

**ASSESSMENT OF GENETIC VARIABILITY AND DIVERSITY OF RICE
ADVANCED LINES FOR SUBMERGENCE TOLERANCE**

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CERTIFICATE

This is to certify that the thesis entitled '**ASSESSMENT OF GENETIC VARIABILITY AND DIVERSITY OF RICE ADVANCED LINES FOR SUBMERGENCE TOLERANCE**' submitted in partial fulfillment of the requirements for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **GENETICS AND PLANT BREEDING** to the College of Agriculture, Shivamogga, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga is a bonafide record of research work carried out by **TASLEEMA SULTANA, ID. No. MA1TAI0348** (tasleema15@gmail.com) during the period of study in this university under my guidance and supervision and no part of this thesis has previously formed the basis for the award of any other degree, diploma, associateship, fellowship or any other similar titles.

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(Tasleema Sultana)

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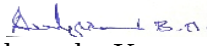
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ABSTRACT

The present investigation was conducted at College of Agriculture, KSNUAHS, Shivamogga during *Kharif* 2020. Twenty-six rice advanced lines and four checks were screened for submergence tolerance under submerged conditions. Genetic variability, character association and genetic diversity were studied under non-submergence. Under submerged conditions, highest survival percentage was observed for KHP-11×MM-1-3-1. Genetic variability studies revealed high PCV, GCV, heritability and genetic advance for survival and stem elongation percentages. Phenotypic correlation for physiological traits revealed a significant positive correlation of survival percentage with harvest index and grain yield. Under non-submergence, analysis of variance revealed the presence of high significant differences for all the characters studied. Genetic variability studies revealed high estimates of PCV, GCV, heritability and genetic advance for number of tillers per plant, number of productive tillers per plant, test weight and grain yield. Correlation studies revealed a significant positive association of 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, panicle fertility, test weight, straw yield and harvest index with grain yield. Path analysis disclosed highest direct positive effect on grain yield by test weight. Mahalanobis D² statistics grouped thirty rice advanced lines into six clusters. Maximum inter-cluster distance was observed between cluster III and IV. Molecular diversity analysis done using fifteen SSR markers revealed the presence of high molecular diversity among the rice advanced lines and grouped them into eight clusters according to UPGMA clustering system. Top-performing rice advanced lines were selected based on grain yield and its related traits. KHP-11×MM-1-3-1 recorded significantly higher yield (6637.50 kg/ha) than presently cultivated variety KHP-11 (5160 kg/ha) which is used as check. Hence, KHP-11 × MM-1-3-1 may be advanced to Multi-location trials, Farm trials and proposed for variety release in hill zone area of Karnataka.

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ಮುಳುಗುವಿಕೆಯ ಸಹಿಷ್ಣುತೆಗೆ ಭತ್ತದ ಸುಧಾರಿತ ತಳಿಗಳ ಅನುವಂಶಿಕ ವ್ಯತ್ಯಾಸ ಮತ್ತು ವೈವಿಧ್ಯತೆಯ ಮೌಲ್ಯಮಾಪನ

(ತಸ್ಲೀಮಾ ಸುಲ್ತಾನ)

ಸಾರಾಂಶ

ಪ್ರಸ್ತುತ ಅಧ್ಯಯನದಲ್ಲಿ ಇಪ್ಪತ್ತಾರು ಸುಧಾರಿತ ಭತ್ತದ ತಳಿಗಳನ್ನು ಹಾಗೂ ನಾಲ್ಕು ಚೆಕ್‌ಗಳನ್ನು ನೀರು ಮುಳುಗಡೆಯ ಸಹಿಷ್ಣುತೆಗೆ ಕೆ.ಶಿ.ನಾ.ಕೃ.ತೋ.ವಿ.ವಿ., ಶಿವಮೊಗ್ಗದಲ್ಲಿ ೨೦೨೦ ರ ಮುಂಗಾರು ಋತುವಿನಲ್ಲಿ ಪರಿಶೀಲಿಸಲಾಯಿತು ಹಾಗೂ ಅನುವಂಶ ವ್ಯತ್ಯಾಸ, ಅನುವಂಶಿಕ ವೈವಿಧ್ಯತೆಯನ್ನು ಒತ್ತಡವಿಲ್ಲದ ಸಾಮಾನ್ಯ ಭತ್ತ ಬೆಳೆಯುವ ಸ್ಥಿತಿಯಲ್ಲಿ ಅಧ್ಯಯನ ಮಾಡಲಾಗಿದೆ. ಕೆ.ಹೆಚ್.ಪಿ - ೧೧ × ಎಂ.ಎಂ.-೧-೩-೧ ಸುಧಾರಿತ ತಳಿಯು ಉಳಿದ ಎಲ್ಲ ತಳಿಗಳಿಗಿಂತ ಉತ್ತಮ ಇಳುವರಿ ಮತ್ತು ನೀರು ಮುಳುಗುವಿಕೆಗೆ ಹೆಚ್ಚಿನ ಸಹಿಷ್ಣುತೆ ತೋರಿದೆ. ಅನುವಂಶ ವ್ಯತ್ಯಾಸ ಅಧ್ಯಯನದಲ್ಲಿ ನೀರು ಮುಳುಗಡೆಯ ಸಹಿಷ್ಣುತೆ, ಕಾಂಡ ಉದ್ದವಾಗುವ ಸಾಮರ್ಥ್ಯವು ಹಾಗೂ ಹೆಚ್ಚಿನ ವಿಭಿನ್ನಾರ್ಥ ಗುಣಾಂಶ (ಪಿ.ಸಿ.ವಿ.) ಮತ್ತು ವ್ಯತ್ಯಾಸದ ವಂಶವಾಹಿ ಗುಣಾಂಶ (ಜಿ.ಸಿ.ವಿ.) ಹೊಂದಿರುತ್ತವೆ. ಒತ್ತಡವಿಲ್ಲದ ಸಾಮಾನ್ಯ ಭತ್ತ ಬೆಳೆಯುವ ಸ್ಥಿತಿಯಲ್ಲಿ, ವ್ಯತ್ಯಾಸದ ವಿಶ್ಲೇಷಣೆಯು ಅಧ್ಯಯನ ಮಾಡಿದ ಎಲ್ಲಾ ಗುಣಗಳಿಗೆ ಹೆಚ್ಚಿನ ಗಮನಾರ್ಹ ವ್ಯತ್ಯಾಸಗಳನ್ನು ತೋರಿಸಿತು. ಪ್ರತಿ ಸಸ್ಯದಲ್ಲಿನ ತೆಂಡೆಗಳ ಸಂಖ್ಯೆ, ಪ್ರತಿ ಸಸ್ಯದ ಉತ್ಪಾದಕ ತೆಂಡೆಗಳ ಸಂಖ್ಯೆ, ಪರಿಕ್ಷಾತೂಕ ಮತ್ತು ಧಾನ್ಯದ ಇಳುವರಿಗಳು ಹೆಚ್ಚಿನ ಪಿಸಿವಿ ಮತ್ತು ಜಿಸಿವಿಯನ್ನು ಬಹಿರಂಗಪಡಿಸಿವೆ. ಪರಸ್ಪರ ಸಂಬಂಧದ ಅಧ್ಯಯನದಲ್ಲಿ ಸಸ್ಯದ ಎತ್ತರ, ಪ್ರತಿ ಸಸ್ಯಕ್ಕೆ, ತೆಂಡೆಗಳ ಸಂಖ್ಯೆ, ಪ್ರತಿ ಸಸ್ಯದ ಉತ್ಪಾದಕ ತೆಂಡೆಗಳ ಸಂಖ್ಯೆ, ತೆನೆಯ ಉದ್ದ, ಪ್ರತಿ ತೆನೆಗೆ ತುಂಬಿದ ಧಾನ್ಯಗಳ ಸಂಖ್ಯೆ, ತೆನೆಯ ಫಲವತ್ತಿ, ಪರಿಕ್ಷಾತೂಕ, ಒಣಹುಲ್ಲಿನ ಇಳುವರಿ ಮತ್ತು ಕೊಯ್ಲಿನಲ್ಲಿ ಗಮನಾರ್ಹ ಸಕಾರಾತ್ಮಕ ಸಂಬಂಧವನ್ನು ಬಹಿರಂಗಪಡಿಸಿದೆ. ಧಾನ್ಯ ಇಳುವರಿಯೊಂದಿಗೆ ಸೂಚ್ಯಂಶ, ಪಥ ವಿಶ್ಲೇಷಣೆಯು ಪರಿಕ್ಷಾತೂಕದ ಮೂಲಕ ಧಾನ್ಯದ ಇಳುವರಿ ಮೇಲೆ ಹೆಚ್ಚಿನ ನೇರ ಧನಾತ್ಮಕ ಪರಿಣಾಮವನ್ನು ವಿಶ್ಲೇಷಿಸಿದೆ. ಮಹಾಲನೋವಿಸಿ ಡಿ^೨ ಅಂಕಿ ಅಂಶಗಳು ಅನುಸಾರ ಮೂವತ್ತು ಭತ್ತದ ಸುಧಾರಿತ ತಳಿಗಳನ್ನು ಆರು ಗುಂಪುಗಳಾಗಿ ವರ್ಗೀಕರಿಸಲಾಯಿತು. ಗುಂಪು ೩ ಮತ್ತು ಗುಂಪು ೪ ರ ನಡುವೆ ಗರಿಷ್ಠ ಅಂತರ ಕಂಡು ಬಂದಿದೆ. ಹದಿನೈದು ಎಸ್.ಎಸ್.ಆರ್. ಮಾರ್ಕರ್‌ಗಳನ್ನು ಬಳಸಿಕೊಂಡು ಮಾಡಿದ ಆಣ್ವಿಕ ವೈವಿಧ್ಯತೆಯ ವಿಶ್ಲೇಷಣೆಯಲ್ಲಿ ಭತ್ತದ ಸುಧಾರಿತ ತಳಿಗಳಲ್ಲಿ ಹೆಚ್ಚಿನ ಆಣ್ವಿಕ ವೈವಿಧ್ಯತೆಯ ಉಪಸ್ಥಿತಿಯನ್ನು ಬಹಿರಂಗಪಡಿಸಿತು ಮತ್ತು ಯು.ಪಿ.ಜಿ.ಎಂ.ಎ. ಗುಂಪುಗಾರಿಕೆಯ ವ್ಯವಸ್ಥೆಯು ಅವುಗಳನ್ನು ಎಂಟು ಗುಂಪುಗಳಾಗಿ ವರ್ಗೀಕರಿಸಿದೆ. ಇಳುವರಿ ಮತ್ತು ಅದರ ಸಂಬಂಧಿತ ಗುಣಲಕ್ಷಣಗಳ ಮೇಲೆ ಕೆ.ಎಚ್.ಪಿ.- ೧೧ × ಎಂ.ಎಂ.-೧-೩-೧ ಸುಧಾರಿತ ಭತ್ತದ ತಳಿಯನ್ನು ಅತ್ಯುತ್ತಮ ಎಂದು ಪರಿಗಣಿಸಲಾಗಿದೆ. ಆದ್ದರಿಂದ ಕೆ.ಎಚ್.ಪಿ.-೧೧ × ಎಂ.ಎಂ.-೧-೩-೧ ಅನ್ನು ವಿಭಿನ್ನ ಸ್ಥಳಗಳ ಪರಿಶೀಲನೆಗೆ ಮತ್ತು ಫಾರ್ಮ್ ಟ್ರೇಲ್‌ಗಳಿಗೆ ಮುಂದುವರಿಸಬಹುದಾಗಿದೆ, ಹಾಗೂ ಕರ್ನಾಟಕದ ಗುಡ್ಡಗಾಡು ಪ್ರದೇಶಗಳಲ್ಲಿ ಬಿಡುಗಡೆಗಾಗಿ ಪ್ರಸ್ತಾಪಿಸಬಹುದಾಗಿದೆ.

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INTRODUCTION

I INTRODUCTION

Rice, botanically seed of *Oryza sativa* belonging to the family *Gramineae* with more than 110,000 cultivated varieties, is a staple food for more than half of the world's population and is a major source of income in many Asian countries. It is grown in more than 100 countries in 154 million hectares, with 90 per cent of the total global production from Asia. Rice provides 21 per cent of global human per capita energy and 15 per cent of per capita protein. Rice protein ranks high in nutritional quality due to its true digestibility of 88 per cent, which is the highest among cereals. The protein quality is around 0.55, which is also higher compared to other cereals. Besides carbohydrates and proteins, rice also provides essential amino acids, minerals (P, Mg, Ca), vitamins (Folic acid) and fiber.

Rapid population growth is imparting increased pressure on already strained food producing resources. According to the reports of the Population Foundation of India, by 2030 India will have a population of 1546 million and 1824 million by the end of 2050 (CRRRI-vision 2050), which results in increased demand for rice from 117.47 million tonnes to 137.30 million tonnes by 2050 (FAOSTAT, 2018). In addition to this, elevating drift of climate change like surge in temperature, melting of glaciers, altered precipitations and shifting seasons are threatening agriculture and food security. In the future, rice production must continue to grow at least as rapidly as the population, if not faster. Rice research that develops new technologies has a pivotal role in meeting this need and contributing to global efforts directed at poverty alleviation.

