plant was from 25.15 grams to 45.80 grams with a mean of 38.48 grams showing significant variation. R×T-9-1-11 achieved lowest grain yield of 25 grams. While R×T-9-1-14 recorded highest grain yield of 45 grams. For this feature, high PCV and moderate GCV were valued at 23.16 and 18.48 per cent, respectively. A high GAM of 30.38 and high heritability of 63.67 per cent were observed.

4.2 Genetic divergence among advanced breeding lines of rice for grain yield and its attributing traits

In order to efficiently use genetically divergent parents in a hybridization programme, it is helpful to examine a large number of germplasm lines/genotypes for genetic diversity using D^2 statistics. Forty five advanced breeding lines of rice along with five checks were subjected to a Mahalanobis D^2 analysis for the current study.

4.2.1 Clustering pattern of advanced breeding lines of rice

Seven clusters from 45 advanced breeding lines of rice along with five checks were obtained based on the D^2 statistics. The lines were formed into groups in such a way that within each cluster, the D^2 statistics value was smaller than those between the clusters. Table 4.2.1 represents the clustering patterns of all the 45 advanced breeding lines of rice along with five checks.

The clustering pattern obtained revealed that biggest cluster formed was cluster I which had 40 lines within it. This was followed by cluster II, III, IV and V each with two lines present in the cluster; cluster VI and VII were found to have one line in it.

4.2.2 Intra and inter clusters distance

The distance for the 45 advanced breeding lines of rice along with five checks were assessed within the cluster and also between the distance of two clusters. As presented in table 4.2.2. Cluster V exhibited a maximum intra cluster distance of 29.51 when compared with all the seven clusters, which was followed by cluster IV (27.19), cluster I (26.49) and cluster III (24.06). The inter cluster distance was exhibited highest between cluster VI and cluster VII (210.25), followed by distance between cluster II and cluster V (162.58) indicating that the lines within these clusters are highly diverse. The inter cluster distance lowest was noticed between cluster IV and cluster VII (40.54) followed by cluster III and cluster IV (44.18) indicating that the traits within the clusters were less diverse.

4.2.3 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 by seven clusters are presented in Table 4.2.3.

4.2.3.1 Days to 50 per cent flowering

Days to 50 per cent flowering was found to have highest cluster mean value of 122.00 for cluster III, followed by cluster IV (111.50). Lowest value of clustermean was recorded for cluster VII (95.00), followed by cluster V (96.00).

Table 4.2.1 Clustering pattern of advanced breeding lines of rice based on D^2 values

Cluster number	Number of genotypes	Genotypes
I	40	R×T-7-4-2, R×T-6-4-5, R×T-2-4-5, R×T-3-6-7, R×T-4-5-1, R×T-5-9-5, R×T-3-4-2, R×T-2-7-8, R×T-8-9-9, R×T-9-1-2, R×T-8-9-10, R×T-9-1-3, R×T-8-9-11, R×T-9-1-4, R×T-8-9-12, R×T-9-1-5, R×T-9-1-6, R×T-8-9-14, R×T-8-9-15, R×T-9-1-8, R×T-8-9-16, R×T-9-1-9, R×T-8-9-17, R×T-9-1-10, R×T-9-1-11, R×T-8-9-19, R×T-9-1-12, R×T-8-9-20, R×T-9-1-13, R×T-8-9-21, R×T-9-1-14, R×T-4-1-15, R×T-8-9-23, R×T-6-1-16, R×T-8-9-5, R×T-9-1-17, R×T-8-9-25, R×T-9-1-18, R×T-8-9-26, R×T-8-9-27
II	2	R×T-8-9-13, R×T-9-1-19
III	2	Tunga, KHP-11
IV	2	RNR-15048, BPT-5204
V	2	R×T-9-1-7, R×T-8-9-22
VI	1	R×T-8-9-18
VII	1	JGL-1798

Table 4.2.2 Intra and inter cluster distances for yield and its component characters in advanced breeding lines of rice

	I	II	III	IV	V	VI	VII
I	**26.49**	84.01	68.17	103.73	44.31	51.03	130.12
II		**16.57**	104.24	88.59	162.58	56.68	142.47
III			**24.06**	44.18	114.08	117.40	80.78
IV				**27.19**	158.96	132.90	40.53
V					**29.51**	93.53	155.02
VI						**0.00**	210.25
VII							**0.00**

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

Table 4.2.3 Cluster means for yield and its component characters in advanced breeding lines of rice

Cluster/Character	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}
I	105.03	134.76	167.72	15.16	14.77	22.23	237.25	233.63	95.41	28.71	3.30	37.53
II	105.00	134.50	157.90	15.70	15.45	22.03	271.95	269.60	97.18	30.61	4.45	38.80
III	122.00	152.00	127.80	17.69	16.75	22.20	244.43	231.72	93.54	31.63	3.32	45.58
IV	111.50	141.50	106.40	17.78	17.60	20.95	276.60	258.94	95.53	25.78	3.95	44.30
V	96.00	124.00	164.63	17.05	15.28	20.53	203.90	199.63	96.24	28.05	2.85	33.45
VI	110.50	140.50	170.40	10.80	10.10	16.55	196.35	196.35	95.01	24.35	3.84	29.70
VII	95.00	125.00	98.50	21.50	20.90	24.15	360.20	327.65	93.85	24.90	3.70	44.30

Where,

X_1 = Days to 50 per cent flowering
X_2 = Days to maturity
X_3 = Plant height (cm)
X_4 = Number of tillers per plant
X_5 = Number of productive tillers per plant
X^6 = Panicle length (cm)
X_7 = Number of spikelets per panicle
X_8 = Number of filled grains per panicle
X_9 = Spikelet fertility (%)
X_{10} = Test weight (g)
X_{11} = Length breadth ratio
X_{12} = Grain yield per plant (g)

4.2.3.2 Days to maturity

The cluster mean value was maximum for days to maturity for cluster III (152.00), followed by cluster IV (141.50). The cluster mean value was minimum for cluster IV (124.00), followed by cluster VII (125.00).

4.2.3.3 Plant height (cm)

Plant height exhibited the maximum cluster mean value of 170.40 for cluster VI, followed by cluster I (167.72). Whereas lowest cluster mean value was observed for cluster VII (98.50) followed by cluster IV (106.40).

4.2.3.4 Number of tillers per plant

Number of tillers per plant exhibited highest cluster mean value in cluster VII (21.50), followed by cluster IV (17.78) and lowest cluster mean value was found for cluster VI (10.80) followed by cluster I (15.16).

4.2.3.5 Number of productive tillers per plant

Maximum cluster mean value was found for the number of productive tillers per plant in cluster VII (20.90) followed by cluster IV (17.60). Whereas mean cluster value was lowest for cluster VI (10.10) followed by cluster I (14.77).

4.2.3.6 Panicle length (cm)

Panicle length exhibited highest cluster mean value of 24.15 cm by the cluster VI, followed by cluster I (22.23 cm). Cluster VI (20.53cm) followed by cluster V (16.55cm), exhibited lowest cluster mean value.

4.2.3.7 Number of spikelets per panicle

The highest cluster mean value of 360.20 was noticed for the trait numberof spikelets per panicle in cluster VII, followed by cluster IV (276.60). However, cluster mean value was lowest for cluster VI (196.35), followed by cluster V (203.90).

4.2.3.8 Number of filled grains per panicle

The number of filled grains per panicle exhibited the highest cluster mean value of 327.65 by cluster VII, followed by cluster II (269.60). Also, lowest cluster mean was noticed for cluster VI (196.35), followed by cluster V (199.63).

4.2.3.9 Spikelet fertility (%)

The maximum cluster mean value for spikelet fertility was noticed by cluster II (97.18), followed by cluster V (96.24). The lowest cluster mean value wasobserved for cluster III (93.54) followed by cluster VII (93.85).

4.2.3.10 Test weight (g)

Test weight exhibited highest cluster mean value of 31.61 g in cluster III followed by cluster II (30.61g). Whereas lowest cluster mean value was noticed in cluster VI (24.35 g) followed by cluster VII (24.90 g).

4.2.3.11 Length breadth ratio

Length breadth ratio recorded highest cluster mean value for cluster II(4.45), followed by cluster IV (3.95). However, the lowest cluster mean was recorded by cluster V (2.85), followed by cluster I (3.30).

4.2.3.12 Grain yield per plant (g)

Grain yield per plant recorded highest cluster mean value in cluster III (45.58 g), followed by cluster IV and VII (44.30 g). Cluster mean value was observed to be lowest for cluster VI (29.70 g), followed by cluster V (33.45 g).

4.2.4 Contribution of different characters towards divergence

The contribution of the traits studied towards genetic divergence in percentage was recorded and represented in Table 4.2.4.

Among all the characters studied for yield and its attributing traits percentage contribution to total divergence differed in different traits; grain length breadth ratio (21.7 %) contributed the highest for diversity among the lines, followed by plant height (15.8%), days to 50 per cent flowering (12.0%), number of spikelets per panicle (11.6 %), grain yield (9.9%), panicle length (7.3%), number of tillers per plant (6%), number of productive tillers per plant (4.4%), test weight (4.2%), number of filled grains per panicle (2.9%), spikelet fertility (2.7%) and days to maturity (1.5%).

4.3 Phenotypic correlation analysis for yield and its attributing traits.

To ascertain the nature of the relationship between yield and its corresponding features under non-submergence conditions, phenotypic correlation among 12 quantitative characters was determined and is shown in Table 4.3.1.

4.3.1 Correlation of grain yield per plant with other characters

Number of tillers per plant (r = 0.62), number of productive tillers per plant (r = 0.68), panicle length (r = 0.57), number of filled grains per panicle (r = 0.72), number of spikelets per panicle (r = 0.70), spikelet fertility (r = 0.58), test weight (r = 0.37), and length to breadth ratio (r = 0.25) were all found to be significantly and positively correlated with grain yield. Days to 50 per cent flowering had a non-significant negative association with grain yield (r = -0.14), as did days to maturity (-0.08) and plant height (-0.13).