Among all the climatic stress conditions, the most significant and fast-rising issue is an increase in water level, *i.e.*, flooding, primarily seen in lowland rice-growing areas of south and south-east Asia. Heavy rainfall, tides in coastal regions, overflow of rivers and canals result in floods. Flooding causes either complete or partial submergence of the crop, affecting about 10 to 15 million hectares of rice fields every year, accounting for loss of a billion US dollars (Anon., 2018). Further, it is anticipated that areas under floods will increase considerably due to the rise in sea level caused due to melting of polar ice caps. Hence, lowland farmers have no other option better than rice, as it is semi-aquatic and capable of surviving under submerged conditions because of its ability to overcome oxygen limitation for a substantial period. Under submerged conditions, rice manages to survive either by resistance (inherent metabolic

adaptations) or by avoidance (elongation of the stem to keep the leaves above the water surface) (Das and Uchimiya, 2002).

Submergence can be characterized as complete and incomplete based on the depth of the floodwater. If the water depth is more than 100 cm, it is complete submergence. It may persist for several months in deep water areas. The genotypes acclimatized to this condition show rapid stem elongation to withstand rising water levels by consuming more carbohydrates to escape submergence. Incomplete submergence majorly occurs due to the overflowing of rivers or heavy rainfall. Here, flooding occurs for less than 14 days. In this condition, the tolerant genotypes retain good chlorophyll content and undergo limited stem elongation. When the floodwater level is 25 to 50 cm for a few weeks to several months, it is called stagnant or prolonged partial flooding (Vergera *et al.*, 2014).

Submergence tolerance can be defined as the ability of the plant to survive and continue to grow even after being completely submerged in water for several days. Both susceptible and tolerant rice varieties tolerate complete submergence for a considerable period, but susceptible varieties are damaged more rapidly than tolerant ones. Majority of the present-day cultivated rice varieties are not adapted to submerged conditions. Thus, farmers tend to grow low-yielding local landraces with poor quality. Traits desirable for complete submergence and prolonged partial submergence tolerance vary. Hence, identifying tolerant sources with a high survival rate associated with high yield in different degrees of submergence is of utmost importance.

Advanced breeding lines can be defined as the plants whose germplasm has been manipulated to form the parental material from which new varieties or hybrids are developed. These lines have been developed in breeding programmes. They have a narrow genetic base and contain valuable germplasm. They include nearly homozygous lines, mutant lines, transgenic lines, *etc.* These lines are almost stabilized and can be used for screening for desirable characters and released as varieties.

To identify and develop the best genotype suitable for specific environmental conditions, we need to carry out appropriate screening and estimate a large number of genotypes under such environmental conditions. Screening is done by focusing on the traits adapted to the stress conditions, which provide the ability for the plant to thrive. Hence, accurate information regarding the nature and magnitude of such positively contributing traits towards tolerance is necessary.

Developing a superior genotype for a desirable trait requires the presence of variability for that trait as a prerequisite to start the breeding programme. So, the first and foremost step for breeders is assembling the variation or creating it if not present. To achieve this, examining the available germplasm for variability and diversity is obligatory.

When breeders breed for any stress, the ultimate target is to get a higher yield. As yield is a quantitative character, we need to have a sound knowledge regarding the effect of all the yield attributing characters and which among them are essential. This information helps in the selection of better parents, which can be utilized in breeding programmes to get superior progeny (hybrids as well as transgressive segregants).

For designing effective breeding programmes, the knowledge of genetic diversity among the genotypes and their relationships is necessary. The diversity of the genotypes is due to variation in the expression of genes governing various traits. As genes determine the phenotypic characteristics of an organism, their variation results in the production of individuals with characters varied at morphological and/or molecular levels. This can be assessed at both morphological levels as well as using molecular markers.

Among all the molecular markers which revolutionized the characterization of genotypes for variation, SSR (Simple Sequence Repeats) have evolved as the most popular and versatile genetic markers in plant systems. SSR markers, also called microsatellites, are co-dominant, highly polymorphic, easy to use and economical, making them suitable for studying the population structure.

With due consideration of all the elements as mentioned earlier, the present study has been formulated with the following objectives:

1. To evaluate rice advanced lines for submergence tolerance
2. To assess genetic variability in rice advanced lines
3. To study character association for grain yield and its related traits
4. To assess genetic diversity in rice advanced lines

REVIEW OF LITERATURE

II REVIEW OF LITERATURE

The literature pertaining to the experiment is reviewed and presented under the following headings.

2.1 To evaluate rice advanced lines for submergence tolerance

2.2 To assess genetic variability in rice advanced lines

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

2.4 To assess genetic diversity in rice advanced lines

2.1 To evaluate rice advanced lines for submergence tolerance

Among all the abiotic stresses, submergence is the third most crucial stress of 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 the rice advanced lines for their tolerance to submerged conditions can be helpful. In this regard, similar works related to the screening and evaluation of rice genotypes for submergence tolerance have been reviewed and presented below.

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

Das *et al.* (2009) investigated various implications of floodwater affecting seedling survival after submergence using rice genotypes with varied tolerance for submergence. They found that warm floodwater decreases plant survival and turbid water augments plant mortality. Plants survived better in cool water, and survival decreased by 8 per cent per unit increase in water temperature above 26 °C. Even the most tolerant rice cultivar FR13A experienced higher mortality with turbid floodwater. Correlation studies revealed that cultivars with the capacity to maintain higher biomass, higher chlorophyll, and non-structural carbohydrate concentrations after submergence had higher survival.

Sarkar *et al.* (2009) conducted an experiment during *Kharif* 2005–07 under rainfed lowlands and controlled submergence. Under flash-flooding, genotypes with Sub1 survived complete submergence stress with turbid water for up to 12 days, whereas genotypes without Sub1 did not survive. Swarna Sub1 gave a higher grain yield than 'Swarna' with a yield advantage of 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 submergence caused more significant damage than 14 days submergence in SUB1 introgressed cultivars. Survival percentage reduced when plants were submerged for more periods. The survival percentage of landraces was more compared to SUB1 introgressed cultivars.

Akinwale *et al.* (2012) evaluated submergence tolerance of 20 rainfed lowland rice cultivars with floodwater depth of 1.5 m for 14 days in a randomized complete block design with three replications. Thirty days old seedlings were submerged for 14 days under 100 cm of water, followed by the 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 significant cultivar differences. Percentage survival varied from 3.2 to 97.5 per cent. Plant elongation during submergence was negatively correlated with survival ($r = -0.80$), indicating the importance of reduced elongation growth.

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 other groups and 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 to 15 days. Due to the absence of *Sub1* loci, elite Vietnamese varieties such as Khangdan 18, Bacthom 7 and OM6976, and IR42 (sensitive check) were completely destroyed after 13 to 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. They 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 at Los Banos, Philippines, in the wet season of 2009. The results showed that SUB1 introgression rice lines had higher survival than non-SUB1 and did not much elongate their shoots during submergence. In the sensitive genotypes, submergence decreased the panicle number, grain number per panicle and panicle fertility. Consequently, the yield declined. The SUB1 introgression lines had higher chlorophyll concentration and less depletion in soluble sugar and starch after submergence. Introgression of the SUB1 into high-yielding varieties improved submergence tolerance without affecting yield potential. The study indicates that introgression of the SUB1 into taller type rice varieties should be done to compensate the effect of suppressed elongation.

Ranawake *et al.* (2014) screened 25 rice cultivars for submergence tolerance at seedling and vegetative stages. At the seedling stage, germinated seedlings were grown for two weeks and subjected to 5-day, 9-day and 14-day complete submergence stress in separate experiments. The experiment was repeated using 6-week-old plants for the vegetative stage. Survival rate and plant height were recorded. At 5-day, 9-day and 14-day submergence periods, 100 per cent, 32 per cent and 24 per cent of rice cultivars survived respectively, at the seedling stage. Whereas 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 seedling (20 %) and vegetative stages (17.5 %). All survived rice cultivars elongated (100 %) under 14-day submergence stress at seedling and vegetative stages. Some rice cultivars reduced the plant height at 5-day and 9-day complete submergence stresses at seedling and vegetative stages. There was a correlation between elongation and survival percentage of rice cultivars and it depends on the growth stage and submergence period.

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. 80 to 100 per cent of survival was shown by 12 cultivars. Five cultivars showed more than 70 per cent survival.

Nishanth *et al.* (2017) studied 525 germplasm lines and screened for survival percentage under submergence. They were scored from 1 to 9 using IRRI standard method. Among all the lines, none of them scored 1 with 100 per cent survival, two lines (Jaladhi and IET 21465) scored 3 with 96 per cent survival, 68 lines scored 5 with 75 to 94 per cent survival rate, 230 lines scored 7 with a survival rate between 50 to 74 per cent and 225 lines scored 9 with less than 49 per cent survival rate. Among the checks, FR13A showed the highest survival rate of 96 per cent and Jyothi showed the least survival rate of 8 per cent.

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

Wening *et al.* (2019) evaluated 95 lines and four rice checks for submergence tolerance in the Indonesia Centre of Rice Research using augmented design with five blocks. In the submergence condition, the experiment was conducted in a submergence pool and in optimal conditions, the investigation was conducted in an irrigated field. The selection methods 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 tolerant and can be used for the breeding programme.

2.2 To assess genetic variability in rice advanced lines

The 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 the breeding programme in crops like rice.

Vanaja and Babu, (2007) evaluated the genetic variability for 10 quality parameters in 56 high-yielding diverse rice genotypes. Phenotypic and genotypic coefficients of variation revealed the existence of considerable 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 potentiality of these parameters in breeding programmes.

Pandey *et al.* (2009) evaluated 40 rice genotypes for genetic variability by studying 12 quantitative characters. Analysis of variance revealed the presence 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.

Adilakshmi *et al.* (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 due to the preponderance of the additive gene action under submergence. Ear bearing tillers recorded low genetic advance and 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 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 indicating that enough variability is present in the material. Among them, grain yield per plant (30.52-31.18 %) and filled grains per panicle (26.05-26.86 %) were found to have high GCV and PCV. Almost all the characters showed a slight variation between PCV and GCV, revealing little influence of the environment in expressing these traits. The characters showing high GCV and PCV were highly heritable and have high genetic advance revealing that they are governed by additive gene action and direct selection for these traits can be made.

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 significant for all the traits indicating the existence of genetic variability for all the characteristics 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 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 on genetic variability using 44 diverse rice genotypes. The analysis of variance revealed the presence of significant differences among the genotypes for all the traits indicating the presence of a sufficient amount of variability among the genotypes for various characters. High estimates of the genotypic and phenotypic coefficient of variations were observed for number of grains per panicle, grain yield per plant, straw yield per plant and harvest index indicating wider genetic variation for these traits. High values of heritability coupled with high genetic advance as per cent of mean were observed for number of grains per panicle, grain yield per plant, straw yield per plant, harvest index, 1000-grain weight, grain L/B ratio and amylose content indicating selection may be effective for these characters.

Pradhan *et al.* (2015) evaluated 30 rice cultivars under normal and submerged situations to study the genetic basis of yield variations. High significant difference among the genotypes was present for all the characters except for fertility percentage and grain yield per plant under normal conditions and except for grain yield per plant under submerged conditions. Most of the traits exhibited a higher magnitude of GCV and PCV under submerged conditions except panicle length and plot yield. High heritability estimates associated with moderate to high genetic gain was observed for days to 50 per cent flowering, plant height, grain number and 1000-grain weight indicating the presence of additive gene effects. Hence, selection based on phenotypic performance would be effective.

Devi *et al.* (2016) studied variability on 27 rice genotypes. Higher estimates of PCV and GCV were observed for yield per plant (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 is exhibited by effective tillers, plant height, flag leaf length, filled grains per panicle, test weight, yield per plant, head rice recovery and length/breadth ratio indicating the preponderance of additive gene action providing a good scope for further improvement by selection.

Venkatesan *et al.* (2016) investigated the submergence tolerance of 26 rice genotypes with check Swarna Sub1. Based on the characters like days to first flowering, plant height, number of tillers per plant, number of panicles per plant, panicle length, test weight, photosynthetic rate, stomatal conductance, intercellular CO₂ concentration, transpiration rate and grain yield per plant, diversity analysis was made. The analysis of variance revealed the presence of variability among the genotypes for all the eleven characters taken under study both in normal and submergence conditions.

Gour *et al.* (2017) conducted an investigation to estimate the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (GA) in 83 rice genotypes. Analysis of variance indicated the presence of significant differences among the genotypes for different morphological characters. High GCV and PCV were observed for grain yield per plant, panicle weight per plant, biological yield per plant, filled spikelets per plant, test weight, harvest index, number of tillers per plant. Whereas, moderate GCV and PCV were observed for plant height. High heritability coupled with high genetic advance as per cent of mean was observed for grain yield per plant, panicle weight per plant, biological yield per plant, filled spikelets per plant, harvest index, test weight, number of tillers per plant, panicle length per plant. Whereas, high heritability coupled with moderate genetic advance as per cent of mean was recorded for days to 50 per cent flowering and days to maturity. The filled spikelets per plant, harvest index, biological yield per plant showed high genetic advance that helped in effective and reliable selection through these characters for crop improvement.

Lahari *et al.* (2017) carried out the present investigation at the College of Agriculture, Shivamogga during summer 2016 to screen 107 rice genotypes and 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 Randomized Complete Block Design with two replications under submergence during *Kharif* 2016 to evaluate genetic variability. The analysis of variance revealed a significant difference among the genotypes for all the characters. High PCV and GCV coupled with high heritability and high GAM were recorded in number of tillers per plant, productive tillers per plant, grain yield per plant, straw yield per plant, and absolute growth rate.

Ram *et al.* (2017) carried out the present investigation to study the genetic parameters for yield and yield attributing characters in 100 rice genotypes. Analysis of variance revealed the presence of significant differences for all the traits under study, indicating enough variability in the material. The characters like grain yield per plant and biological yield exhibited high GCV and PCV. Days to 50 per cent flowering, plant height, days to maturity, spikelet fertility and harvest index recorded low estimates of PCV and GCV. Minor differences between GCV and PCV were recorded for all the characters studied indicating the less environmental influence. The characters like ear bearing tillers, number of grains per panicle, biological yield, test weight and grain yield per plant exhibited high heritability coupled with high genetic advance, indicating that simple selection could effectively improve these characters.

Rashid *et al.* (2017) conducted an experiment to estimate the genetic variability of ten rice genotypes. Analysis of variance for yield and yield contributing traits showed significant ($p < 0.01$) variation among the genotypes. Results showed a higher phenotypic coefficient of variation compared to the genotypic coefficient of variation

for all the traits indicating the influence by the environment. The magnitude of the difference was less, showing the slight impact of the environment. The higher estimates of PCV and GCV were observed for number of filled grains per panicle (27.53; 26.84), number of unfilled grains per panicle (26.76; 25.28) and plant height (23.14; 23.00), indicating the possibility of genetic improvement through direct selection. Days to 50 per cent flowering, days to maturity, panicle length, number of effective tillers per plant, fertility (%), 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 %) and high genetic advance and genetic advance as percentage of mean were found for all the traits indicating the prevalence of additive gene action, which provides a 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 slight, indicating less environmental influence on the characters studied. High to moderate estimates of GCV and PCV were recorded for grain yield per hill, harvest index, spikelets per panicle, tillers per hill, flag leaf length and panicles per hill.

Sumanth *et al.* (2017) conducted the present investigation with 23 rice genotypes for 13 quantitative characters to study genetic variability, heritability and genetic advance. Analysis of variance showed significant differences for all the characters studied. The highest genotypic coefficient of variation and phenotypic coefficient variation 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 indices for crop improvement. High heritability estimates were observed for plant height, flag leaf length, biological yield, spikelets per panicle, panicles per plant. The high genetic advance was observed for the number of spikelets per panicle and plant height, indicating the predominance of additive gene effects and possibilities of effective selection to improve these characters.

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 with high genetic advance 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 the environment in the expression of these characters. High genetic advance coupled with

high heritability suggests that these traits are controlled by additive genes and hence, they should be given priority in selection.

Barik *et al.* (2019) evaluated 88 lowland indigenous landraces for submergence response. Variation in survival rate, shoot elongation, relative growth index, dry matter, chlorophyll, soluble sugar and starch were evaluated under well-drained and completely submerged conditions for two years. The first three components showed 96.82 per cent of total variation among landraces showing wide variation among genotypes. PCV was more than GCV for all the traits. 5 landraces - Samudrabali, Basnamundi, Gadaba, Surudaka, Dokarakuji were most tolerant to submergence. The first three of them even showed greater survival rates than standard submergence tolerant variety FR13A when submerged for 14 days. They elongated more vigorously and accumulated more biomass. So, they can be used for breeding improved submergence tolerant rice varieties.

Manjunatha and Kumara, (2019) conducted the experiment with 64 rice genotypes to study genetic variability, heritability and genetic advance for grain yield and yield-associated traits. The analysis of variance revealed significant differences indicating the existence of genetic variability among the genotypes for all the traits studied. Higher PCV and GCV values were exhibited by panicles per square meter, suggesting the possibility of improving this trait through selection. 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 per cent mean was exhibited for plant height, panicles per square meter. High genetic advance as per cent of mean was recorded by yield, panicles per square meter, plant height and days to 50 per cent flowering.

Singh *et al.* (2019) studied genetic parameters, correlation coefficients among yield and yield components, the direct and indirect effect of yield components on yield in 101 rice genotypes for seven quantitative traits. Analysis of variance revealed that there was a high significant difference for all characters among genotypes. GCV and PCV were highest for the filled grains per panicle, grain yield per plant and ear bearing tillers. Broad sense heritability was highest for plant height (99.6 cm), followed by grain yield per plant (98.8 %) and days to flowering (98.2 %). The genetic advance was highest for the number of filled grains per panicle and grain yield per plant.

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 features studied. The magnitudes of genotypic coefficient of variations were relatively higher for grain yield, 1000-grain weight, and days to heading. The highest broad-sense heritability of 94 per cent was recorded in days to maturity and the lowest heritability of 16 per cent was observed in plant height.

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

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 a great importance to have knowledge of grain yield and its related traits. Hence, the characters which are positively associated with yield have to be identified.

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 spikelets per panicle, total biomass, days to 50 per cent flowering and plant height exhibited a significant positive association with grain yield. Path analysis revealed their direct effects on grain yield. The direct effect of total biomass and harvest index was also high on grain yield. Thus, these traits contribute to the grain yield and can be exploited for further breeding programmes.

Adilakshmi *et al.* (2012) conducted character association studies in 64 rice genotypes. The association analysis indicated a negative association of plant survival percentage with total shoot elongation and relative shoot elongation, whereas a positive association with yield per plant indicated its importance. Path analysis revealed that the traits viz., total shoot elongation, plant survival percentage, 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.

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

Sravan *et al.* (2012) studied the inter-relationship 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 in the 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 the inter-relationship of grain yield and associated characters using 44 diverse rice genotypes. Correlation studies indicated genotypic correlation coefficients were higher in magnitude than the phenotypic correlation coefficients for most of the traits. Grain yield per plant was found positively and significantly associated with plant height, panicle length, number of total tillers per plant, number of effective tillers per plant, number of grains per panicle, harvest index and 1000-grain weight at both genotypic and phenotypic levels indicating that these traits were main yield attributing traits. Path analysis revealed that straw yield per plant had the highest positive direct effect on grain yield followed by grain length, harvest index, days to maturity, protein content, number of total tillers per plant and number of grains per panicle. For maximizing the grain yield per plant, emphasis should be given in the selection of characters such as the number of grains per panicle, straw yield per plant, harvest index and 1000-grain weight.

Rashid *et al.* (2014) studied 20 diverse cultivars of rice for correlation. Among the traits days to heading, days to maturity, number of productive tillers, 1000-grain weight showed a 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 positively correlated with grain yield per plant.

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

Devi *et al.* (2016), studied correlation and path analysis for yield and quality traits in 27 rice genotypes. Grain yield per plant had the highest significant positive association with filled seeds per panicle, plant height, flag leaf length, effective tillers, flag leaf width and panicle length indicating the importance of these characters for yield improvement. At the same time, head rice recovery was found to be significantly and positively correlated with milling percentage and hulling percentage. Path analysis reveals that test weight (3.48), effective tillers (1.57) and filled grains per panicle (1.41) had a positive direct effect on grain yield per plant. Among the quality traits, kernel

length followed by milling percentage and kernel elongation ratio had a direct effect on head rice recovery.

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 the submerged conditions with more than 50 cm of water depth for two weeks at the vegetative stage of the crop. High broad-sense heritability along with high genetic gain over mean was observed for plant height, grains per panicle, test weight, seed yield. 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 and path coefficients from data collected on 83 rice genotypes. Grain yield per plant showed a positive association with panicle weight per plant, biological yield per plant, number of tillers per plant and harvest index, while negative association with plant height. The biological yield per plant had a maximum direct effect on grain yield per plant followed by panicle length per plant, harvest index, filled spikelets per plant, panicle length per plant and days to maturity. Hence, biological yield per plant, harvest index and number of seeds per plant are identified as key traits for developing high yielding genotypes of rice for the future breeding programme.

Lahari *et al.* (2017) carried out the present 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 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 the 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. The highest positive direct effect on grain yield was observed in straw yield per plant and harvest index.

Kar *et al.* (2018) carried out the present investigation is to establish the nature of the relationship between grain yield and yield components by using correlation and path 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. The attributes like days to 50 per cent flowering exhibited a maximum positive direct effect on grain yield followed by plant height, grain yield per plant, fertility percentage and 100-grain weight, indicating the importance of such traits as criteria for selection for the realization of higher productivity.

Sreedhar and Reddy, (2019) studied association among seven traits in 40 rice genotypes. Genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients suggesting a strong genetic association among the yield and yield components. Correlation coefficient analysis showed that the number of productive tillers per m² and test weight exhibited a significant positive correlation with the yield at genotypic and phenotypic levels. A significant negative correlation was observed between the number of filled grains per panicle and yield. Path coefficient analysis revealed that a positive direct effect of the number of productive tillers per m² and days to 50 per cent flowering on grain yield at both genotypic and phenotypic levels.

Singh *et al.* (2019) studied genetic parameters, correlation coefficients among yield and yield components, the direct and indirect effect of yield components on yield in 101 rice genotypes for seven quantitative traits. A significant positive association of grain yield with 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 ($r_g=0.9999$, $r_p=0.997$), days to heading and grain yield ($r_g=0.9999$, $r_p=0.9276$), and days to maturity and grain yield ($r_g=0.9796$, $r_p=0.9174$). A negative and highly significant genetic correlation was observed between plant height and test weight ($r_g=-0.9999$). The results indicated that days to heading, days to maturity, grain yield, 1000-grain weight demonstrating higher heritability and remarkable genetic advance could be considered the most appropriate traits for improvement and selection of trait to achieve stable and high yielding early rice genotypes under rainfed environments.

Nath and Kole, (2021) studied the cause-effect relationship 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, 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. Genotypic path analysis indicated that direct selection for test weight, number of primary and secondary branches per panicle in a positive direction with limited selection for panicle number and spikelet fertility would increase the grain yield.

2.4 To assess genetic diversity in rice advanced lines

For designing effective breeding programmes, the knowledge of greater genetic variation in germplasm and its relationship is necessary. Characterization of germplasm 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 analyzed by D^2 statistics and molecular markers.

Ni *et al.* (2002) evaluated the genetic diversity in thirty-eight rice cultivars and accessions of two wild species (*O. rufipogon* and *O. nivara*) 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 chromosome 6 and 7 and considerably lower diversity on chromosome 2. With stepwise discrimination, two subsets of approximately 30 markers were identified that produced genetic distance matrices and dendrograms that were the same as those produced utilizing all 111 markers. The results suggested that a relatively small number of microsatellite markers could be used to estimate genetic diversity and identify rice cultivars.

Bose and Pradhan (2005) estimated the nature and magnitude of genetic divergence in 35 rice genotypes using Mahalanobis D^2 statistics. The genotypes were grouped into 10 clusters showing a fair 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.

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 intra-cluster distances were lower, reflecting homogeneity of the genotypes within the clusters. Cluster VI contained the highest number of genotypes (12) and cluster IV had 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 clusters III and IV and the lowest between clusters II and VI. Cluster IV showed a high genetic distance from all clusters except cluster II. The genotypes from cluster IV could be hybridized with any of the four clusters genotypes to produce transgressive segregants. Days to flowering, duration and spikelets per panicle were mainly responsible for genetic divergence while considering mean values.

Pandey *et al.* (2009) evaluated 40 rice genotypes for their genetic diversity by studying 12 quantitative characters using cluster analysis. The genotypes were grouped into seven clusters based on Mahalanobis D^2 statistics. Out of total diversity, 86.16 per cent of the divergence was contributed by 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 variation. There was the 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 a Euclidean distance of 3.49, the 30 genotypes were grouped into IV clusters. PCA components explained 38.4 per cent of 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 study, the genotypes were grouped into 11 clusters. The maximum number of 16 and 15 genotypes were grouped under clusters XI and I respectively, while clusters II, IV, V, VI, VIII, IX and X had only two genotypes. The maximum inter-cluster D^2 value was between cluster I and X (32.96), followed by cluster I and IV (32.90). The genotypes in cluster I had wider diversity with varieties in cluster X and cluster IV and these lines may be utilized in further breeding programme for the exploitation of hybrid vigour. The 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, the maximum contribution was made by grain yield (50.87 %) followed by days to 50 per cent flowering (15.02 %), total grains per panicle (10.52 %) and plant height (10.23 %). Grain yield, days to 50 per cent flowering, total grains per panicle and plant height together contribute 86.62 per cent towards total divergence. Therefore, these characters may be given importance during the hybridization programme.

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 spikelets per panicle, 1000 grain weight and total biomass.

Upadhyay *et al.* (2011) conducted a study intending to develop molecular tags for rice lines. A set of 29 rice varieties were studied for diversity using SSR markers. A total of 87 alleles were produced that were 100 per cent polymorphic. Twelve sets of SSR primers amplified specific alleles in 14 genotypes. The PIC value ranged from 0.57 (RM313) to 0.98 (RM442 and RM163) with an average of 0.78 and an average genetic similarity of 0.38 was observed among the popular varieties. The maximum

similarity of 0.82 was observed between Jayshree and Sarjoo52 and the minimum similarity of 0.05 between Jaya and Pusa Basmati 1. Cluster analysis revealed PCA of rice microsatellite data from 20 primer pairs separated the four early varieties and landraces from recently evolved varieties by the first and second principal component, representing 15 and 12.2 per cent of diversity in the sample. Out of 29 genotypes, 14 genotypes 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 D² analysis revealed a considerable amount of diversity in the material. The genotypes were grouped into nine clusters. Cluster I and III constituted the 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 programme. 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 two to eleven, 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. Polymorphic Information Content (PIC) values ranged from 0.157 to 0.838, with an average of 0.488, revealing that more variation was present among the studied varieties. The PIC values indicated that RM401 might be the best marker for identification and diversity estimation of rice varieties followed by RM566, RM3428, RM463 and RM8094 markers. The UPGMA cluster dendrogram created in this study identified five clusters with a similarity coefficient of 0.50. The SSR polymorphism and diversity could likely be attributed to pedigree. In this study, eight SSR markers (RM10713, RM279, RM424, RM6266, RM1155, RM289, RM20224, and RM5371) were identified that produced specific alleles only in the aromatic rice varieties. They were helpful in varietal identification and DNA fingerprinting of these varieties. The findings of this study should be helpful for varietal identification and could help in background selection in backcross breeding programs.