Table 4.2.4 Contribution of different traits towards total divergence

SL NO.	Character	Contribution %
1	Length breadth ratio	21.7
2	Plant height	15.8
3	Days to50 per cent flowering	12.0
4	Number of spikelets per panicle	11.6
5	Grain yield per plant	9.9
6	Panicle length	7.3
7	Number of tillers per plant	6.0
8	Others	16

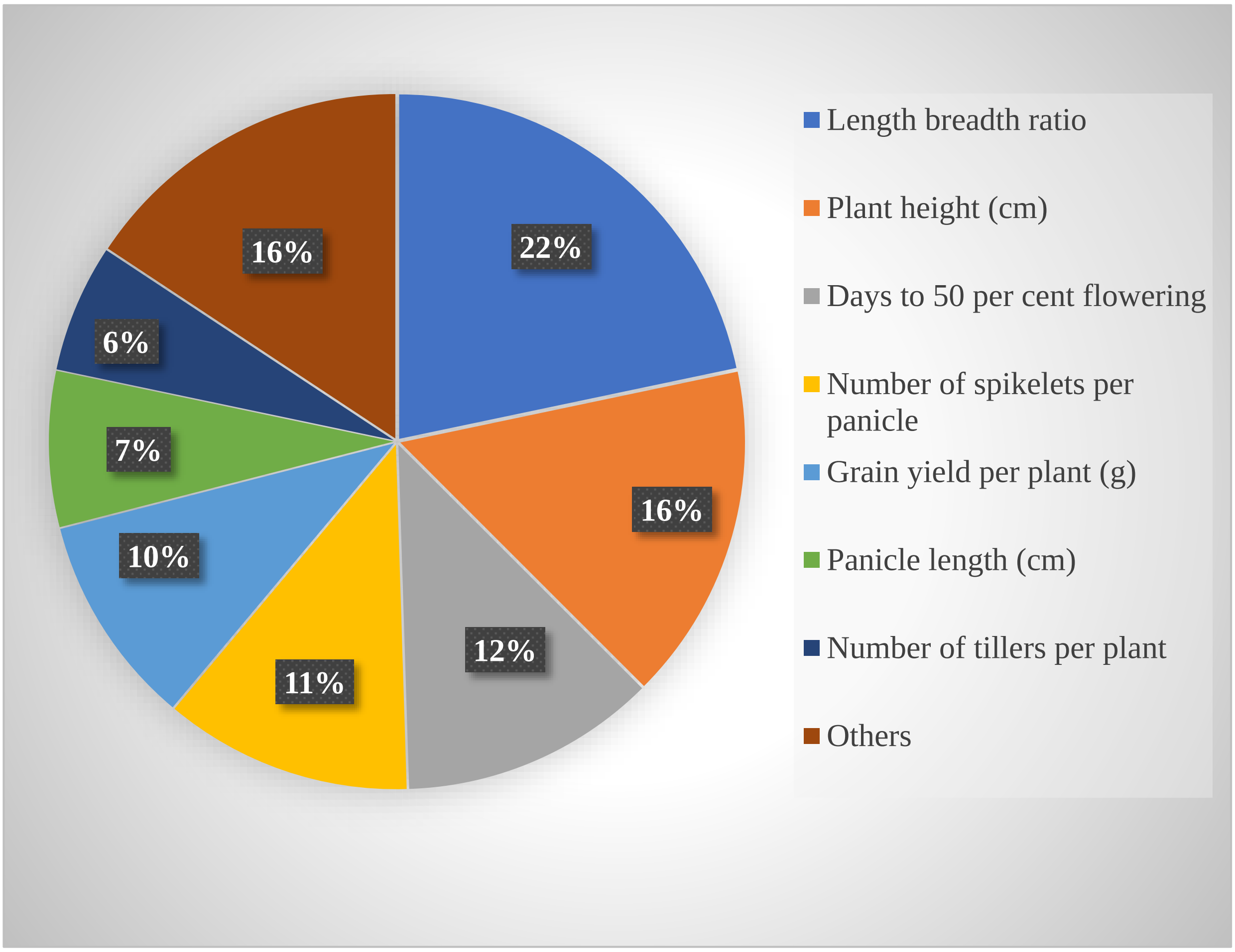

Fig 1: Per cent contribution of different traits towards total divergence

Table 4.3.1 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}	
1	0.82**	-0.23*	-0.22*	-0.27**	-0.26**	-0.28**	-0.33**	-0.33**	-0.03	-0.08	-0.14	X_1
	1	-0.27**	-0.14	-0.17	-0.28**	-0.28**	-0.31**	-0.30**	0.053	-0.08	-0.08	X_2
		1	-0.24*	-0.20*	0.08	-0.10	-0.04	0.19	0.08	-0.28**	-0.13	X_3
			1	0.84**	0.43**	0.35**	0.35**	0.34**	0.21*	0.27**	0.62**	X_4
				1	0.52**	0.43**	0.45**	0.42**	0.30**	0.24^*	0.68**	X_5
					1	0.46**	0.50**	0.41**	0.38**	0.09	0.57**	X_6
						1	0.97**	0.45**	0.05	0.14	0.70**	X_7
							1	0.53**	0.16	0.16	0.72**	X_8
								1	0.42**	0.08	0.58**	X_9
									1	0.05	0.25*	X_{10}
										1	0.37**	X_{11}
											1	X_{12}

*, ** - significant at 5% and 1% level respectively.

Where,

X_1- Days to 50 per cent flowering
X_2- Days to maturity
X_3- Plant height (cm)
X_4- Number of tillers per plant
X_5- Number of productive tillers per plant
X_6- Panicle length (cm)
X_7- Number of spikelets per panicle
X_8- Number of filled grains per panicle
X_9- Spikelet fertility (%)
X_{10}- Test weight (g)
X_{11}- Length breadth ratio
X_{12}- Grain yield per plant (g)

4.3.2 Correlation among yield attributing characters

4.3.2.1 Days to 50 per cent flowering

Days to 50 per cent flowering showed a substantial positive correlation with days to maturity (0.82). It showed a significant negative correlation (-0.23) with plant height, (-0.22) number of tillers per plant, (-0.27) number of productive tillers per plant, (-0.33) number of filled grains per panicle, (-0.28) number of spikelets per panicle, (-0.26) panicle length and (-0.33) spikelet fertility. Non-significant negative correlation with (-0.08) grain length and breadth ratio and test weight (-0.03).

4.3.2.2 Days to maturity

Days to maturity have shown a significant positive correlation with days to 50 per cent flowering (0.82). It exhibited a positive correlation with test weight (0.05). It exhibited significant negative correlation with plant height (-0.27), panicle length (-0.28), number of filled grains per panicle (-0.31), number of spikelets per panicle (-0.28) and spikelet fertility (-0.30). It exhibited a non-significant negative correlation with number of tillers per plant (-0.14), number of productive tillers per plant (-0.17) and grain length and breadth ratio (-0.08).

4.3.2.3 Plant height (cm)

A non-significant positive association was shown by plant height with panicle length (0.08) spikelet fertility (0.19)and test weight (0.08). With days to 50 per cent flowering (-0.23), days to maturity (-0.27), number of tillers per plant (-0.24), number of productive tillers per plant (-0.20) and grain length and breadth ratio (-0.28), was found to be significantly negatively correlated with grain yield. A non-significant negative correlation was found with number of filled grains per panicle (-0.04) and number of spikelets per panicle (-0.10).

4.3.2.4 Number of tillers per plant

Number of tillers per plant showed a significant positive correlation with number of productive tillers per plant (0.84), panicle length (0.43), number of filled grains per panicle (0.35), number of spikelets per panicle (0.35), spikelet fertility (0.34), test weight (0.21) and grain length breadth ratio (0.27). Whereas a significant negative correlation was found with days to 50 per cent flowering (-0.22), days to maturity (-0.14) and plant height (-0.24).

4.3.2.5 Number of productive tillers per plant

Significant positive correlation were found between number of productive tillers per plant and number of tillers per plant (0.84), panicle length (0.52), number of filled grains per panicle (0.45), number of spikelets per panicle (0.43), spikelet fertility (0.42), test weight (0.30) and grain length and breadth ratio (0.24). Significant negative correlation with plant height (-0.20) and days to 50 per cent flowering (-0.27) were observed. In contrast, a non-significant negative association was seen for days to maturity (-0.17).

4.3.2.6 Panicle length (cm)

Panicle length was noticed to have a significant positive correlation with all the traits like number of tillers per plant (0.43), number of productive tillers per plant (0.52), number of filled grains per panicle (0.50), number of spikelets per panicle (0.46), spikelet fertility (0.41) and test weight (0.38). Non-significant positive correlation with plant height (0.08) and grain length and breadth ratio (0.09). Significant negative correlation with days to 50 per cent flowering (-0.26) and days to maturity (-0.28).

4.3.2.7 Number of spikelets per panicle

Number of spikelets per panicle exhibited a significant positive correlation with number of tillers per plant (0.35), number of productive tillers per plant (0.43), panicle length (0.46), spikelet fertility (0.45) and number of filled grains per panicle (0.97). A non-significant positive correlation was seen with test weight (0.05) and grain length breadth ratio (0.14). Significant negative with days to 50 per cent flowering (-0.28) and days to maturity (-0.28) and non-significant negative correlation with plant height (-0.10).

4.3.2.8 Number of filled grains per panicle

A significant positive correlation with number of filled grains per panicle was accompanied by the number of tillers per plant (0.35), number of productive tillers per plant (0.45), panicle length (0.50), number of spikelets per panicle (0.97) and spikelet fertility (0.53). A non-significant positive correlation was noticed with test weight (0.16) and grain length and breadth ratio (0.16). There is a significant negative correlation with days to 50 per cent flowering (-033.) and days to maturity (-0.31) and a non-significant negative correlation plant height (-0.04).

4.3.2.9 Spikelet fertility (%)

Spikelet fertility had a significant positive association with the number of tillers per plant (0.34), number of productive tillers per plant (0.42), panicle length (0.41), number of filled grains per panicle (0.53), number of spikelets per panicle (0.45) and test weight (0.42). A non-significant positive association with spikelet fertility was exhibited by plant height (0.19) and grain length and breadth ratio (0.08). Significant negative correlation was exhibited by days to 50 per cent flowering (-0.33) and days to maturity (-0.30).

4.3.2.10 Test weight (g)

Test weight exhibited a significant positive correlation with number of tillers per plant (0.21), number of productive tillers per plant (0.30), panicle length (0.38) and spikelet fertility (0.42). Whereas a positive non-significant correlation was found with days to maturity (0.05), plant height (0.08), number of filled grains per panicle (0.16), number of spikelets per panicle (0.05) and grain length and breadth ratio (0.05). A non-significant negative correlation was exhibited by days to 50 per cent flowering (-0.04).

4.3.2.11 Length breadth ratio

A significant positive association with grain length and breadth ratio was shown by number of tillers per plant (0.27), number of productive tillers per plant (0.24) and test weight (0.05). A non-significant positive correlation was exhibited by panicle length (0.09), test weight (0.05), number of filled grains per panicle (0.16), number of spikelets per panicle(0.14) and spikelet fertility (0.08). Whereas a negative significant association was observed for plant height (-0.28), a non-significant negative association was observed for daysto 50 per cent flowering (-0.08) and days to maturity (-0.08).

4.4 Screening of advanced breeding lines of rice for submergence tolerance

Forty five advanced breeding lines of rice along with two susceptible local checks Jyothi, BPT-5204 and two tolerant national checks FR13A, Swarna sub-1 were evaluated for survival percentage under submerged conditions. The evaluation was done by taking observation of the number of plants that survived 14 days after de-submergence and scored from 1 to 9 according to the Standard Evaluation Method recommended by the International Rice Research Institute (IRRI) 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 5.6 to 96.0 per cent. None of the advanced breeding lines of rice had 100 per cent survival with a score of 1, whereas only one rice genotype Swarna sub-1 recorded the highest survival rate of 96 per cent with a score of 3. FR13A scored 5 with a survival percentage of 85 per cent. Five lines including R×T-8-9-25, R×T-8-9-17, R×T-8-9-14, R×T-5-9-5, R×T-2-4-5 scored 7 with a survival percentage of 50 per cent. Forty lines including Jyothi and BPT-5204 scored 9 with the survival percentage range between 0 to 49 per cent, R×T-7-4-2 (11.1%), R×T-6-4-5 (11.1%), R×T-3-6-7 (22.2%), R×T-4-5-1 (27.8%), R×T-3-4-2 (11.1%), R×T-2-7-8 (5.6%), R×T-8-9-9 (5.6%), R×T-9-1-2 (5.6%), R×T-8-9-10 (5.6%), R×T-9-1-3 (5.6%), R×T-8-9-11 (11.1%), R×T-9-1-4 (5.6%), R×T-8-9-12 (11.1%), R×T-9-1-5 (27.8%), R×T-8-9-13 (5.6%), R×T-9-1-6 (44.4%), R×T-9-1-7 (27.8%), R×T-8-9-15 (5.6%), R×T-9-1-8 (27.8%), R×T-8-9-16 (5.6%), R×T-9-1-9 (5.6%), R×T-9-1-10 (5.6%), R×T-8-9-18 (5.6%), R×T-9-1-11 (5.6%), R×T-8-9-19 (11.1%), R×T-9-1-12 (11.1%), R×T-8-9-20 (44.4%), R×T-9-1-13 (22.2%), R×T-8-9-21 (5.6%), R×T-9-1-14 (5.6%), R×T-8-9-22 (44.4%), R×T-4-1-15 (27.8%), R×T-8-9-23 (11.1%), R×T-6-1-16 (16.7%), R×T-8-9-5 (44.4%), R×T-9-1-17(16.7%), R×T-9-1-18 (5.6%), R×T-8-9-26 (11.1%), R×T-9-1-19 (16.7%), R×T-8-9-27 (11.1%), Jyothi (30.0%) and BPT-5204 (22.2%).

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

Line no	Genotypes	Survival percentage (%)	Score
1	R×T-7-4-2	11.1	9
2	R×T-6-4-5	11.1	9
3	R×T-2-4-5	50.0	7
4	R×T-3-6-7	22.2	9
5	R×T-4-5-1	27.8	9
6	R×T-5-9-5	50.0	7
7	R×T-3-4-2	11.1	9
8	R×T-2-7-8	5.6	9
9	R×T-8-9-9	5.6	9
10	R×T-9-1-2	5.6	9
11	R×T-8-9-10	5.6	9
12	R×T-9-1-3	5.6	9
13	R×T-8-9-11	11.1	9
14	R×T-9-1-4	5.6	9
15	R×T-8-9-12	11.1	9
16	R×T-9-1-5	27.8	9
17	R×T-8-9-13	5.6	9
18	R×T-9-1-6	44.4	9
19	R×T-8-9-14	50.0	7
20	R×T-9-1-7	27.8	9
21	R×T-8-9-15	5.6	9
22	R×T-9-1-8	27.8	9
23	R×T-8-9-16	5.6	9
24	R×T-9-1-9	5.6	9
25	R×T-8-9-17	50.0	7
26	R×T-9-1-10	5.6	9
27	R×T-8-9-18	5.6	9
28	R×T-9-1-11	5.6	9
29	R×T-8-9-19	11.1	9
30	R×T-9-1-12	11.1	9
31	R×T-8-9-20	44.4	9
32	R×T-9-1-13	22.2	9
33	R×T-8-9-21	5.6	9
34	R×T-9-1-14	5.6	9
35	R×T-8-9-22	44.4	9
36	R×T-4-1-15	27.8	9
37	R×T-8-9-23	11.1	9
38	R×T-6-1-16	16.7	9
39	R×T-8-9-5	44.4	9
40	R×T-9-1-17	16.7	9
41	R×T-8-9-25	50.0	7
42	R×T-9-1-18	5.6	9
43	R×T-8-9-26	11.1	9
44	R×T-9-1-19	16.7	9
45	R×T-8-9-27	11.1	9
46	Jyothi	30.0	9
47	BPT-5204	22.2	9
48	FR 13A	85.0	5
49	Swarna sub1	96.0	3

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

Score	Survival percentage	No. of genotypes	Genotypes
1	100%	0	Nil
3	95-99%	1	Swarna sub 1
5	75-94%	1	FR 13A
7	50-74%	5	R×T-2-4-5, R×T-8-9-14, R×T-5-9-5, R×T-8-9-17, R×T-8-9-25
9	0-49%	42	R×T-7-4-2, R×T-6-4-5, R×T-3-6-7, R×T-4-5-1, R×T-3-4-2, R×T-2-7-8, R×T-8-9-9, R×T-9-1-2, R×T-8-9-10, R×T-9-1-3, R×T-8-9-11, R×T-9-1-4, R×T-8-9-12, R×T-9-1-5, R×T-8-9-13, R×T-9-1-6, R×T-9-1-7, R×T-8-9-15, R×T-9-1-8, R×T-8-9-16, R×T-9-1-9, R×T-9-1-10, R×T-8-9-18, R×T-9-1-11, R×T-8-9-19, R×T-9-1-12, R×T-8-9-20, R×T-9-1-13, R×T-8-9-21, R×T-9-1-14, R×T-8-9-22, R×T-4-1-15, R×T-8-9-23, R×T-6-1-16, R×T-8-9-5, R×T-9-1-17, R×T-9-1-18, R×T-8-9-26, R×T-9-1-19, R×T-8-9-27, Jyothi, BPT-5204

Among the national checks, Swarna sub-1 had the highest survival percentage of 96.0 per cent and FR13A had a survival percentage of 85.0 per cent and local checks Jyothi and BPT-5204 had a survival percentage of 30.0 and 22.2 per cent, respectively.

Out of 45 advanced breeding lines of rice, most of the lines (40) scored 9 with survival per cent ranging from 0 to 49 per cent. The highest survival percentage of 96 per cent was reported by national check Swarna sub-1. Among advanced breeding lines of rice R×T-8-9-25, R×T-8-9-17, R×T-8-9-14, R×T-5-9-5, R×T-2-4-5 scored 7 with a survival percentage of 50 per cent. Whereas checks Jyothi and BPT-5204 had the lowest survival percentage of score 9. Among advanced breeding lines of rice R×T-7-4-2, R×T-6-4-5, R×T-3-6-7, R×T-4-5-1, R×T-3-4-2, R×T-2-7-8, R×T-8-9-9, R×T-9-1-2, R×T-8-9-10, R×T-9-1-3, R×T-8-9-11, R×T-9-1-4, R×T-8-9-12, R×T-9-1-5, R×T-8-9-13, R×T-9-1-6, R×T-9-1-7, R×T-8-9-15, R×T-9-1-8, R×T-8-9-16, R×T-9-1-9, R×T-9-1-10, R×T-8-9-18, R×T-9-1-11, R×T-8-9-19, R×T-9-1-12, R×T-8-9-20, R×T-9-1-13, R×T-8-9-21, R×T-9-1-14, R×T-8-9-22, R×T-4-1-15, R×T-8-9-23, R×T-6-1-16, R×T-8-9-5, R×T-9-1-17, R×T-9-1-18, R×T-8-9-26, R×T-9-1-19, R×T-8-9-27 with score of 9. A list of the genotypes evaluated for submergence and 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 45 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 recorded for these parameters presented in Table 4.5.1.