Rani *et al.* (2013) screened 64 rice genotypes under submergence conditions to study the diversity pattern and to identify and develop varieties suitable for flood-prone areas. The genotypes were grouped into eight clusters. The maximum of 22 genotypes were grouped into cluster I followed by cluster II consisting of 14 genotypes. Clusters IV and VI were with single genotype, indicating the highest heterogeneity among the

genotypes. Maximum inter-cluster distances were observed between clusters IV and VIII (3269.73) and V and VIII (3248.71). The maximum contribution to total divergence was observed from traits viz., test weight, relative shoot elongation, grain yield per plant and days to 50 per cent flowering, 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, fast recovery after de-submergence. These groups are extreme for traits associated with submergence tolerance.

Kodihalli *et al.* (2014) studied genetic diversity among 49 local rice genotypes using Mahalanobis D^2 statistics under submergence. Based on genetic distance, these genotypes were grouped into six clusters. Cluster I was the largest with 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 per plant and grain yield per plant contributed significantly to genetic diversity. Cluster II was characterized by maximum mean value for the majority of these characters. Hence, Doddiga and Hasuli may be used as parents in the future breeding programmes. Genotypes of Cluster III and V may be inter-crossed 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 VI. The minimum genetic diversity was found between Cluster III and IV. They concluded that cultivars like IRRI-3, IRRI-4, KSK-133, SR-57, IRR15 and SRS-64 can be used for hybridization and improvement 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 values for each of the 24 SSR loci. A total of 68 alleles were detected across 16 genotypes by using these 24 SSR markers. The number of alleles per locus varied from 2 (RM 338, RM 452, RM 171) to 6 (RM 585, RM 249, RM 481, RM 162). The PIC values varied from 0.36 (RM 1) to 0.86 (RM 249), with an average of 0.62 per locus. Based on the information generated, the genotypes got separated into six different clusters. Cluster I comprised of 4 genotypes separated from each other at a similarity value of 0.40. Cluster II is comprised of 3 landraces separated at a similarity value of 0.45. Cluster III is comprised of 3 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 is comprised of 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 analyzed based on Mahalanobis D^2 statistics and grouping of clusters was done by Tocher's method. In D^2 analysis, genotypes were grouped into three different clusters in normal and five clusters in submergence. Genotypes Swarna *Sub1*, AURL 41051, AURL 4135, AURL 4139, AURL 4125 were predicted as best according to their performance in normal and submergence conditions. 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. The genotypes from the above clusters when taken as parents would produce superior progenies and hybrids for submergence tolerance.

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 correlation existed between the mean genetic similarity and the mean seedling vigour estimated by shoot length under submergence among the tested varieties. Results suggested the usefulness of the SSR marker system to assess genetic diversity in rice germplasm in relation to their seedling vigour under submergence.

Devi et al. (2017) used microsatellite (SSR) markers to determine the allelic diversity and relationship among 30 Basmati rice genotypes. 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 a different level of polymorphism among the genotypes indicating the robust nature of SSR markers. Among all the primers, RM 107 produced the highest number of alleles (5 alleles) followed by RM127, RM131, RM154 (four alleles), RM11, RM85, RM128 (three alleles), RM5, RM17, RM30, RM38, RM55, RM84, RM130, RM156, RM335 RM338, RM341 (two alleles) and lowest number (single) of alleles were observed in RM18 and RM273. Polymorphic Information Content (PIC value) ranged from 0.556 (RM273) to 0.995 (RM273). Clustering analysis based on UPGMA grouped the genotypes into three main clusters I, II and III, comprising 9, 7 and 14 genotypes, respectively.

Lahari *et al.* (2017) carried out the present 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 Randomized Complete Block Design with two replications under submergence during *Kharif* 2016 to evaluate 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 maximum contribution towards genetic divergence. Hence, from the present investigation three promising genotypes viz., IET 19171, IET 17393 and IET 18508 have been identified as high-yielding submergence tolerant rice varieties.

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 159 bands. Out of them, 30 bands were polymorphic and 129 were monomorphic. The least genetic similarity was found between kalanamak and IR77734-93-2-3-2.

Venkatesan *et al.* (2018) studied the submergence tolerance of 26 rice genotypes with check Swarna *Sub1*. Genetic divergence was analyzed based on Mahalanobis D^2 statistics and the grouping of clusters by Tocher's method. The analysis of variance revealed the presence of variability among genotypes for all the characters both under normal and submergence conditions. In D^2 analysis, 26 genotypes were grouped into three different clusters in normal and five in submergence conditions. The maximum intra-cluster distance was observed between clusters III and I in normal and clusters III and V in submergence conditions.

Tripathi et al. (2020) conducted the present study to assess the genetic diversity among 27 rice cultivars with 12 SSR markers. A total of 40 alleles were detected across 27 rice cultivars tested. PIC values varied widely among SSR loci tested and they 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.*, clusters I and II with a similarity coefficient of 0.13. Cluster I was divided into two minor sub-groups, IA and IB with 5 and 8 genotypes, respectively. These subgroups were further subdivided into minor groups. Similarly, the second main cluster, *i.e.*, Cluster II, was also subdivided into two minor sub-groups that are IIA and IIB, having 5 and 9 genotypes, respectively. These subgroups were further divided into minor groups. This indicated presence of considerable diversity in the genotypes studied and the most diverse cultivars were IR98846-2-1-2-3 and IR14D201

MATERIAL AND METHODS

III MATERIAL AND METHODS

The present investigation was conducted at the College of Agriculture, Navile, KSNUAHS, Shivamogga under artificially created submergence conditions. The details of material used and methods employed in screening for submergence tolerance, genetic variability, character association and diversity studies in rice advanced lines, and statistical tools used in drawing inferences are described in this chapter.

3.1 Experiment I: Evaluation of rice advanced lines for submergence tolerance

3.1.1 Experimental material

The material used for the present study consisted of thirty rice advanced lines, including Swarna sub-1 and FR13A as tolerant checks at the national level, KHP-11 and KHP-13 as local checks, which were collected from the Department of Genetics and Plant Breeding, College of Agriculture, Shivamogga. The investigation was carried out during *Kharif* 2020 at the College of Agriculture, Navile, Shivamogga. The list of rice advanced lines included in the study are presented in Table 1.

3.1.2 Experimental methods

3.1.2.1 Experimental layout and cultural operations

The experiment was laid out in Randomised Complete Block Design (RCBD) with two replications to evaluate the rice advanced lines. Thirty rice advanced lines along with the checks were sown during *Kharif* 2020 for raising the nursery. Twenty-one days old seedlings were transplanted manually into the main field at the rate of single seedling per hill in RCBD design with a spacing of 20 cm row to row and 15 cm plant to plant.

3.1.2.2 Screening for submergence tolerance

The transplanted seedlings were left for one week for proper establishment and then submerged in water with a depth of 50 to 60 cm for 15 days. The crop was then de-submerged and the cultural operations and plant protection measures were taken up according to the recommended package of practices to maintain a good and healthy plant stand.

The number of plants survived fifteen days after de-submergence were recorded to calculate the survival percentage. The number of seedlings before submergence and

the number of seedlings that survived after submergence were noted. The percentage of survivors of each genotype was calculated.

The survival percentage was calculated as (number of survived hills at 15 days of re-emergence) / (number of hills before submergence) *100 and were scored based on Standard Evaluation System for Rice (SES) (IRRI, 1988)

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

3.2 Experiment II: Genetic variability, diversity and character association studies among the rice advanced lines with regards to yield and yield attributing traits under the non-submergence condition

3.2.1 Experimental material

Thirty rice advanced breeding lines of F₆ generation, including tolerant National checks Swarna sub-1 and FR13A, KHP-11 and KHP-13 as local checks collected from the Department of Genetics and Plant Breeding, College of Agriculture, Shivamogga were used to study genetic variability, diversity and character association for yield and yield attributing traits. The investigation was carried out during *Kharif* 2020 at the College of Agriculture, Navile, Shivamogga. The list of rice advanced lines included in the study are presented in Table 1.

3.2.2 Experimental methods

3.2.2.1 Experimental layout and cultural operations

Experimental material was laid out in the field by following Randomised Complete Block Design (RCBD) with two replications. Seeds of all the thirty rice advanced lines, including checks were sown to raise nursery bed during *Kharif* 2020 at the College of Agriculture, Navile, Shivamogga. Twenty-one-day-old seedlings were transplanted manually to the main field at the rate of one seedling per hill in RCBD with two replications. The recommended package of practices were followed in order to maintain a healthy and good crop stand.



Plate 1: Extent of damage caused among rice advanced breeding lines under submergence condition



Plate 2: An overview of experimental plot of rice under non-submergence condition

Table 1: List of rice advanced breeding lines taken for the experiment

Line No.	Genotype
1	KPR2 × IS-9-2-2-2
2	KPR2 × IS-1-4-1-2
3	KPR2 × IS-9-2-2-1
4	KPR2 × IS × Gandhasali-2-4-4
5	KPR-2 × IS × Gandhasali 2-4-4-3
6	KPR-2 × IS × Gandhasali 2-4-4-2
7	Jyothi × Tunga-4-3
8	Jyothi × Tunga-4-6
9	Jyothi × Tunga-2-6-1
10	Jyothi × Tunga-4-5
11	Jyothi × Tunga-2-4
12	Gandhsali × Hyd-5-2-2-4-2-2
13	Gandhsali × Hyd-5-3-4-1-3-4
14	Gandhsali × Hyd-5-1-4-1-4
15	IS × Hyd-3-2-1-2-2
16	IS × Hyd-3-1-1-2-2
17	Jyothi × KPR-1BC2F64-4
18	Jyothi × KPR-1BC2F64
19	Jyothi × KPR-1-BC2F6-4-3-2
20	Jyothi × KPR-1-BC2F6-4-8-2
21	Jyothi × KPR-1-BC2F6-2-1-1-1-1-1
22	Jyothi × KPR-1-BC3F3-1-4
23	HYD-5 × ISBC3F5-5-2-1-2
24	KHP-11 × MM-1-3-1
25	IS × Hyd-5-1-1-2-2
26	KPR-2 × IS-1-3
Check 27	KHP-11
Check 28	KHP-13
Check 29	FR-13A
Check 30	Swarna sub-1

3.2.2.2 Method of sampling and recording observations

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

3.2.2.2.1 Survival Percentage (%)

Survival percentage was calculated as (number of survived hills at 15 days of re-emergence) / (number of hills before submergence) * 100 and were scored based on Standard Evaluation System for Rice (SES) (IRRI, 1988).

3.2.2.2.2 Stem elongation percentage (%)

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

3.2.2.2.3 Days to 50 percent flowering

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

3.2.2.2.4 Days to maturity

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

3.2.2.2.5 Plant height (cm)

The height of the plant from the base of the plant to the tip excluding awn was measured at maturity of the plant and recorded in centimeters using a metal scale.

3.2.2.2.6 Number of tillers per plant

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

3.2.2.2.7 Number of productive tillers per plant

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

3.2.2.2.8 Panicle length (cm)

Length of the panicle was measured from flag leaf node to the tip of panicle excluding awns if any and recorded in centimeters using metal scale.

3.2.2.2.9 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 filled grains per panicle.

3.2.2.2.10 Number of grains per panicle / Number of spikelets per panicle

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

3.2.2.2.11 Spikelet fertility / Panicle 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 calculated by dividing the average number of filled grains of five panicles by the average number of spikelets of five panicles and expressed in percentage.

3.2.2.2.12 Test weight (g)

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

3.2.2.2.13 Length / Breadth (L/B) ratio

The length and breadth of five randomly selected grains was recorded using scale. 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.

3.2.2.2.14 Straw yield per plant (g)

Weight of the straw per plant was taken after sun drying, the constant weight is recorded and expressed in grams.

3.2.2.2.15 Harvest index

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

3.2.2.2.16 Grain yield (kg/ha)

The total weight of the grains from five plants in each rice advanced line was measured in grams and averaged to obtain the per plant yield. The yield per hectare is calculated using the plant population.

3.3 DNA Marker/SSR Marker based diversity analysis

3.3.1 Genetic material

Cup sowing was done for thirty rice advanced lines including the checks and two parents during *Rabi* 2020 and leaf samples were collected. DNA isolation was carried out from the samples as per CTAB (Cetyl Trimethyl Ammonium Bromide) method described by Doyle and Doyle (1990). The protocol followed for DNA isolation is as follows,

3.3.2 Requirements

- Leaf samples (collected freshly from the cup sown seedlings).
- Cetyl Trimethyl ammonium bromide (CTAB) extraction buffer (100ml)
 - CTAB 3 % (w/v)
 - Tris HCl (pH 8.0) 100 mM
 - Sodium Chloride 5 M
 - EDTA 20 mM

(Autoclave Tris, Sodium Chloride and EDTA and add 3 % CTAB (w/v) after autoclaving and preheat the buffer before using).