4.5.1.1.Survival percentage

The survival per cent exhibited a mean value of 25.34 per cent with a range of 5.6 per cent to 96.0 per cent. High GCV (56.38) and PCV (59.66) along with high heritability (89.30), was recorded for survival percentage coupled with high genetic advance as per cent mean (109.74).

4.5.1.2.Stem elongation (%)

The mean stem elongation of 33.90 per cent with the range from 10.86 to 52.92 per cent was obtained. High GCV (31.38) and PCV (33.48) were recorded for stem elongation per cent. High heritability of 87.84 per cent. Per cent for stem elongation was seen with high genetic advance as per cent mean value of 60.58.

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

SL NO.	Character	Mean	Range		GCV (%)	PCV (%)	h^2bs (%)	GAM (%)
			Minimum	Maximum				
1	Survival percentage	25.34	8.33	95.00	56.38	59.66	89.30	109.74
2	Stem elongation (%)	33.90	10.86	52.92	31.38	33.48	87.84	60.58

Where,

GCV = Genetic coefficient of variation

PCV = Phenotypic coefficient of variation

H2 (bs) = Heritability (broad sense)

GAM = Genetic advance as per cent mean

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

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

4.6.1 Survival percentage

Survival percentage under stress condition showed a significant positive correlation with grain yield (0.53) and a significant negative correlation was seen with stem elongation percentage (-0.31).

4.6.2 Stem elongation (%)

A non-significant negative correlation was exhibited by stem elongation percentage with survival percentage (-0.13), Whereas grain yield exhibited a significant negative correlation of value -0.31.

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 line, there are significant difference observed for the following five traits. The per cent difference for various traits between submergence and non-submergence condition revealed that days to 50 per cent flowering showed an increased number of days for flowering than non-submergence while the rest of the traits (number of tillers per plant, number of productive tillers per plant and test weight) exhibited decreased mean value under stress than under non-submergence. The comparison is represented in 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 45 advanced breeding lines of rice was found to be highest for R×T-3-4-2 (23.50%) followed by R×T-8-9-17 (21.24%) and the difference was found to be minimum for R×T-9-1-19 (3.45%) followed by R×T-2-7-8 (4.93%).

4.7.1.2 Number of tillers per plant

The maximum per cent difference in the number of tillers by advanced breeding lines of rice on comparing under submergence with non-submergence was found to be in R×T-4-5-1 (74.44%) followed by R×T-3-6-7 (73.4%). while the minimum difference was exhibited by R×T-8-9-27(12.7%) followed by R×T-9-1-12 (13.1%). The number of tillers per plant obtained was decreased under submergence condition than under non-submergence condition due to stress impact.

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	-0.13	0.53**
Stem elongation (%)		1	-0.31**
Grain yield per plant			1

**- significance at 1% level.

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

SL NO.	Genotypes	**Days to 50 percent flowering**		
		Submergence	Non-submergence	Change in % Mean
1	R×T-7-4-2	109.50	102.50	6.83
2	R×T-6-4-5	110.00	93.50	17.65
3	R×T-2-4-5	106.50	97.00	9.79
4	R×T-3-6-7	107.50	92.00	16.85
5	R×T-4-5-1	110.00	101.50	8.37
6	R×T-5-9-5	113.00	99.00	14.14
7	R×T-3-4-2	113.00	91.50	23.50
8	R×T-2-7-8	117.00	111.50	4.93
9	R×T-8-9-9	114.00	102.50	11.22
10	R×T-9-1-2	112.00	97.50	14.87
11	R×T-8-9-10	111.00	102.50	8.29
12	R×T-9-1-3	114.00	103.00	10.68
13	R×T-8-9-11	114.00	103.50	10.14
14	R×T-9-1-4	115.00	98.50	16.75
15	R×T-8-9-12	110.50	98.00	12.76
16	R×T-9-1-5	110.00	99.00	11.11
17	R×T-8-9-13	105.00	95.50	9.95
18	R×T-9-1-6	112.00	100.50	11.44
19	R×T-8-9-14	114.00	99.00	15.15
20	R×T-9-1-7	109.50	102.00	7.35
21	R×T-8-9-15	105.50	98.50	7.11
22	R×T-9-1-8	116.00	100.00	16.00
23	R×T-8-9-16	110.00	99.00	11.11
24	R×T-9-1-9	105.00	93.00	12.90
25	R×T-8-9-17	117.00	96.50	21.24
26	R×T-9-1-10	113.00	99.00	14.14
27	R×T-8-9-18	110.50	97.00	13.92
28	R×T-9-1-11	107.50	99.00	8.59
29	R×T-8-9-19	115.00	103.00	11.65
30	R×T-9-1-12	110.50	96.00	15.10
31	R×T-8-9-20	110.00	104.50	5.26
32	R×T-9-1-13	110.00	94.50	16.40
33	R×T-8-9-21	103.50	98.00	5.61
34	R×T-9-1-14	114.00	104.50	9.09
35	R×T-8-9-22	104.50	87.00	20.11
36	R×T-4-1-15	106.50	101.00	5.45
37	R×T-8-9-23	105.00	95.00	10.53
38	R×T-6-1-16	115.00	98.50	16.75
39	R×T-8-9-5	106.50	101.00	5.45
40	R×T-9-1-17	110.00	99.00	11.11
41	R×T-8-9-25	103.00	98.00	5.10
42	R×T-9-1-18	110.00	97.00	13.40
43	R×T-8-9-26	110.50	99.00	11.62
44	R×T-9-1-19	105.00	101.50	3.45
45	R×T-8-9-27	112.50	96.50	16.58

Table 4.7.1b 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×T-7-4-2	9.60	13.70	29.90
2	R×T-6-4-5	7.30	15.50	52.90
3	R×T-2-4-5	9.80	14.00	30.00
4	R×T-3-6-7	4.50	16.90	73.40
5	R×T-4-5-1	4.20	16.40	74.40
6	R×T-5-9-5	7.60	13.60	44.10
7	R×T-3-4-2	7.00	14.00	50.00
8	R×T-2-7-8	9.20	14.00	34.30
9	R×T-8-9-9	5.20	16.50	68.50
10	R×T-9-1-2	9.80	14.50	32.40
11	R×T-8-9-10	5.80	13.50	57.00
12	R×T-9-1-3	7.70	12.70	39.40
13	R×T-8-9-11	8.40	15.20	44.70
14	R×T-9-1-4	5.30	14.30	62.90
15	R×T-8-9-12	4.50	15.50	71.00
16	R×T-9-1-5	8.60	13.20	34.80
17	R×T-8-9-13	7.70	18.00	57.20
18	R×T-9-1-6	5.70	14.30	60.10
19	R×T-8-9-14	6.70	15.60	57.10
20	R×T-9-1-7	5.10	15.20	66.40
21	R×T-8-9-15	7.40	15.90	53.50
22	R×T-9-1-8	8.20	17.50	53.10
23	R×T-8-9-16	7.40	17.00	56.50
24	R×T-9-1-9	10.50	13.80	23.90
25	R×T-8-9-17	6.40	14.30	55.20
26	R×T-9-1-10	7.50	13.80	45.70
27	R×T-8-9-18	8.40	10.80	22.20
28	R×T-9-1-11	6.30	11.10	43.20
29	R×T-8-9-19	5.80	12.40	53.20
30	R×T-9-1-12	8.60	9.90	13.10
31	R×T-8-9-20	6.70	11.70	42.70
32	R×T-9-1-13	9.50	12.50	24.00
33	R×T-8-9-21	7.50	10.80	30.60
34	R×T-9-1-14	8.30	15.20	45.40
35	R×T-8-9-22	8.60	18.90	54.50
36	R×T-4-1-15	10.60	12.50	15.20
37	R×T-8-9-23	6.50	11.10	41.40
38	R×T-6-1-16	7.70	11.50	33.00
39	R×T-8-9-5	10.30	14.60	29.50
40	R×T-9-1-17	7.80	11.50	32.20
41	R×T-8-9-25	10.20	12.90	20.90
42	R×T-9-1-18	8.50	14.80	42.60
43	R×T-8-9-26	10.30	16.50	37.60
44	R×T-9-1-19	7.10	13.40	47.00
45	R×T-8-9-27	16.58	19.00	12.70

Table 4.7.1c 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×T-7-4-2	9.60	13.10	26.72
2	R×T-6-4-5	6.70	16.00	57.99
3	R×T-2-4-5	9.80	19.80	50.38
4	R×T-3-6-7	4.50	17.70	74.58
5	R×T-4-5-1	3.90	16.00	75.55
6	R×T-5-9-5	7.60	13.90	45.32
7	R×T-3-4-2	7.00	16.40	57.32
8	R×T-2-7-8	9.20	13.20	30.30
9	R×T-8-9-9	5.20	11.10	53.15
10	R×T-9-1-2	8.60	11.70	26.50
11	R×T-8-9-10	5.80	10.30	43.41
12	R×T-9-1-3	7.10	12.60	43.65
13	R×T-8-9-11	8.40	15.30	44.92
14	R×T-9-1-4	5.30	14.30	62.94
15	R×T-8-9-12	4.50	15.90	71.70
16	R×T-9-1-5	8.60	15.90	45.91
17	R×T-8-9-13	7.70	16.80	54.17
18	R×T-9-1-6	5.70	15.80	63.92
19	R×T-8-9-14	6.50	13.20	50.76
20	R×T-9-1-7	4.70	13.90	66.06
21	R×T-8-9-15	7.40	14.60	49.32
22	R×T-9-1-8	8.20	14.80	44.59
23	R×T-8-9-16	7.40	16.20	54.32
24	R×T-9-1-9	10.40	12.40	15.79
25	R×T-8-9-17	6.30	14.70	57.14
26	R×T-9-1-10	7.30	13.70	46.52
27	R×T-8-9-18	8.40	10.10	16.83
28	R×T-9-1-11	6.30	11.10	43.24
29	R×T-8-9-19	5.80	12.40	53.23
30	R×T-9-1-12	8.60	12.50	31.20
31	R×T-8-9-20	6.70	11.70	42.74
32	R×T-9-1-13	9.50	12.50	24.00
33	R×T-8-9-21	7.50	10.50	28.57
34	R×T-9-1-14	8.30	13.60	38.97
35	R×T-8-9-22	8.60	16.70	48.50
36	R×T-4-1-15	10.60	12.40	14.17
37	R×T-8-9-23	6.50	11.40	42.98
38	R×T-6-1-16	7.70	14.00	44.80
39	R×T-8-9-5	10.10	15.30	33.99
40	R×T-9-1-17	7.70	15.80	51.27
41	R×T-8-9-25	10.20	12.90	20.93
42	R×T-9-1-18	8.50	14.60	41.78
43	R×T-8-9-26	10.30	14.70	29.93
44	R×T-9-1-19	7.10	13.30	46.62
45	R×T-8-9-27	7.10	15.00	52.51