- 0.2 % β - Mercaptoethanol (added freshly).
- Tris EDTA (TE) buffer
 - Tris HCl (pH 8.0) 10 mM
 - EDTA (pH 8.0) 1 mM

(Dissolved and made up to 100 ml, autoclave and stored at 4 °C)

- 2 % Polyvinyl Poly Pyrrolidone (PVP)
- Ice cold Isopropanol
- Chloroform: Isoamyl alcohol 24:1 (v/v)

- Sodium acetate (3.0 M, pH 7.0) (pH adjusted using glacial acetic acid)
- Absolute ethanol and 70 % ethanol (stored at -20 °C)
- RNase A: 10 mg/ml (RNase A was dissolved in TE buffer and stored at -20 °C).

3.3.3 Protocol for DNA extraction

- The leaf samples (approximately 2 g) were cut into small bits with sterile scissors and transferred to pre-chilled mortar.
- The leaf tissues were frozen using liquid nitrogen and ground into a fine powder.
- The fine powder was allowed to thaw in 5 ml of preheated extraction buffer in polypropylene centrifuge tubes and incubated for 45 minutes at 65 °C in a water bath with occasional mixing.
- The Micro Centrifuge Tubes (MCTs) were centrifuged for 10 minutes at 13,000 rpm at 25°C and the supernatant was transferred to a fresh set of MCTs.
- An equal volume of chloroform: Isoamyl alcohol mixture (24:1) v/v was added to the supernatant and mixed by inversions for 15 minutes.
- The contents of MCTs were centrifuged at 10,000 rpm for 10 minutes at room temperature.
- The clear aqueous phase was transferred to a new sterile tube and equal volume of ice-cold isopropanol was added and mixed gently by inversion and then kept in the freezer at 4°C for precipitation of DNA.
- Using blunt end tips, the precipitate was pooled out into a micro centrifuge tube and air-dried after removing supernatant by a brief spin.
- 500µl of chloroform: Isoamyl alcohol mixture was added and centrifuged at 10,000 rpm for 10 minutes at room temperature.
- The aqueous phase was transferred to another micro centrifuge tube without disturbing the inner phase.
- To this, 2.5 volume of chilled isopropanol and 1/10 volume of sodium acetate were added and kept for incubation overnight.
- It was centrifuged and the supernatant was discarded.
- To this, 500 µl of each 70 % and 100 % ethanol was subsequently used to wash the DNA by centrifugation.
- The alcohol was discarded and the DNA was completely air-dried and the DNA pellet was dissolved in 50 µl of TE and stored at 4°C.

3.3.4 DNA quality assay using agarose gel electrophoresis

Material

6X loading dye

- 30 % Glycerol (v/v)
- 0.25 % Bromophenol blue (w/v)
- 0.25 % Xylene cyanol (w/v)

(Dissolved in sterile double distilled water and the volume is made up to 100 ml)

50X Tris Acetate EDTA buffer (TAE)

- Tris base 242 g
- 57.1 ml Glacial Acetic Acid
- 100 ml 0.5M EDTA

(Dissolved in 800 ml of sterile double distilled water and volume made up to 1000 ml)

100bp Ladder

- 40 µl loading dye
- 10 µl 100bp ladder
- 120 µl sterilized double distilled water

(Total volume made up to 170 µl)

3.3.5 Protocol

- Agarose gel of 0.8 per cent (0.8 g agarose in 100 ml TAE buffer) was prepared for checking the presence of the isolated genomic DNA.
- The required amount of agarose powder was added in the TAE buffer and was heated in the oven to dissolve the powder.
- About 6 µl of EtBr was added for every 100 ml of TAE buffer taken to dissolve agarose powder.
- The solution was cooled to around 45 °C temperature and poured onto the gel casting apparatus and kept undisturbed for solidification.
- 3 µl of DNA sample was mixed with 1µl of 10 X loading dye; they were loaded in the wells of the solidified gel and were run at 120V.

3.3.6 Quantification of DNA

The genomic DNA was quantified spectrophotometrically both at 260 nm and 280 nm wavelengths. The absorbance at 260 nm allows the calculation of DNA concentration in the sample. An OD of 1 at 260 nm corresponds to 50 ng of double-stranded DNA. A pure sample of DNA shows the ratio of OD 260 / 280 as 1.8. A ratio

less than 1.8 indicates contamination in isolation either with phenol or with proteins. The values higher than 1.8 indicate the presence of RNA in isolation.

3.3.7 Normalization of the DNA concentration

Normalization of the DNA concentration was done to bring all the DNA concentrations to a relatively equal level (25 ng μl^{-1}) by appropriate dilutions for PCR reaction. Dilution was done with TE buffer.

3.3.8 PCR reaction mixture

PCR for candidate gene markers was performed in a total volume of 10 μl containing 4 μl 1X PCR Master Mix (Takara Master Mix), 4 μl nuclease-free water, 0.50 μl of each forward and reverse primers, 1 μl genomic DNA. The PCR amplification conditions of the present study are mentioned in Table 2.

3.3.9 Agarose gel electrophoresis

Agarose gel (3.00 %) was prepared using electrophoresis grade agarose in a volume of electrophoresis buffer (1X TAE) sufficient for casting a gel. Ethidium bromide was added at the concentration of 10 mg / ml of gel. The gel was allowed to solidify fully before removing the combs and loading the sample. 10 μl of PCR products were loaded into the wells. A voltage of 100 V was given for a period of two and half hours for the separation of PCR fragments. The gel was viewed under a UV trans-illuminator and the DNA banding pattern was captured in a gel documentation instrument.

3.3.10 Selection of Primers

Primers for the present investigation were selected based on previous worker's data. Fifteen simple sequence repeats (SSR) markers were selected and details of the primers are mentioned in Table 3.

3.3.11 Screening of SSR markers

Fifteen selected SSR markers were screened across thirty rice advanced lines and two parents to assess the molecular diversity.

Table 2: PCR amplification conditions

Steps	Temperature	Time	No. of cycles
Initial denaturation	95 °C	5 minutes	1
Denaturation	94 °C	30 seconds	35
Annealing	*	60 seconds	
Extension	72 °C	45 seconds	
Final extension	72 °C	10 minutes	1
Hold	4°C	Forever	

*Annealing temperature differs with primers

Table 3: List of SSR primers linked to submergence tolerance used in the present investigation

Sl. No.	Primers	Chromosome number	Annealing temp. (°C)	Forward sequence	Reverse sequence
1	RM140	1	55 °C	GGCAGAGAGAGCTGCATCTC	GACGACGACGAACCCAAC
2	RM170	6	55 °C	TCGCGCTTCTTCCTCGTCGACG	CCCGCTTGCAGAGGAAGCAGCC
3	RM58	6	55 °C	TGCCTCTTCCCTGGCTCCCCCTG	GGCATGCCGATGAAATGCATG
4	RM583	1	55 °C	AGATCCATCCCTGTGGAGAG	GCGAACTCGCGTTGTAAATC
5	RM10890	1	55 °C	GCTTCGGCTCTTTCATTCACTGG	GCGATTATAGGAGCGCTATGTGG
6	RM2	7	55 °C	TACGTGTCACCGCTTCCT	ATGTCCGGGATCTCATCG
7	RM212	1	55 °C	CCACTTTCAGCTACTACCAG	CACCCATTGTGTCTCTCATTATG
8	RM3825	1	55 °C	AAAGCCCCCAAAAGCAGTAC	GTGAAACTCTGGGGTGTTCG
9	RM6463	1	50 °C	AGGCACAGAGCGAAACCG	CCAAAGCGCTTCAAGTACGTC
10	RM5869	2	55 °C	TCTCTGCAACCTACGCACAC	GCGGCTGGAGAACATGAC
11	RM22	3	55 °C	GGTTTGGAGCCCATATCT	CTGGGCTTCTTTTCACTCGTC
12	RM36	3	55 °C	CAACTATGCACCATTTGTCGC	GTACTCCACAAGACCGTACC
13	RM163	5	55 °C	ATCCATGTGCGCCTTTATGAGGA	CGCTACCTCCTTCACTTACTAGT
14	RM3859	7	55 °C	TTGCAGATCGGTTTCCACTG	GGTCCTGGATTTCATGGTGTG
15	RM263	2	55 °C	CCCAGGCTAGCTCATGAACC	GCTACGTTTGAGCTACCACG

3.3.12 Scoring of bands

Polymorphic Information Content (PIC) values were calculated for each SSR locus based on Anderson *et al.* (1993). The major allele frequency and Polymorphism Information Content (PIC) values were determined using Power Marker Version 3.25 (Liu and Muse, 2005). The amplified bands were scored for each SSR primer pair based on the presence or absence of bands, generating a binary data matrix of 1 and 0 for each marker system. All the matrices were then analyzed using the NTSYS pc statistical package version 2.2. The data matrices were used to calculate genetic similarity based on Jaccard's similarity coefficients and a dendrogram displaying relationships among thirty rice advanced lines was constructed.

3.4 Statistical analysis

3.4.1 Analysis of variance (ANOVA)

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

Analysis was done using 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	$SSg/(r-1)(t-1) = MSSE$	
Total	(rt-1)	tSS		

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

The sum of squares can be obtained as follows,

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

Where, CF= correction factor

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

Where, r= number of replications

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

Where, t= number of genotypes

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

3.4.1.1 Mean

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

$$\text{Mean} = \frac{\sum_{i=1}^n x_i}{n}$$

Where,

x_i = i^{th} observation of a population

n = number of observations

3.4.1.2 Range

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

3.4.1.3 Standard error

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

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

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

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

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

Where,

r = number of replications

MSSE= error mean sum of square

3.4.1.5 Critical difference (CD)

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

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

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

3.4.1.6 Coefficient of variation (CV)

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

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

3.4.2 Estimation of genetic parameters

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

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

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

3.4.3 Coefficient of variability

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

3.4.3.1 Phenotypic coefficient of variation (PCV)

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

3.4.3.2 Genotypic coefficient of variation (GCV)

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

Where,

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

σ_p = phenotypic standard deviation

σ_g = genotypic standard deviation

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

3.4.4 Heritability (h^2) broad sense

Heritability in broad sense for all the characters was computed by the formula suggested by Lush (1949).

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

Where,

σ_g^2 = genotypic variance

σ_p^2 = phenotypic variance

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

3.4.5 Genetic advance (GA)

3.4.5.1 Predicted genetic advance

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

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

Where,

h^2 = heritability

K = selection differential at given intensity

σ_p = phenotypic standard deviation

3.4.5.2 Genetic advance as per cent mean (GAM)

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

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

Where,

GA = Genetic advance

$\bar{X}$ = General mean

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

3.4.6 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.

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

$$r_{p(x,y)} = \frac{\text{Cov}_{p(x,y)}}{\sqrt{\sigma_{p(x)}^2 \cdot \sigma_{p(y)}^2}}$$

Where,

r_p and r_g are phenotypic and genotypic correlations, respectively.

$\text{Cov}_{p(x,y)}$ and $\text{Cov}_{g(x,y)}$ are phenotypic and genotypic covariance between the characters, x and y.

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

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

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

3.4.7 Path coefficient analysis

The direct or indirect effect of yield attributing traits to yield was calculated using correlation coefficients as given by Wright (1921) and illustrated by Dewey and Lu (1959). Analysis was done using WINDOSTAT software (Version 9.2) and R software.

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

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

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

Where,

P_{01}, P_{02}, P_{0p} are the direct path coefficients of variables 1, 2, 3..... p on the dependent variable 0.

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

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

$$P_{0x}^2 = 1 - (P_{01}^2 + 2 P_{01} P_{02} r_{12} + 2 P_{01} P_{03} r_{13} + \dots + P_{02}^2 + 2 P_{02} P_{03} r_{23} + \dots + P_{0p}^2)$$

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

0.0 to 0.09 : Negligible

0.10 to 0.19 : Low

0.20 to 0.29 : Moderate

0.30 to 0.99 : High

>1.00 : Very high

3.4.8 Genetic diversity

3.4.8.1 Mahalanobis' D^2 analysis

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

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

Where,

D^2 = square of generalized distance

λ_{ij} = reciprocal of the common dispersal matrix

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

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

Since, the formula for computation requires the inversion of higher order determinants, the transformation of the original correlated unstandardized character means (Xs) to the standardized uncorrelated variable (Ys) was done to simplify the

computational procedure. The D^2 values were obtained as the corresponding uncorrelated (Ys) values of any two uncorrelated genotypes (Rao, 1952).

3.4.8.2 Clustering of D^2 values

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

Intra cluster distance:

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

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

Where,

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

n = number of all possible combinations.

Inter cluster distance

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

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

Where,

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

n_i = number of lines in cluster i.

n_j = number of lines in cluster j.

EXPERIMENTAL RESULTS

IV EXPERIMENTAL RESULTS

The present investigation was conducted to evaluate the rice advanced lines for submergence tolerance and to study the morphological and physiological traits related to submergence tolerance, nature and magnitude of genetic variability and diversity with respect to grain yield and yield attributing characters among thirty rice advanced lines and their association with each other in non-submergence conditions. The experimental results are presented in this chapter under the following sub-headings.

- 4.1 Evaluation of rice advanced lines for submergence tolerance
- 4.2 Morphological and physiological studies of rice advanced lines
- 4.3 Phenotypic correlation studies among physiological parameters with grain yield
- 4.4 Genetic variability parameters for grain yield and yield attributing characters
- 4.5 Phenotypic correlation among yield and yield attributing traits
- 4.6 Path coefficient analysis for grain yield and yield attributing characters
- 4.7 Genetic divergence among grain yield and yield attributing traits
- 4.8 Molecular diversity studies in rice advanced lines using SSR markers linked to submergence tolerance
- 4.9 Superior rice advanced lines identified for yield and yield attributing traits.

4.1 Evaluation of rice genotypes for submergence tolerance

The observations for the survival of the rice advanced lines under submerged conditions were recorded to find the survival percentage of thirty rice advanced lines including two local checks KHP-11 and KHP-13 as well as two national checks FR13A and Swarna sub-1. The observations were taken by counting the number of plants that survived fifteen days after de-submergence and were scored from 1 to 9 according to the Standard Evaluation Method recommended by the International Rice Research Institute (IRRI).

The survival per centage of the evaluated rice advanced lines ranged from 5 to 100. Only one rice advanced line KHP-11 × MM-1-3-1(100 %) recorded score of 1 with 100 per cent survival, there was no rice advanced line which scored 3, 2 genotypes IS × Hyd-3-2-1-2-2 (85 %), KPR-2 × IS-1-3 (75 %) scored 5 with survival percentage between 94 per cent and 75 per cent, 4 rice advanced lines KPR-2 × IS-9-2-2-1(60 %), Jyothi × Tunga-4-6 (55 %), Jyothi × KPR-1-BC3F3-1-4 (55 %) and Jyothi × KPR-1BC2F6-4-3-2 (55 %) scored 7 with survival percentage in the range of 50 to 74 per cent and 19 genotypes KPR-2 × IS-1-4-1-2 (45 %), Jyothi × Tunga-4-5 (45 %),

Gandhasali × Hyd-5-3-4-1-3-4 (45 %), IS × Hyd-5 (45 %), Jyothi × Tunga-4-3 (40 %), IS × Hyd-3 (35 %), Jyothi × Tunga-2-4 (35 %), KPR2 × IS × Gandhasali-2-4-4-3 (35 %), Gandhasali × Hyd-5-2-2-4-2-2 (30 %), Jyothi × KPR-1BC2F6-4-4 (30 %), Jyothi × KPR-1-BC2F6-2-1-1-1-1-1 (30 %), Jyothi × KPR-1BC2F64 (25 %), KPR-2 × IS × Gandhasali-2-4-4 (25 %), Jyothi × Tunga-2-6-1 (15 %), Jyothi × KPR-1BC2F6-4-8-2 (15 %), Hyd-5 × ISBC3F5-5-2-1-2 (15 %), Gandhasali × Hyd-5-1-4-1-4 (10 %), KPR × IS × Gandhasali-2-4-4-2 (10 %) and KPR2×IS-9-2-2-2 (5 %) scored 9 with 0 to 49 per cent of survival percentage. Among the national checks Swarna sub-1 has got 100 per cent mean survival percentage which was higher than other national check FR13A which got survival percentage of 85 per cent and local checks KHP-11 and KHP-13 with 85 per cent and 75 per cent of mean survival percentage, respectively.

The highest survival percentage of 100 per cent was noticed in one rice advanced line KHP-11 × MM-1-3-1 as well as check Swarna sub-1. The lowest survival percentage of 5 per cent was noticed in one rice advanced line KPR2 × IS-9-2-2-2. Most of the genotypes scored 9 having 0 to 49 per cent survival. The list of genotypes evaluated for submergence, survival percentage and classification according to the IRRI Standard Evaluation System is presented in Table 4 and Table 5.

4.2 Morphological and physiological studies of rice advanced lines

4.2.1 Genetic variability studies for physiological parameters

Stem elongation and survival percentages studied for the rice advanced lines under submerged conditions were subjected to variability analysis. These parameters exhibited a wide range of Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), Heritability (broad sense) and Genetic Advance as per cent Mean (GAM). The details are presented in Table 6.

4.2.1.1 Survival percentage (%)

The survival percentage recorded high GCV (60.49 %) and PCV (61.87 %) along with high heritability (95.62 %) coupled with high genetic advance as per cent mean (121.86 %). The mean survival percentage was found to be 45.51 per cent with the range from 5.00 per cent (KPR2 × IS-9-2-2-2) to 100.00 per cent (KHP-11 × MM-1-3-1).

Table 4: Classification of rice advanced breeding lines based on survival percentage under submergence based on IRRI Standard Evaluation System

Score	Survival percentage	Genotypes
1	100 %	KHP-11 × MM-1-3-1
3	95-99 %	-
5	75-94 %	IS × Hyd-3-2-1-2-2, KPR-2 × IS-1-3
7	50-74 %	KPR-2 × IS-9-2-2-1, Jyothi × KPR-1BC2F6-4-3-2, Jyothi × Tunga-4-6, Jyothi × KPR-1BC3F3-1-4
9	0-49 %	KPR-2 × IS-1-4-1-2, Jyothi × Tunga-4-5, IS × Hyd-5, Gandhasali × Hyd-5-3-4-1-3-4, Jyothi × Tunga-4-3, IS × Hyd-3, Jyothi × Tunga-2-4, KPR2 × IS × Gandhasali-2-4-4-3, Gandhasali × Hyd-5-2-2-4-2-2, Jyothi × KPR-1BC2F6-4-4, Jyothi × KPR-1-BC2F6-2-1-1-1-1-1, Jyothi × KPR-1BC2F64, KPR-2 × IS × Gandhasali-2-4-4, Jyothi × Tunga-2-6-1, Jyothi × KPR-1BC2F6-4-8-2, Hyd-5 × ISBC3F5-5-2-1-2, Gandhasali × Hyd-5-1-4-1-4, KPR × IS × Gandhasali-2-4-4-2, KPR2 × IS-9-2-2-2

Table 5: List of advanced breeding lines taken for the experiment with their respective survival percentage and IRRI Standard Evaluation System score

Line No.	Genotype	Survival percentage (%)	Score
1	KPR2 × IS-9-2-2-2	5	9
2	KPR2 × IS-1-4-1-2	45	9
3	KPR2 × IS-9-2-2-1	60	7
4	KPR2 × IS × Gandhasali-2-4-4	25	9
5	KPR-2 × IS × Gandhasali 2-4-4-3	35	9
6	KPR-2 × IS × Gandhasali 2-4-4-2	10	9
7	Jyothi × Tunga-4-3	40	9
8	Jyothi × Tunga-4-6	55	7
9	Jyothi × Tunga-2-6-1	15	9
10	Jyothi × Tunga-4-5	45	9
11	Jyothi × Tunga-2-4	35	9
12	Gandhsali × Hyd-5-2-2-4-2-2	30	9
13	Gandhsali × Hyd-5-3-4-1-3-4	45	9
14	Gandhsali × Hyd-5-1-4-1-4	10	9
15	IS × Hyd-3-2-1-2-2	85	5
16	IS × Hyd-3	35	9
17	Jyothi × KPR-1BC2F64-4	30	9
18	Jyothi × KPR-1BC2F64	25	9
19	Jyothi × KPR-1-BC2F6-4-3-2	55	7
20	Jyothi × KPR-1-BC2F6-4-8-2	15	9
21	Jyothi × KPR-1-BC2F6-2-1-1-1-1-1	30	9
22	Jyothi × KPR-1-BC3F3-1-4	55	7
23	HYD-5 × ISBC3F5-5-2-1-2	15	9
24	KHP-11 × MM-1-3-1	100	1
25	IS × Hyd-5	45	9
26	KPR-2 × IS-1-3	75	5
27	KHP-11	85	5
28	KHP-13	75	5
29	FR-13A	85	5
30	Swarna SUB 1	100	1

Table 6: Estimates of mean, range, variability, heritability and genetic advance as per cent mean for physiological parameters

Sl. No	Characters	Mean $\pm$ SE _m	Range		GCV (%)	PCV (%)	h ² (bs) (%)	GAM (%)	CV (%)	CD @ 5%	CD @ 1%
			Min	Max							
1	Survival Percentage (%)	45.51 $\pm$ 4.17	5	100	60.49	61.87	95.62	121.86	12.94	12.08	16.28
2	Stem elongation (%)	35.25 $\pm$ 3.28	16.19	55.32	28.44	31.38	82.38	53.25	13.17	9.51	12.83

4.2.1.2 Stem elongation percentage (%)

High GCV (28.44) and PCV (31.38) were obtained for stem elongation percentage. Heritability for stem elongation percentage was 82.38 per cent and genetic advance as per cent mean was 53.25. The mean was 35.25 per cent, ranging from 16.19 (KPR2 × IS-9-2-2-2) to 55.32 per cent (Gandhsali × Hyd-5-1-4-1-4). The highest stem elongation was recorded in Gandhsali × Hyd-5-1-4-1-4 (55.32 %) followed by Jyothi × KPR-1-BC2F6-2-1-1-1-1 (52.44 %) and the lowest was recorded in KPR2 × IS-9-2-2-2 (16.19 %) followed by HYD-5 × IS-BC3F5-5-2-1-2 (20.97 %).

4.3 Phenotypic correlation studies among physiological parameters with grain yield

The phenotypic correlation of physiological parameters viz., stem elongation percentage, survival percentage and harvest index were studied with yield per plant as a dependent trait. The details are furnished in Table 7.

Under submergence conditions, survival percentage showed a significant positive correlation with harvest index (0.2767) and grain yield (0.6241). Whereas, it showed a significant negative correlation with stem elongation percentage (-0.2991).

Stem elongation percentage showed a negative non-significant correlation with harvest index (-0.0273) and grain yield (-0.2193). Harvest index manifested a significant positive correlation with grain yield (0.4368).

4.4 Genetic variability parameters for grain yield and yield attributing characters

The analysis of variance for various morphological characters showed significant difference for all the characters studied, which indicated that the rice advanced lines under study were genetically diverse. The analysis of variance for all the fourteen traits is given in Table 8. Mean values for all the characters studied are provided in Appendix I.

The genetic variability parameters viz., mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) and genetic advance as per cent mean (GAM) for all the fourteen traits under study are furnished in Table 9.

Table 7: Phenotypic correlation coefficients for yield and submergence tolerance traits

	Survival percentage (%)	Stem elongation (%)	Harvest Index (%)	Grain yield (kg/ha)
Survival percentage (%)	1	-0.2991*	0.2767*	0.6241**
Stem elongation (%)		1	-0.0273	-0.2193
Harvest index (%)			1	0.4368**
Grain yield (g)				1

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

Table 8: Analysis of variance for yield and its component characters in rice advanced lines in control conditions

Source of variation	df	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Total number of tillers per plant	Number of productive tillers per plant	Panicle length (cm)	No. of filled grains per panicle
Replication	1	2.44	0.83	239.95	7.27	5.44	2.02	203.12
Genotype	29	216.85**	201.27**	644.68**	36.17**	42.43**	10.85**	1135.50**
Error	29	0.81	0.17	67.18	4.88	3.28	1.01	135.26
CD (5%)		1.85	2.01	16.79	4.53	3.71	2.05	23.82
CD (1%)		2.49	2.72	22.65	6.11	5.01	2.77	32.14
CV (%)		0.78	0.66	7.27	11.44	10.17	4.48	9.97

Source of variation	df	Total no. of spikelets per panicle	Panicle fertility (%)	Test weight (g)	Length – Breadth ratio	Straw yield (g)	Harvest index	Grain yield (kg/ha)
Replication	1	177.35	13.00	0.05	0.03	14.05	4.26	218264.90
Genotype	29	1930.56**	480.73**	101.71**	0.42**	77.68**	136.37**	2619051.00**
Error	29	156.98	41.68	0.79	0.004	7.58	17.20	183470.80
CD (5%)		25.67	13.22	1.82	0.13	5.64	8.49	877.40
CD (1%)		34.62	17.84	2.46	0.17	7.61	11.46	1183.60
CV (%)		8.23	8.59	3.59	1.96	9.08	8.53	9.24

Table 9: Estimation of mean, range, variability, heritability and genetic advance as per cent mean for yield and yield-related traits

Sl. No	Characters	Mean $\pm$ SE _m	Range		PCV (%)	GCV (%)	h ² (bs) (%)	GAM (%)
			Min	Max				
1	Days to 50 per cent flowering	115 $\pm$ 0.63	104	139	9.02	8.98	99.25	18.44
2	Days to maturity	150 $\pm$ 0.69	137	167	6.71	6.68	99.04	13.69
3	Plant height (cm)	112.77 $\pm$ 5.79	89.58	156.56	16.72	15.08	81.12	27.96
4	Number of tillers per plant	19.31 $\pm$ 1.56	11.05	30.37	23.46	20.47	76.21	36.82
5	Number of productive tillers per plant	17.82 $\pm$ 1.28	9.55	29.37	26.83	24.83	85.64	47.33
6	Panicle length (cm)	22.40 $\pm$ 0.70	15.95	25.80	10.87	9.90	83.04	18.59
7	Number of filled grains per panicle	116.59 $\pm$ 8.22	61.06	158.32	21.61	19.18	78.71	35.05
8	Total number of spikelets per panicle	152.24 $\pm$ 8.86	90.50	202.78	21.22	19.56	84.96	37.14
9	Panicle fertility (%)	75.19 $\pm$ 4.56	45.12	98.74	21.49	19.70	84.04	37.21
10	Test weight (g)	24.74 $\pm$ 0.63	11.45	33.25	28.93	28.71	98.46	58.69
11	Length breadth ratio	3.21 $\pm$ 0.04	2.26	4.48	14.31	14.17	98.11	28.93
12	Straw yield (g)	30.33 $\pm$ 1.94	14.90	43.31	21.52	19.52	82.23	36.46
13	Harvest index	48.63 $\pm$ 2.93	21.84	62.24	18.02	15.87	77.60	28.80
14	Grain yield (kg/ha)	4637.38 $\pm$ 302.88	2281.50	6637.50	25.52	23.79	86.91	45.69

4.4.1 Days to 50 per cent flowering

Days to 50 per cent flowering ranged from 104 to 139 days with a mean of 115 days. Jyothi × KPR-1-BC2F6-4-3-2 was the earliest to flower at 104 days and KPR-2 × IS -1-3 was late to flower at 139 days. Low PCV and GCV of 9.02 and 8.98 per cent was recorded, respectively. The character exhibited high heritability (99.25 %) with moderate genetic advance as per cent mean (18.44).