Table 4.7.1d Estimates of per cent difference for test weight under submergence and non-submergence condition

SL NO.	Genotypes	**Test weight (g)**		
		Submergence	Non-submergence	Change in % Mean
1	R×T-7-4-2	19.92	27.40	27.30
2	R×T-6-4-5	16.42	20.40	19.49
3	R×T-2-4-5	21.34	26.90	20.52
4	R×T-3-6-7	18.92	22.30	15.23
5	R×T-4-5-1	18.30	24.70	25.85
6	R×T-5-9-5	22.00	24.00	8.33
7	R×T-3-4-2	20.85	22.00	5.20
8	R×T-2-7-8	18.55	29.30	36.78
9	R×T-8-9-9	22.45	27.50	18.51
10	R×T-9-1-2	21.36	29.90	28.48
11	R×T-8-9-10	25.30	26.40	4.00
12	R×T-9-1-3	29.41	30.00	1.97
13	R×T-8-9-11	19.94	29.10	31.48
14	R×T-9-1-4	24.30	27.60	11.84
15	R×T-8-9-12	26.06	27.20	4.01
16	R×T-9-1-5	21.85	24.50	10.72
17	R×T-8-9-13	21.12	24.10	12.20
18	R×T-9-1-6	25.07	27.30	8.24
19	R×T-8-9-14	21.56	26.50	18.67
20	R×T-9-1-7	22.59	25.90	12.73
21	R×T-8-9-15	25.08	27.00	7.09
22	R×T-9-1-8	24.76	26.00	4.77
23	R×T-8-9-16	24.54	26.00	5.58
24	R×T-9-1-9	25.47	28.30	10.06
25	R×T-8-9-17	21.78	22.80	4.55
26	R×T-9-1-10	23.00	24.00	4.17
27	R×T-8-9-18	25.90	27.90	7.30
28	R×T-9-1-11	20.78	22.00	5.37
29	R×T-8-9-19	27.80	29.00	4.14
30	R×T-9-1-12	20.94	27.50	23.96
31	R×T-8-9-20	26.03	28.00	6.99
32	R×T-9-1-13	23.94	25.00	4.05
33	R×T-8-9-21	25.09	26.60	5.68
34	R×T-9-1-14	24.94	27.60	9.56
35	R×T-8-9-22	23.62	25.70	8.06
36	R×T-4-1-15	32.00	34.70	7.78
37	R×T-8-9-23	21.11	25.50	17.05
38	R×T-6-1-16	21.25	26.90	21.01
39	R×T-8-9-5	21.80	22.70	3.75
40	R×T-9-1-17	22.33	28.40	21.34
41	R×T-8-9-25	23.16	26.00	10.84
42	R×T-9-1-18	26.06	29.50	11.51
43	R×T-8-9-26	22.46	25.00	10.14
44	R×T-9-1-19	25.80	27.90	7.66
45	R×T-8-9-27	24.11	32.50	25.80

4.7.1.3 *Number of productive tillers per plant*

The number of productive tillers exhibited the highest per cent difference of 75.55 by R×T-4-5-1 followed by 74.58 per cent by R×T-3-6-7. Whereas the minimum per cent difference was shown by R×T-4-1-15 (14.17%) followed by R×T-9-1-9 (15.79%). The number of productive tillers obtained will be decreased under submergence condition than under non-submergence condition due to stress impact.

4.7.1.4 *Test weight*

Test weight per cent difference was noticed to be lowest in R×T-9-1-3 (1.97%) followed by R×T-8-9-5 (3.75%). Highest per cent difference was found inR×T-2-7-8 (36.78%) followed by R×T-8-9-11 (31.48%). Test weight also showed a mean reduction under stress condition than under non-submergence.

DISCUSSION

V DISCUSSION

Nearly half of the world's population is fed by the leading grain crop rice (*Oryza sativa* L). When it comes to ensuring food security, rice is crucial. The current yield levels must be boosted up to 121 million tonnes by 2050 to fulfill the needs of India's growing population and combat food security; the production of rice must be expanded by over two million tonnes annually. Although the development activity stated in the recent past for rice production has yielded many incredible outcomes, demand for this crop exceeds production owing to population increase at an exponential rate and a decline in the amount of fertile land available for this crop to expand.

The landrace FR13A ('Dhalaputia' in Orissa) has been identified by NRRI, Cuttack as a truly tolerant genotype to submergence condition. Different mechanisms of tolerance to submergence condition have been carried out extensively using this landrace. Similar research has been conducted in the current investigation to screen the advanced breeding lines of rice for submergence tolerance. Screening of the advanced breeding lines of rice at 50-60 cm depth of water for about 14 days for submergence tolerance.

The current research entitled **"Assessment of Genetic Variability in Advanced Breeding Lines of Rice (*Oryza sativa* L.) and their Comparative Study under Submergence"** was conducted in a Randomised Complete Block Design (RCBD) with two replications at ZAHRS, Navile, Shivamogga and AHRS Kathalagere, mainly with the aim for estimating genetic parameters for yield and its attributing traits among the advanced breeding lines of rice, assessing the genetic diversity available among rice advanced breeding lines of rice and degree of association of grain yield with its component traits. Also, screening of the rice genotypes for submergence tolerance at 50-60 cm depth of water for about 14 days to evaluate for submergence tolerance.

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

5.3 Phenotypic correlation analysis for 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 per plant

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 important objectives 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 inheritance factors like yield and their corresponding attributes. Population diversity is essential for any breeding programme and is crucial for crop improvement for any desired feature. Therefore, determining the gene pool's level of diversity is the first and most crucial stage in every breeding effort. Critical evaluation of genetic variability metrics like the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance is required for any crop improvement effort in plant breeding.

5.1.1 Analysis of variance for grain yield and its attributing characters

Significant genetically diverse differences were seen across advanced breeding lines of rice for a variety of attributes, indicating that selection will be successful. Manjunatha *et al.* (2019), Sudeepthi *et al.* (2019) and other authors cited the same outcomes.

5.1.2 Genetic variability parameters for grain yield and its attributing characters

In the current investigation, low phenotypic and genotypic coefficients of variation were recorded for days to 50 per cent flowering and days to maturity. Similar findings were reported for both traits by Edukondalu *et al.* (2017), Nishanth *et al.* (2017), Rashid *et al.* (2017), Sumanth *et al.* (2017), Tiwari *et al.* (2019), Sudeepthi *et al.* (2020) and Demeke *et al.* (2022) obtained similar results for days to 50 per cent flowering and on par results were obtained for days to maturity by Murali *et al.* (2023). The occurrence of low estimate values of phenotypic and genotypic coefficients of variation indicates that the selection of these characters for the crop improvement program will be inappropriate.

Spikelet fertility was found to have low genotypic and phenotypic coefficients of variation. The results obtained are similar to the results by Ram *et al.* (2017), Sudeepthi *et al.* (2020) and Nath and Kole (2021).

PCV and GCV obtained were moderate for panicle length and plant height. The findings of moderate PCV are in accordance with Dhanwani *et al.* (2013) for panicle length and low GCV was obtained in accordance with Chamar *et al.* (2021) and Demeke *et al.* (2022). Edukondalu *et al.* (2017), Gour *et al.* (2017) and Demeke *et al.* (2022) for plant height. Moderate estimates of GCV and PCV indicate that there is reasonable scope for enhancing crop yield through the selection of these traits.

Number of tillers per plant and number of productive tillers per plant were found to exhibit moderate PCV and GCV values and similar results were reported by Dhanwani *et al.* (2013), Devi *et al.* (2016), Edukondalu *et al.* (2017), Srujana *et al.* (2017) and Sumanth *et al.* (2017).

Length breadth ratio were found to exhibit moderate PCV and GCV values and similar results were reported by Dhanwani *et al.* (2013) and Edukondalu *et al.* (2021). Grain yield was found to exhibit high PCV in accordance with Ram *et al.* (2017), Edukondalu *et al.* (2017) and moderate GCV in accordance with Tiwari *et al.* (2019) and Sudeepthi *et al.* (2020).

The traits *viz.,* number of spikelets per panicle, number of filled grains per panicle and test weight recorded moderate PCV and GCV. Similar results were observed by Demeke *et al.* (2022) for number of filled grains per panicle, number of spikelets per panicle and test weight. However, these traits expressed high heritability with high genetic advance as per cent mean where similar findings were reported by Tiwari *et al.* (2019).

For all the characters studied, it was found that phenotypic coefficients of variation values were more than the corresponding genotypic coefficients of variation. Sumanth *et al.* (2017), Chamar *et al.* (2021) and Demeke *et al.* (2022) have reported higher PCV estimates than GCV estimates for all the characters evaluated. A narrow difference between PCV and GCV was observed indicating that environmental influence is less and genetic factors contribute the most to variability in these characters.