4.4.2 Days to maturity

The mean days to maturity was found to be 150 days ranging from 137 to 167 days. Jyothi × KPR-1-BC2F6-4-8-2 was the earliest to mature at 137 days, while Jyothi × KPR-1-BC2F6-2-1-1-1-1-1 (167 days) was late to mature. The PCV and GCV were 6.71 and 6.68 per cent, respectively. A high heritability estimate of 99.04 per cent with moderate GAM (13.69 %) was observed.

4.4.3 Plant height (cm)

Plant height ranged from 89.58 cm to 156.56 cm with a mean value of 112.77 cm. HYD-5 × ISBC3F5-5-2-1-2 recorded a minimum height of 89.58 cm and the maximum plant height of 156.56 cm was recorded by IS × Hyd-3-2-1-2-2. The PCV and GCV were 16.72 and 15.08 per cent, respectively. High heritability (81.12 %) and high GAM (27.96 %) was recorded by this trait.

4.4.4 Number of tillers per plant

It was found that the number of tillers per plant significantly differed among rice advanced lines. It ranged from 11.05 to 30.37 with a mean value of 19.31. Gandhsali × Hyd-5-1-4-1-4 recorded the lowest number of tillers per plant, *i.e.*, 11.05, whereas KHP-11 × MM-1-3-1 recorded the highest number of tillers with 30.37 tillers per plant. Phenotypic and genotypic coefficients of variability observed were 23.46 and 20.47 per cent, respectively. High heritability of 76.21 per cent and high genetic advance as per cent mean of 36.82 were noticed.

4.4.5 Number of productive tillers per plant

A significant difference among the rice advanced lines for the number of productive tillers per plant was noticed. The number of productive tillers per plant varied significantly from 9.55 to 29.37 with a mean value of 17.82. KHP-11 × MM-1-3-1 recorded the highest number of productive tillers and Gandhsali × Hyd-5-1-4-1-4 recorded the lowest. Among checks, FR13A recorded the highest number of productive tillers per plant (24.85). PCV and GCV were 26.83 and 24.83 per cent, respectively, coupled with a high heritability of 85.64 per cent and GAM of 47.33 was noticed.

4.4.6 Panicle length (cm)

The panicle length exhibited a wide range of variability among the studied rice advanced lines. It ranged from 15.95 to 25.80 cm with a mean value of 22.40 cm. The highest panicle length was recorded by IS × Hyd-3-2-1-2-2 (25.80 cm) followed by KHP-11 × MM-1-3-1 (24.80 cm) and lowest by HYD-5 × ISBC3F5-5-2-1-2 (15.95 cm) followed by Jyothi × KPR-1-BC2F6-4-8-2 (16.75 cm). Moderate PCV (10.87 %) and low GCV (9.90 %) coupled with high heritability (83.04 %) and moderate GAM (18.59 %) was recorded.

4.4.7 Number of filled grains per panicle

The number of filled grains per panicle recorded moderate GCV (19.81 %) with high PCV (21.61 %) coupled with high heritability (78.71 %) and high GAM (35.05 %). The mean value was found to be 116.59 with the range of 61.06 to 158.32. The minimum number of filled grains per panicle was recorded by IS × Hyd-3, whereas Jyothi × KPR-1-BC2F6-4-8-2 showed the maximum number of filled grains per panicle.

4.4.8 Total number of spikelets per panicle

The total number of spikelets per panicle recorded moderate GCV (19.56 %) with high PCV (21.22 %) coupled with high heritability (84.96 %) and high GAM (37.14 %). The mean value was found to be 152.24 with the range of 90.50 to 202.78. The maximum number of spikelets per panicle was recorded by Jyothi × Tunga-4-6, whereas Jyothi × KPR-1-BC2F6-4-8-2 showed the minimum number of spikelets per panicle.

4.4.9 Panicle fertility (%)

The mean panicle fertility was 75.19 per cent which ranged from 45.12 to 98.74 per cent. Jyothi × Tunga-4-5 showed the highest panicle fertility and the lowest panicle fertility was recorded by Gandhsali × Hyd-5-1-4-1-4. High PCV and moderate GCV of 21.49 and 19.70 per cent, respectively with a high heritability of 84.04 per cent and GAM of 37.21 per cent were noticed.

4.4.10 Test weight (g)

Test weight ranged from 11.45 to 33.25 g with a mean of 24.74 g. The lowest test weight was recorded by Gandhsali × Hyd-5-1-4-1-4 and KHP-11 × MM-1-3-1 had the highest test weight. The PCV and GCV were 28.93 and 28.71 per cent, respectively. High heritability (98.46 %) with high GAM (58.69 %) was noticed.

4.4.11 Length breadth ratio

The length breadth ratio of the rice advanced lines under study ranged from 2.26 to 4.48 with a mean value of 3.21. Jyothi × KPR-1-BC2F6-4-8-2 recorded the highest length breadth ratio while Jyothi × Tunga-4-6 recorded the lowest. The PCV and GCV were moderate, i.e., 14.31 and 14.17, respectively. High heritability of 98.11 per cent and high genetic advance as per cent mean of 28.93 was observed.

4.4.12 Straw yield per plant (g)

Straw yield per plant ranged from 14.90 to 43.31 g with a mean of 30.33 g. The lowest straw yield was recorded by Gandhsali × Hyd-5-1-4-1-4 and KPR2 × IS-1-4-1-2 had the highest straw yield. The PCV and GCV for this character were 21.52 and 19.52 per cent, respectively. High heritability (82.23 %) coupled with high GAM (36.46 %) was exhibited by this trait.

4.4.13 Harvest index

Harvest index varied significantly from 21.84 to 62.24 per cent with a mean of 48.63 per cent. Jyothi × KPR-1-BC3F3-1-4 recorded the lowest harvest index (21.84 %) and the highest was recorded by IS × Hyd-3-2-1-2-2 (62.24 %). The PCV and GCV recorded for this character were 18.02 and 15.87, respectively. Heritability of 77.60 per cent with the GAM of 28.80 was observed.

4.4.14 Grain yield (kg/ha)

Grain yield varied significantly from 2281.50 to 6637.50 kg/ha with a mean of 4637.38 kg/ha. The lowest grain yield of 2281.50 kg/ha was recorded by Gandhsali × Hyd-5-1-4-1-4 followed by HYD-5 × ISBC3F5-5-2-1-2 (2849.25 kg/ha) and KHP-11 × MM-1-3-1 had the highest grain yield of 6637.50 kg/ha followed by IS × Hyd-3-2-1-2-2 (6534.00 kg/ha). The PCV and GCV for this character were 25.52 and 23.79 per cent, respectively. High heritability of 86.91 per cent with a high GAM of 45.69 was exhibited.

4.5 Phenotypic correlation among yield and yield attributing traits

Phenotypic correlations among fourteen characters studied was calculated to determine the nature of the association between yield and yield attributing traits under submergence conditions and are presented in Table 10.

4.5.1 Correlation of grain yield with other characters

A significant positive association was found between grain yield with plant height ($r = 0.549$), number of tillers per plant ($r = 0.509$), number of productive tillers per plant ($r = 0.597$), panicle length ($r = 0.444$), number of filled grains per panicle ($r = 0.418$), total number of spikelets per panicle ($r = 0.267$), panicle fertility ($r = 0.488$),

test weight ($r = 0.571$), straw yield ($r = 0.303$) and harvest index ($r = 0.437$). Whereas, positive non-significant association of grain was found with days to 50 per cent flowering ($r = 0.180$) and days to maturity ($r = 0.151$). While non-significant negative correlation was found for length breadth ratio ($r = -0.047$).

4.5.2 Correlation among yield attributing characters

4.5.2.1 Days to 50 per cent flowering

Days to 50 per cent flowering exhibited a significant positive correlation with days to maturity (0.933). It showed a non-significant positive correlation with plant height (0.169), number of tillers per plant (0.081), number of productive tillers per plant (0.184), number of filled grains per panicle (0.090), total number of spikelets per panicle (0.108), test weight (0.187), length breadth ratio (0.104), straw yield (0.012), harvest index (0.157). The non-significant negative association with panicle length (-0.186) and panicle fertility (-0.054) was manifested.

4.5.2.2 Days to maturity

Days to maturity (0.933) exhibited a significant positive correlation with days to 50 per cent flowering. A non-significant positive correlation was exhibited by plant height (0.211), number of tillers per panicle (0.117), number of productive tillers per panicle (0.211), number of filled grains per plant (0.169), the total number of spikelets per panicle (0.173), test weight (0.158) and harvest index (0.167). A non-significant negative association of days to maturity was observed with panicle length (-0.072), panicle fertility (-0.017), length breadth ratio (-0.054) and straw yield (-0.057).

Table 10: Phenotypic correlation among yield and yield-related characters under submergence

	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄
X ₁	1.000	0.933**	0.169	0.081	0.184	-0.186	0.090	0.108	-0.054	0.187	0.104	0.012	0.157	0.180
X ₂		1.000	0.211	0.117	0.211	-0.072	0.169	0.173	-0.017	0.158	-0.054	-0.057	0.167	0.151
X ₃			1.000	0.249	0.442**	0.273*	0.179	0.301*	0.116	0.406**	-0.072	0.067	0.280*	0.549**
X ₄				1.000	0.845**	0.542**	0.300*	0.440**	0.288*	0.358**	-0.358**	0.133	0.286*	0.509**
X ₅					1.000	0.487**	0.383**	0.392**	0.389**	0.545**	-0.229	0.168	0.301*	0.597**
X ₆						1.000	0.524**	0.587**	0.433**	0.281*	-0.526**	0.192	0.271*	0.444**
X ₇							1.000	0.606**	0.733**	0.368**	-0.306**	0.504**	-0.015	0.418**
X ₈								1.000	0.117	0.217	-0.640**	0.273*	0.059	0.267*
X ₉									1.000	0.519**	-0.046	0.521**	-0.086	0.488**
X ₁₀										1.000	-0.271*	0.310*	0.023	0.571**
X ₁₁											1.000	-0.142	0.181	-0.047
X ₁₂												1.000	-0.388**	0.303*
X ₁₃													1.000	0.437**
X ₁₄														1.000

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

Where,

X₁= Days to 50 per cent flowering
 X₂= Days to maturity
 X₃= Plant height (cm)
 X₄= number of tillers per plant
 X₅=Number of productive tillers per plant
 X₆= Panicle length (cm)
 X₇= number of filled grains per panicle
 X₈= Total number of spikelets per panicle
 X₉= Panicle fertility (%)
 X₁₀= Test weight (g)
 X₁₁= Length breadth ratio
 X₁₂= Straw yield (g)
 X₁₃= Harvest index
 X₁₄= Grain yield (kg/ha)

4.5.2.3 Plant height

Plant height showed to be positive significantly associated with the number of productive tillers per plant (0.442), panicle length (0.273), the total number of spikelets per panicle (0.301), test weight (0.406) and harvest index (0.280). A non-significant positive association with days to 50 per cent flowering (0.169), days to maturity (0.211), number of tillers per plant (0.249), number of filled grains per panicle (0.179), panicle fertility (0.116) and straw yield (0.067). A non-significant negative correlation was found with the length breadth ratio (-0.072).

4.5.2.4 Number of tillers per plant

The number of tillers per plant showed a significant positive correlation with the number of productive tillers per plant (0.845), panicle length (0.542), the number of filled grains per panicle (0.300), total number of spikelets per panicle (0.440), panicle fertility (0.288), test weight (0.358) and harvest index (0.286). Whereas the non-significant positive correlation was found with days to 50 per cent flowering (0.081), days to maturity (0.117), plant height (0.249) and straw yield (0.133). Plant height was found to be negatively significantly correlated with length breadth ratio (-0.358).

4.5.2.5 Number of productive tillers per plant

Significant positive association of the number of productive tillers per plant was exhibited with plant height (0.442), number of tillers per plant (0.845), panicle length (0.487), number of filled grains per panicle (0.383), total number of spikelets per panicle (0.392), panicle fertility (0.389), test weight (0.545) and harvest index (0.381). Whereas, the positive non-significant association was found with days to 50 per cent flowering (0.184), days to maturity (0.211) and straw yield (0.168). The negative non-significant correlation was observed with the length breadth ratio (-0.229).