Although information on the variability and its extent present in the lines for traits studied, together with the influence of environment, can be obtained from phenotypic and genotypic coefficients of variation, a pertinent estimate of the extent of inheritance of the traits cannot be supplied. As a result, the heritability of a trait will give plant breeders a chance to decide how much selection pressure needs to be applied in the crop development programme for a specific environmental state. High heritability in the broad sense combined with high genetic progress as a percentage serve as direct selection criteria because they provide estimates of the traits transmissibility, which shows how well selection has worked to improve the characters (Johnson *et al.*, 1955).

5.1.3 Heritability and genetic advance

Heritability is the measurement of genetic variability transmitted from previous generations (Lush, 1949). Heritability in a broad sense accompanied by high genetic advance as per cent mean, serve as a direct parameter for selection, estimatingthe index of trait transmissibility. All these traits are controlled mostly by additive gene action, indicating the effectiveness of selection for the trait's improvement(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. 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 Divya *et al.* (2018) and Edukondalu *et al.* (2017) explained about high heritability for panicle length and number of productive tillers per plant. For the trait like spikelet fertility results were on par with Sravan *et al.* (2012) and Sandeep *et al.* (2018). Similar results of high heritability were obtained by Sravan *et al*. (2012) and Chamar *et al*. (2021) for grain yield.

Genetic advance as per cent of mean estimates the measure of the genetic gain obtained under selection. Genetic advance as per cent mean was higher 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, grain length and breadth ratio and grain yield. However, moderate genetic advance as per cent mean was noticed for days to 50 per cent flowering, days to maturity and panicle length. Low GAM was exhibited by the trait spikelet fertility. Results obtained were in accordance with Gour *et al.* (2017), Prasad *et al.* (2017), Ram *et al*. (2017), Srujana *et al*. (2017) and Demeke *et al*. (2022), for days to 50 per cent flowering and days to maturity and panicle length. Low genetic advance as per cent mean for spikelet fertility was reported. Similar results were recorded by Tiwari *et al.* (2019).

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, grain length and breadth ratio and grain yield were found to be in accordance with results obtained by Edukondalu *et al*. (2017) and Demeke *et al*. (2022). Nandan *et al.* (2010) obtained similar results for panicle length, number of spikelets per panicle, number of filled grains per panicle and test weight. The results of Divya *et al.* (2018) results were on par for grain yield per plant, 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. Biswajith *et al.* (2017) reported on par results for the number of spikelets per panicle, plant height, test weight and grain yield.

In the current investigation, traits *viz.*, plant height, panicle length, number of spikelets per panicle, number of filled grains per panicle, test weight and grain yield 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 Genetic divergence among advanced breeding lines of rice for grain yield and its attributing traits

Forty five advanced breeding lines of rice along with five checks were grouped into seven clusters based on D^2 statistics. The groups formed were in such a way that within each cluster lines had smaller values of D^2 statistics compared to those existing between the clusters. The clustering pattern obtained revealed that the biggest cluster formed was cluster I which had forty lines. This was followed by cluster II, III, IV and V each with two lines present in the cluster; cluster VI and VII were found to have one line in it. The results complied with the results of Khalequzzaman *et al.* (2008), Pandey *et al.* (2009), Kodihalli and Dushyanthakumar (2014).

5.2.1 Average intra and inter clusters distance

Cluster V exhibited the maximum intra cluster distance (29.51), followed by cluster IV (27.19). Because of the greater amount of diversity existing among themselves the lines present within these two groups could be utilised better for the hybridisation programme. Hence, hybridisation is effectively utilised by selecting the lines of cluster V and cluster IV followed by cluster I and cluster III.

Cluster VI with one line (R×T-8-9-18) and cluster VII with one line (JGL-1798) were found to be most divergent because of the maximum inter cluster distance existing between them followed by cluster II (R×T-8-9-13, R×T-9-1-19) with clusterV (R×T-9-1-7, R×T-8-9-22). Clusters with the highest inter cluster distance will have more genetic diversity and such lines belonging to the clusters will be utilised for hybridisation program.

Meanwhile, those clusters with minimum inter cluster distance will be found to have narrow genetic diversity and hybridisation between them will not exhibit better heterosis. Therefore, it is better to select those lines having clusters with more inter cluster distance than with low inter cluster distance. Cluster IV (RNR-15048, BPT-5204) and cluster VII (JGL-1798) recorded the minimum inter cluster distance between them followed by cluster III (Tunga, KHP-11) and cluster IV (RNR-15048, BPT-5204).

The 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 hybrids development.

5.2.2 Cluster means analysis

Cluster VII (JGL-1798) was found to have maximum cluster mean value for number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle, panicle length. It indicates that lines selected from this cluster could be directly selected and utilised in crop improvement programme. Cluster III (Tunga, KHP-11) exhibited highest mean value for most of the traits like days to 50 per cent flowering, days to maturity, test weight and grain yield per plant. Cluster II (R×T-8-9-13, R×T-9-1-19) was found to have the maximum cluster mean value for spikelet fertility and grain length and breadth ratio. Cluster VI (R×T-8-9-18) was found to have a maximum cluster mean value for plant height.

Simiar results were reported by Bose and Pradhan (2005), Venkatesan *et al.* (2016) and Lahari *et al.* (2017). They inferred that, for hybridisation programme selection of parents should be done from the two clusters which have higher inter cluster distance so that maximum variability should be obtained in the segregating generations and for transgressive segregants to be generated.

5.2.3 Contribution of different characters towards divergence

Among all the characters studied for yield and its attributing traits, the percentage contribution to total divergence was differed in different traits grain length breadth ratio, plant height, days to 50 per cent flowering, number of spikelets per panicle, grain yield, panicle length, number of tillers per plant, number of productive tillers per plant, test weight and number of filled grains per panicle all together contributed for 95.80 per cent towards total divergence. Bose and Pradhan (2005), Kodihalli and Dushyanthakumar (2014) and Lahari *et al.* (2017) emphasized the contribution, grain length breadth ratio, plant height, days to 50 per cent flowering, number of spikelets per panicle. Therefore, these traits should be considered more for selecting the more diverse parents in programs of hybridisation.

Genotypes that belong to the cluster VI and VII, II and V showed more inter cluster distance and the traits like grain length breadth ratio, plant height, days to 50 per cent flowering, number of spikelets per panicle, grain yield, panicle length, number of tillers per plant, number of productive tillers per plant should be given more importance for the best parents selection in hybridisation program.

5.3 Phenotypic correlation analysis for yield and its attributing traits

5.3.1 Correlation of grain yield with other characters

Grain yield was found to have a 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 length breadth ratio. A non-significant negative correlation was found for days to 50 per cent flowering, days to maturity and plant height.

The results obtained were found to be similar with the results of Mushtaq *et al.* (2021) which depicted a positive and significant association of number of tillers per plant, number of effective tillers per plant, panicle length and test weight with grain yield. Niharika *et al*. (2022) reported a significant positive association of grain yield with number of tillers per plant and number of productive tillers per plant. Singh *et al.* (2020) obtained similar results of a positive significant association of panicle length with grain yield. Lohiteswara *et al*. (2021) showed similar results of grain yield having a significant positive association with number of filled grains per panicle and spikelet fertility. Babu *et al.* (2012) and Zahid *et al.* (2006) showed similar results of grain yield having a significant positive association with number of filled grains per panicle and number of spikelets per panicle, respectively. The results of Kumar (2022) are in accordance with a positive significant association of test weight with grain yield. Whereas non-significant negative association of plant height with grain yield was reported by Dhavaleshvar *et al*. (2019). The results of Reddy *et al.* (2022) depicted a negative and non-significant association of grain yield with days to 50 per cent flowering, days to maturity and plant height.

5.3.2 Correlation among yield components

Days to 50 per cent flowering have shown a significant positive correlation with days to maturity. It exhibited a significant negative correlation with plant height, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, number of spikelets per panicle, panicle length and spikelet fertility and non-significant negative correlation with grain length breadth ratio and test weight. The results obtained are in accordance with Reddy *et al.* (2022) for a positive association of days to 50 per cent flowering with days to maturity and a significant negative association of days to 50 per cent flowering with plant height, number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle and panicle length. Significant negative association of days to 50 per cent flowering with grain and length ratio are similar to that of results obtained by Mushtaq *et al.* (2021).

Days to maturity had a positive correlation with days to 50 per cent flowering. It exhibited a significant negative correlation with plant height, panicle length, number of filled grains per panicle, number of spikelets per panicle and spikelet fertility with the days to maturity. It exhibited a non-significant negative correlation with the number of tillers per plant, the number of productive tillers per plant and grain length breadth ratio. It exhibited a positive correlation with test weight. Results in accordance with traits like days to 50 per cent flowering, test weight, grain length and breadth ratio as reported by Mushtaq *et al.* (2021) and Dhavaleshvar *et al.* (2019). Similar results for plant height and panicle length were reported by Reddy *et al.* (2022). Number of spikelets per panicle recorded a negative association by Shreedhar *et al.* (2019). Similar results for spikelet fertility were reported by Dhavaleshvar *et al.* (2019). Number of tillers per plant and number of productive tillers per plant as reported by Dhavaleshvar *et al.* (2019) and Reddy *et al.* (2022).

A non-significant positive association was shown by plant height with panicle length, spikelet fertility and test weight. With days to 50 per cent flowering, days to maturity, number of tillers per plant, number of productive tillers per plant and grain length breadth ratio was found to be significantly negatively correlated with grain yield. A non-significant negative correlation was found with number of filled grains per panicle and number of spikelets per panicle. Positive association was shown by plant height with panicle length and test weight and significant negative association with the number of tillers per plant and number of productive tillers per plant and non-significant negative association with the number of spikelets per panicle which was similar to results of Dhavaleshvar *et al.* (2019). For panicle length and spikelet fertility, which showed a positive association the same results were quoted by Niharika *et al.* (2022b). Significant negative association with days to 50 per cent flowering and days to maturity was on par with the results of Kumar (2022).

Number of tillers per plant showed a significant positive correlation with number of productive tillers per plant, panicle length, number of filled grains per panicle, total number of spikelets per panicle, spikelet fertility, test weight and grain length breadth ratio. A significant negative correlation was found with days to 50 per cent flowering, days to maturity and plant height. A significant positive association of the number of tillers per plant with number of productive tillers per plant, panicle length, number of filled grains per panicle, number of spikelets per panicle and test weight was found to be in accordance with Niharika *et al.* (2022). Similar results were reported by Mushtaq *et al.* (2021) for panicle length and number of productive tillers per plant. Kumar (2022) reported a positive association of the number of tillers per plant with grain length and breadth ratio. The significant negative association of the number of tillers per plant with days to 50 per centflowering and days to maturity was in accordance with Kumar (2022). Niharika *et al.* (2022) obtained a significant negative correlation for plant height.

Number of productive tillers per plant exhibited a 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. Significant negative correlation was observed with plant height and days to 50 per cent flowering. Whereas with days to maturity, a non-significant negative correlation was observed. Significant association of number of productive tillers per plant with number of tillers per plant, panicle length and test weight was in accordance with Reddy *et al*. (2022). The results of a positive significant association of the number of productive tillers per plant with spikelet fertility are similar to Singh *et al*. (2018). Niharika *et al*. (2022) reported the same findings of a significant association of the number of productive tillers per plant with number of filled grains per panicle and number of spikelets per panicle. The significant negative association of the number of productive tillers per plant with plant height and days to 50 per cent flowering was on par with Reddy *et al*. (2022).

Panicle length displayed a significant positive correlation with allthe 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 and test weight. A non-significant positive correlation with plant height and grain length breadth ratio. Significant negative correlation with days to 50 per cent flowering and days to maturity. Dhavaleshvar *et al.* (2019) found the results on par as those reported in the experiment for number of tillers per plant, number of productive tillers per plant and test weight. Similar results were obtained by Niharika *et al*. (2022). Bhutta *et al*. (2019) found a positive significant association for number of spikelets perpanicle and spikelet fertility. Niharika *et al*. (2022) obtained a positive significant correlation for number of filled grains per panicle. A positive, non-significant association with plant height and grain length breadth ratio was recorded by Singh *et al*. (2018). Kumar (2022) recorded on par results for days to 50 per cent flowering and days to maturity.

Number of spikelets per panicle exhibited a significant positive correlation with the number of tillers per plant, number of productive tillers per plant, panicle length, spikelet fertility and the number of filled grains per panicle. A non-significant positive correlation was seen with the test weight and grain length breadth ratio. Significant negative with days to 50 per cent flowering, days to maturity and non-significant negative correlation with plant height. Niharika *et al*. (2022) reported similar findings for number of tillers per plant, number of productive tillers per plant panicle length. Similar reports were also found for panicle length and spikelet fertility by Dhavaleshvar *et al.* (2019). A non-significant association of number of spikelets per panicle with plant height was obtained by Dhavaleshvar *et al.* (2019). Similar results were also obtained by Noatia *et al*. (2021). Katkani *et al.* (2023) reported a similar association for days to 50 per cent flowering and days to maturity.

A significant positive correlation with number of filled grains per panicle was accompanied by number of tillers per plant, number of productive tillers per plant, panicle length, the number of spikelets per panicle and spikelet fertility. A non-significant positive correlation was noticed with test weight and grain length breadth ratio. Significant negative correlation with days to 50 per cent flowering, days to maturity and a non-significant negative correlation with plant height. Niharika *et al.* (2022b) found results similar to the current investigation studies for traits like the number of tillers per plant, number of productive tillers per plant, panicle length, number of spikelets per panicle and spikelet fertility. Singh *et al.* (2018) reported a positive association of number of filled grains with test weight. Naotia *et al.* (2021) found similar results for plant height. Katkani *et al.* (2023) reported a similar association for days to 50 per cent flowering and days to maturity.

Spikelet fertility had a significant 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 and test weight. A non-significant positive association with spikelet fertility was exhibited by plant height and length/breadth ratio. A significant negative correlation was exhibited by days to 50 per cent flowering, days to maturity. Dhavaleshvar *et al.* (2019) reported on par results for number of tillers and number of productive tillers per plant. The results obtained were found in harmony with the findings of Singh *et al*. (2018) for the 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. Katkani *et al.* (2023) found the results similar to the current investigation studies for traits like days to 50 per cent flowering and days to maturity.

Test weight exhibited a significant positive correlation with number of tillers per plant, number of productive tillers per plant, panicle length and spikelet fertility. Whereas positive non-significant correlation was recorded with days to maturity, plant height, number of filled grains per panicle, number of spikelets per panicle and grain length/breadth ratio. A non-significant negative correlation was exhibited by days to 50 per cent flowering. For number of tillers per plant, number of productive tillers per plant and panicle length by Niharika *et al.* (2022). Similar results were obtained by Kumar (2022) for panicle length. Niharika *et al*. (2022) reported a similar association for days to maturity and Mushtaq *et al.* (2021) for days to 50 per cent flowering. The results obtained were found in harmony with the findings of Sridhar *et al.* (2016) for plant height and number of spikelets per panicle.

A significant positive association with length breadth ratio was shown by number of tillers per plant, productive tillers per plant, panicle length and test weight. For panicle length and test weight significant positive association was recorded by

Mushtaq *et al.* (2021). A non-significant positive correlation was exhibited by the number of filled grains per panicle, the number of spikelets per panicleand spikelet fertility. Whereas a negative significant association was observed for plant height, a non-significant negative association was observed for daysto 50 per cent flowering and days to maturity. Mushtaq *et al.* (2021) reported results similar to that obtained for days to 50 per cent flowering, days to maturity. Singh *et al*. (2018) reported similar findings for plant height. Singh *et al.* (2020) reported a similar association of grain length breadth ratio and with number of spikelets per panicle.

According to the results obtained grain yield had a 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 and test weight indicating that all the above-mentioned traits should be given importance during crop improvement and selection of plants.

5.4 Screening of advanced breeding lines of rice for submergence tolerance

Screening of advanced breeding lines of rice under submergence will be helpful in selecting the lines which are superior and tolerant to submergence condition. Forty five advanced breeding lines of rice were evaluated and the best lines identified will thrive better when they are subjected to stressful situations. The study was conducted on survival percentage of advanced breeding lines of rice which revealed that Swarna sub-1 (check), including R×T-8-9-25, R×T-8-9-17, R×T-8-9-14, R×T-5-9-5, R×T-2-4-5 had highest survival per cent. Whereas, Jyothi, BPT-5204, R×T-7-4-2, R×T-6-4-5, R×T-3-6-7, R×T-4-5-1, R×T-3-4-2, R×T-2-7-8, R×T-8-9-9, R×T-9-1-2, R×T-8-9-10, R×T-9-1-3, R×T-8-9-11, R×T-9-1-4, R×T-8-9-12, R×T-9-1-5, R×T-8-9-13, R×T-9-1-6, R×T-9-1-7, R×T-8-9-15, R×T-9-1-8, R×T-8-9-16, R×T-9-1-9, R×T-9-1-10, R×T-8-9-18, R×T-9-1-11, R×T-8-9-19, R×T-9-1-12, R×T-8-9-20, R×T-9-1-13, R×T-8-9-21, R×T-9-1-14, R×T-8-9-22, R×T-4-1-15, R×T-8-9-23, R×T-6-1-16, R×T-8-9-5, R×T-9-1-17, R×T-9-1-18, R×T-8-9-26, R×T-9-1-19, R×T-8-9-27 had least survival percentage.

Sarkar *et al.* (2009), Linh *et al.* (2013), Nugraha *et al.* (2013), Nishanth *et al*. (2017) and Gautam *et al.* (2018) have reported in accordance with 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.

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

For any line under submergence condition to be tolerant, the pre-requisite is to have a high survival percentage and good re-emergence after being subjected to a brief period of submergence. The study conducted on survival percentage of advanced breeding lines of rice revealed that Swarna sub-1 (check), R×T-8-9-25, R×T-8-9-17, R×T-8-9-14, R×T-5-9-5, R×T-2-4-5 had highest survival per cent, whereas Jyothi, BPT-5204, R×T-7-4-2, R×T-6-4-5, R×T-3-6-7, R×T-4-5-1, R×T-3-4-2, R×T-2-7-8, R×T-8-9-9, R×T-9-1-2, R×T-8-9-10, R×T-9-1-3, R×T-8-9-11, R×T-9-1-4, R×T-8-9-12, R×T-9-1-5, R×T-8-9-13, R×T-9-1-6, R×T-9-1-7, R×T-8-9-15, R×T-9-1-8, R×T-8-9-16, R×T-9-1-9, R×T-9-1-10, R×T-8-9-18, R×T-9-1-11, R×T-8-9-19, R×T-9-1-12, R×T-8-9-20, R×T-9-1-13, R×T-8-9-21, R×T-9-1-14, R×T-8-9-22, R×T-4-1-15, R×T-8-9-23, R×T-6-1-16, R×T-8-9-5, R×T-9-1-17, R×T-9-1-18, R×T-8-9-26, R×T-9-1-19, R×T-8-9-27 had least mean survival percentage revealed their susceptibility to submergence condition. Similar findings were reported by Sarkar *et al.* (2009), Linh *et al.* (2013) and Nugraha *et al.* (2013), Nishanth *et al*. (2017) and Gautam *et al.* (2018).

The stem elongation percentage was recorded to be highest for R×T-9-1-9 followed by R×T-3-4-2 and the lowest percentage of stem elongation was seen in FR13A and Swarna sub-1 followed by R×T-9-1-12. In the current investigation, the advanced breeding lines of rice having higher stem elongation will have better survival under submerged condition. However, advanced breeding lines of rice with higher 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 lines are found to have better survival percentage, moderate stem elongation and had given better yield even after being subjected to stress condition. Das *et al.* (2005), Sarkar *et al.* (2011), Singh *et al.* (2014) and Oladosu *et al.* (2020),achieved similar results where the study of advanced breeding lines of rice under submerged condition was carried out. Their outcomes obtained revealed that most of the advanced breeding lines of rice having submergence tolerance had the capacity of moderate or limited stem elongation with more survival percentage.

PCV and GCV obtained were higher for stem elongation percentage and survival percentage. Also, there was high heritability coupled with high genetic advance observed for these two traits under submergence. Adilakshmi and Rani (2012) and Kumari *et al.* (2019) revealed similar results *i.e.*, high PCV and GCV coupled with high heritability and high genetic advance for survival percentage and stem elongation percentage. 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 per plant

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

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

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

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

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

The mean per cent difference for various traits between submergence and non-submergence condition revealed that days to 50 per cent flowering showed an increased number of days for flowering while the rest of the traits (number of tillers per plant, number of productive tillers per plant and test weight) exhibited decreasedmean value under stress than under non-submergence.

The per cent difference in days to 50 per cent flowering among 45 rice advanced breeding lines was found to be highest for R×T-3-4-2 followed by R×T-8-9-17 and the difference was found to be minimum for R×T-9-1-19 followed by R×T-2-7-8.

The maximum per cent difference in the number of tillers by advanced breeding lines of rice on comparing under submergence with non-submergence was found to be in R×T-4-5-1 followed by R×T-3-6-7. While the minimum difference was exhibited by R×T-8-9-27 followed by R×T-9-1-12. The number of tillers obtained was decreased under submergence condition than under non-submergence condition due to stress impact.

The number of productive tillers exhibited the highest per cent difference by R×T-4-5-1followed by R×T-3-6-7. Whereas minimum per cent difference was shown by R×T-4-1-15 followed by R×T-9-1-9. The number of productive tillers obtained was decreased under submergence condition than under non-submergence condition due to stress impact.

Test weight per cent difference was noticed to be lowest in R×T-9-1-3 followed by R×T-8-9-5. Highest per cent difference was found in R×T-2-7-8 followed by R×T-8-9-11. Test weight also showed mean reduction under stress condition than non-submergence control.

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, number of productive tillers and test weight where all these traits were found to have lesser value than under non-submergence condition. The results were in agreement with Ranjitha (2019) for grain yield in which decreased grain yield under submergence as compared to under non-submergence condition was noticed for most of the lines under investigation.

Conclusion

- ✓ Forty five advanced breeding lines of rice were assessed for genetic variability, diversity and characters associated with yield and its attributing traits under non submergence.
- ✓ Analysis of variance reported the presence of significant difference for all the yield and its contributing traits analysed among the advanced breeding lines of rice.
- ✓ Genetic variability studies revealed moderate to high PCV and GCV coupled with high heritability and high genetic advance as per cent mean for most of the characters *viz.,* plant height, number of tillers per plant, number of productive tillers per plant, panicle length, number of spikelets per panicle, number of filled grains per panicle, test weight and grain yield. Such high heritability and genetic advance is mainly because of additive gene action which indicates that the selection will be effective.
- ✓ Correlation study reported that a significant positive correlation of grain yield was noticed with the number of tillers per plant, number of productive tillers per plant, panicle length, the number of spikelets per panicle, spikelet fertility, test weight and grain length and breadth ratio.
- ✓ D^2 analysis reported that the inter cluster distance was found to be exhibited maximum by cluster IV and cluster VII followed by the cluster II and cluster V. Hence, the advanced breeding lines of rice that belong to these clusters will have maximum genetic diversity and hence, the highest heterosis can be exploited by crossing genotypes which belong to these clusters.
- ✓ Screening of the advanced breeding lines of rice for submergence tolerance revealed that among 45 advanced breeding lines evaluated, R×T-8-9-25, R×T-8-9-17, R×T-8-9-14, R×T-5-9-5, R×T-2-4-5 reported the highest survival percentage of 50 per cent apart from checks.
- ✓ Hence, the above lines could be proposed for further multilocation trials in the hill zone (lowlands) 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 rice advanced breeding lines for almost all the characters studied indicated hybridization could be carried out for better exploitation of heterosis.
- ✓ Under submergence condition, lines like R×T-8-9-25, R×T-8-9-17, R×T-8-9-14, R×T-5-9-5, R×T-2-4-5 showed better survival than other advanced breeding lines of rice evaluated and hence could be proposed for further screening in different locations of hill zones of Karnataka.

SUMMARY

VI SUMMARY

Rice is an important and major food crop cultivated worldwide and is generally subjected to climate changes and environmental variations. Among such stresses, submergence is the major hindrance to rice production in higher rainfall and lowland areas. Due to global climate change, the water levels are found to be constantly increasing making the condition worsened in such lowland and high rainfall areas. Therefore, hybrids and varieties which are tolerant to submergence have to be developed. Such genotypes developed or identified should be evaluated for variability, diversity and association for yield and its attributing traits.

With consideration of all the above-mentioned points, the current research entitled "Assessment of Genetic Variability in Advanced Breeding Lines of Rice (RNR-15048 × Tunga) and their Comparative Study under Submergence" was conducted at ZAHRS, Shivamogga and AHRS, Kathalagere during *Kharif* 2022. The study involved assessing the genetic variability, genetic diversity present among 45 advanced breeding lines of rice of cross RNR-15048 × Tunga in order to select the more diverse lines, to estimate the association of yield and its contributing characters and to estimate the direct and indirect effects of independent traits studied on the dependent trait like yield.

Forty five advanced breeding lines of rice along with five checks 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. Five plants were randomly selected for each advanced breeding line under each replication and the observations were recorded for the traits *viz.*, days to 50 per cent flowering, days to maturity, plant height, 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, grain length breadth ratio and grain yield.

Analysis of variance revealed the presence of significant difference among the advanced breeding lines of rice for all the traits assessed. The study of genetic variability revealed that GCV and 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, panicle length, number of spikelets per panicle, number of filled grains per panicle, test weight, grain length breadth ratio. The high PCV and moderate GCV are exhibited by traits like number of filled grains per panicle and grain yield. Low PCV and GCV were exhibited by the traits *viz.*, days to 50 per cent flowering, days to maturity and spikelet fertility. All the traits studied recorded high heritability. High Genetic advance as per cent mean 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, panicle length, test weight, grain length and breadth ratio and grain yield. Moderate GAM was exhibited by the traits like days to 50 per cent flowering, days to maturity and panicle length. Spikelet fertility exhibited low GAM.

The correlation study revealed the significant positive association of 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 grain length breadth ratio with grain yield. A non-significant negative association was exhibited by days to 50 per cent flowering, days to maturity and plant height with grain yield.

Forty five advanced breeding lines of rice were grouped into seven clusters based on D^2statistics. Cluster I was found to be the largest with fourty lines, followed by cluster II, III, IV and V each with two lines present in the cluster; cluster VI and VII were found to have one line in it. Cluster V exhibited maximum intra cluster distance followed by cluster IV, cluster I and cluster III. The inter cluster distance was exhibited highest between cluster VI and cluster VII, followed by cluster II and cluster V indicating that the lines within these clusters are highly diverse. The inter cluster distance lowest was noticed between cluster IV and cluster VII followed by cluster III and cluster IV indicating that the traits within the clusters was less diverse.

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

Forty-five advanced breeding lines of rice including four checks, were screened for submergence tolerance during *Kharif* 2022 based on stem elongation percentage and survival percentage. Maximum survival percentage was exhibited by R×T-8-9-25, R×T-8-9-17, R×T-8-9-14, R×T-5-9-5, R×T-2-4-5 compared to other advanced breeding lines of rice. Whereas, Jyothi, , BPT-5204, R×T-7-4-2, R×T-6-4-5, R×T-3-6-7, R×T-4-5-1, R×T-3-4-2, R×T-2-7-8, R×T-8-9-9, R×T-9-1-2, R×T-8-9-10, R×T-9-1-3, R×T-8-9-11, R×T-9-1-4, R×T-8-9-12, R×T-9-1-5, R×T-8-9-13, R×T-9-1-6, R×T-9-1-7, R×T-8-9-15, R×T-9-1-8, R×T-8-9-16, R×T-9-1-9, R×T-9-1-10, R×T-8-9-18, R×T-9-1-11, R×T-8-9-19, R×T-9-1-12, R×T-8-9-20, R×T-9-1-13, R×T-8-9-21, R×T-9-1-14, R×T-8-9-22, R×T-4-1-15, R×T-8-9-23, R×T-6-1-16, R×T-8-9-5, R×T-9-1-17, R×T-9-1-18, R×T-8-9-26, R×T-9-1-19, R×T-8-9-27 recorded least survival percentage.Among checks, Swarna sub-1 exhibited highest survival percentage and BPT-5204 exhibited the lowest survival percentage.

The stem elongation percentage was recorded to be highest for R×T-9-1-9 followed by R×T-3-4-2 and the lowest percentage of stem elongation was seen in R×T-9-1-12. Among check varieties, Jyothi was seen to have highest stem elongation and that of FR13A, Swarna sub-1 recorded lowest 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 percentage and survival percentage. There was high genetic advance coupled with high heritability for the traits.

Under submergence condition, phenotypic correlation for physiological traits assessed revealed that there was a significant positive correlation of survival percentage with grain yield. In contrast, stem elongation percentage exhibited asignificant negative correlation.

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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	Min	Max	Avg	Humidity (%)			Wind Speed(km/hr)		
				Temperature (°C)			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 meterological 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)