4.5.2.6 Panicle length

Panicle length showed a significant positive correlation with plant height (0.273), number of tillers per plant (0.542), number of productive tillers per plant (0.487), number of filled grains per panicle (0.524), the total number of spikelets per panicle (0.587), panicle fertility (0.433), test weight (0.281) and harvest index (0.271). A non-significant positive correlation was found with straw yield (0.192). Whereas the non-significant negative association was manifested with days to 50 per cent flowering (-0.186), days to maturity (-0.072). A significant negative association was observed for length breadth ratio (-0.526).

4.5.2.7 Number of filled grains per panicle

Significant positive correlation with the number of filled grains per panicle was accompanied by the number of tillers per plant (0.300), number of productive tillers per plant (0.383), panicle length (0.524), straw yield (0.504), the total number of spikelets per panicle (0.606), panicle fertility (0.733), test weight (0.368) and straw yield (0.504). Whereas the non-significant positive association was accompanied by days to 50 per cent flowering (0.090), days to maturity (0.169) and plant height (0.179). A non-significant negative association was found with harvest index (-0.015). While the significant positive association was observed for length breadth ratio (-0.306).

4.5.2.8 Total number of spikelets per panicle

Significant positive correlation with the total number of spikelets per panicle was accompanied by plant height (0.301), number of tillers per plant (0.440), number of productive tillers per plant (0.392), panicle length (0.587), number of filled grains per panicle (0.606) and straw yield (0.273). A non-significant positive association was found with days to 50 per cent flowering (0.108), days to maturity (0.173), panicle fertility (0.117), test weight (0.217) and harvest index (0.059). Whereas, a significant negative association was observed for length breadth ratio (-0.640).

4.5.2.9 Panicle fertility

Panicle fertility had a significant positive association with the number of tillers per plant (0.288), number of productive tillers per plant (0.389), panicle length (0.433), number of filled grains per panicle (0.733), test weight (0.519) and straw yield (0.310). A non-significant positive association was exhibited by plant height (0.116) and total number of spikelets per panicle (0.117). Whereas the non-significant negative correlation with panicle fertility was shown by days to 50 per cent flowering (-0.054), days to maturity (-0.017), length breadth ratio (-0.046) and harvest index (-0.086).

4.5.2.10 Test weight

Significant positive association with test weight was shown by plant height (0.406), number of tillers per plant (0.358), number of productive tillers per plant (0.545), panicle length (0.281), number of filled grains per panicle (0.368), panicle fertility (0.519) and straw yield (0.310). A non-significant positive association was shown by days to 50 per cent flowering (0.187), days to maturity (0.158), the total number of spikelets per panicle (0.217) and harvest index (0.023). A significant negative association was found with length breadth ratio (-0.271).

4.5.2.11 Length breadth ratio

Non-significant positive association with the length breadth ratio of the grains was shown by days to 50 per cent flowering (0.104) and harvest index (0.181). A non-significant negative association was recorded by days to maturity (-0.054), plant height (-0.072), number of productive tillers per plant (-0.229), panicle fertility (-0.046) and straw yield (-0.142). Whereas, significant negative association was observed for number of tillers per plant (-0.358), panicle length (-0.526), number of filled grains per panicle (-0.306), total number of spikelets per panicle (-0.640) and test weight (-0.271).

4.5.2.12 Straw yield

A positive significant correlation with straw yield was exhibited by the number of filled grains per panicle (0.504), total number of spikelets per panicle (0.273), panicle fertility (0.521) and test weight (0.310). While the non-significant positive correlation was observed by days to 50 per cent flowering (0.012), plant height (0.067), number of tillers per plant (0.133), number of productive tillers per plant (0.168) and panicle length (0.192). A non-significant negative association was shown by days to maturity (-0.057) and length breadth ratio (-0.142). Whereas a significant negative association was found with harvest index (-0.388).

4.5.2.13 Harvest index

Harvest index was found to have a significant positive association with plant height (0.280), number of tillers per plant (0.286), number of productive tillers per plant (0.301) and panicle length (0.271). A positive non-significant association was found with days to 50 per cent flowering (0.157), days to maturity (0.167), the total number of spikelets per panicle (0.059), test weight (0.023) and length breadth ratio (0.181). A negative non-significant association was found with the number of filled grains per panicle (-0.015), panicle fertility (-0.086) and straw yield (-0.388).

4.6 Path coefficient analysis for grain yield and yield attributing characters

To measure the direct and indirect effect of various independent characters on a dependent character yield, path coefficient analysis was carried out at phenotypic level. The results obtained are presented in Table 11.

4.6.1 Days to 50 per cent flowering

Days to 50 per cent flowering exhibited a negative direct effect on grain yield (-0.0739). The indirect positive effect of days to 50 per cent flowering on grain yield was recorded by panicle length (0.0137) and panicle fertility (0.004). However, it exhibited negative indirect effect *via* days to maturity (-0.0689), plant height (-0.0125), number of tillers per plant (-0.0060), number of productive tillers per plant (-0.0136),

number of filled grains per panicle (-0.0066), total number of spikelets per panicle (-0.0080), test weight (-0.0138), length breadth ratio (-0.0077), straw yield (-0.0009) and harvest index (-0.0116).

4.6.2 Days to maturity

The direct effect of days to maturity on grain yield was positive (0.0921). Days to maturity affected grain yield positive indirectly through days to 50 per cent flowering (0.0859), plant height (0.0194), number of tillers per plant (0.0108), number of productive tillers per plant (0.0195), number of filled grains per panicle (0.0156), the total number of spikelets per panicle (0.0159), test weight (0.0146) and harvest index. However, it exhibited an indirect negative effect on grain yield by panicle length (-0.0066), panicle fertility (-0.0016), length breadth ratio (-0.0050) and straw yield (-0.0053).

4.6.3 Plant height

Plant height showed a positive direct effect on grain yield (0.2444). The positive indirect effect of plant height on grain yield was observed by days to 50 per cent flowering (0.0412), days to maturity (0.0516), number of tillers per plant (0.0607), number of productive tillers per plant (0.1080), panicle length (0.0668), number of filled grains per panicle (0.0437), total number of spikelets per panicle (0.0736), panicle fertility (0.0284), test weight (0.0993), straw yield (0.0163) and harvest index (0.0684). However, it showed a negative indirect effect on grain yield through length breadth ratio (-0.0176).

Table 11: Path coefficient analysis for advanced breeding lines of rice

	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃
X ₁	-0.0739	-0.0689	-0.0125	-0.006	-0.0136	0.0137	-0.0066	-0.008	0.004	-0.0138	-0.0077	-0.0009	-0.0116
X ₂	0.0859	0.0921	0.0194	0.0108	0.0195	-0.0066	0.0156	0.0159	-0.0016	0.0146	-0.005	-0.0053	0.0154
X ₃	0.0412	0.0516	0.2444	0.0607	0.108	0.0668	0.0437	0.0736	0.0284	0.0993	-0.0176	0.0163	0.0684
X ₄	0.0302	0.0433	0.0922	0.3713	0.3139	0.2014	0.1114	0.1632	0.107	0.1329	-0.1328	0.0495	0.106
X ₅	-0.0402	-0.0462	-0.0966	-0.1848	-0.2186	-0.1065	-0.0836	-0.0857	-0.0851	-0.1193	-0.05	-0.0367	-0.0659
X ₆	-0.0305	-0.0119	0.0449	0.0892	0.0801	0.1644	0.0862	0.0965	0.0712	0.0761	-0.0865	0.0316	0.0455
X ₇	0.0032	0.006	0.0063	0.0106	0.0135	0.0185	0.0354	0.0214	0.0258	0.013	-0.0108	0.0178	-0.0005
X ₈	0.0072	0.0115	0.0201	0.0293	0.0262	0.0392	0.0404	0.0667	0.0078	0.0145	-0.0427	0.0182	0.004
X ₉	-0.0029	-0.0009	0.0064	0.0158	0.0213	0.0238	0.04	0.0064	0.0548	0.0284	-0.0025	0.0285	-0.0049
X ₁₀	0.0712	0.0602	0.1546	0.1361	0.2076	0.1066	0.1401	0.0825	0.1973	0.3803	-0.103	0.1179	0.0086
X ₁₁	0.0402	-0.021	-0.0278	-0.1381	-0.0884	-0.2032	-0.1179	-0.247	-0.0178	-0.1046	0.3857	-0.0548	0.0699
X ₁₂	0.0027	-0.0134	0.0156	0.0312	0.0393	0.045	0.1178	0.064	0.1219	0.0725	-0.0332	0.234	-0.0908
X ₁₃	0.0459	0.0489	0.0819	0.0835	0.0882	0.081	-0.0042	0.0175	-0.026	0.0066	0.053	-0.1136	0.2926
r value	0.180	0.151	0.549	0.509	0.597	0.444	0.418	0.267	0.488	0.571	-0.047	0.303	0.437

Residual effect = 0.2403

r = correlation coefficient of component traits with grain yield

Where,

X₁= Days to 50 per cent flowering

X₂= Days to maturity

X₃= Plant height (cm)

X₄= number of tillers per plant

X₅=Number of productive tillers per

X₆= Panicle length (cm)

X₇= number of filled grains per panicle

X₈= Total number of spikelets per

X₉= Panicle fertility (%)

X₁₀= Test weight (g)

X₁₁= Length breadth ratio

X₁₂= Straw yield (g)

X₁₃= Harvest index

X₁₄= Grain yield (kg/ha)

4.6.4 Number of tillers per plant

The number of tillers per plant showed a positive direct effect on grain yield (0.3713). The positive indirect effect of the number of tillers per plant on grain yield was observed by days to 50 per cent flowering (0.0302), days to maturity (0.0433), plant height (0.0922), number of productive tillers per plant (0.3139), panicle length (0.2014), number of filled grains per panicle (0.1114), total number of spikelets per panicle (0.1632), panicle fertility (0.1070), test weight (0.1329), straw yield (0.0495) and harvest index (0.1060). However, it showed a negative indirect effect on grain yield through length breadth ratio (-0.1328).

4.6.5 Number of productive tillers per plant

The number of productive tillers per panicle showed a negative direct effect on grain yield (-0.2186). The negative indirect effect of the number of productive tillers per plant on grain yield was observed by days to 50 per cent flowering (-0.0402), days to maturity (-0.0462), plant height (-0.0966), number of tillers per plant (-0.1848), panicle length (-0.1065), number of filled grains per panicle (-0.0836), total number of spikelets per panicle (-0.0857), panicle fertility (-0.0851), test weight (-0.1193), length breadth ratio (-0.0500), straw yield (-0.0367) and harvest index (-0.0659). It did not show the negative indirect effect on grain yield through any of the characters studied.

4.6.6 Panicle length

Panicle length showed a positive direct effect on grain yield (0.1644). Panicle length manifested a positive indirect effect on grain yield through plant height (0.0449), number of tillers per plant (0.0892), number of productive tillers per plant (0.0801), number of filled grains per panicle (0.0862), total number of spikelets per panicle (0.0965), panicle fertility (0.0712), test weight (0.0761), straw yield (0.0316) and harvest index (0.0455). It showed an indirect negative effect on grain yield through days to 50 per cent flowering (-0.0305), days to maturity (-0.0119) and length breadth ratio (-0.0865).

4.6.7 Number of filled grains per panicle

The number of filled grains per panicle showed a positive direct effect on grain yield (0.0354). The positive indirect effect of the number of filled grains per panicle on grain yield was observed by days to 50 per cent flowering (0.0032), days to maturity (0.0060), plant height (0.0063), number of tillers per plant (0.0106), number of productive tillers per plant (0.0135), panicle length (0.0185), the total number of spikelets per panicle (0.0214), panicle fertility (0.0258), test weight (0.0130) and straw yield (0.0178). However, it showed a negative indirect effect on grain yield through length breadth ratio (-0.0108) and harvest index (-0.0005).

4.6.8 Total number of spikelets per panicle

The total number of spikelets per panicle showed a positive direct effect on grain yield (0.0667). The positive indirect effect of the total number of spikelets per panicle on grain yield was observed by days to 50 per cent flowering (0.0072), days to maturity (0.0115), plant height (0.0201), number of tillers per plant (0.0293), number of productive tillers per plant (0.0262), panicle length (0.0392), number of filled grains per panicle (0.0404), panicle fertility (0.0078), test weight (0.0145), straw yield (0.0182) and harvest index (0.0040). However, it showed a negative indirect effect on grain yield through length breadth ratio (-0.0427).

4.6.9 Panicle fertility

Panicle fertility showed a positive direct effect on grain yield (0.0548). Panicle fertility manifested a positive indirect effect on grain yield through plant height (0.0064), number of tillers per plant (0.0158), number of productive tillers per plant (0.0213), panicle length (0.0238), number of filled grains per panicle (0.0400), the total number of spikelets per panicle (0.0064), test weight (0.0284) and straw yield (0.0285). It showed a indirect negative effect on grain yield through days to 50 per cent flowering (-0.0029), days to maturity (-0.0009), length breadth ratio (-0.0025) and harvest index (-0.0049).

4.6.10 Test weight

Test weight showed a positive direct effect on grain yield (0.3803). The positive indirect effect of test weight on grain yield was observed by days to 50 per cent flowering (0.0712), days to maturity (0.0602), plant height (0.1546), number of tillers per plant (0.1361), number of productive tillers per plant (0.2076), panicle length (0.1066), number of filled grains per panicle (0.1401), the total number of spikelets per panicle (0.0825), panicle fertility (0.1973), straw yield (0.1179) and harvest index (0.0086). However, it showed a negative indirect effect on grain yield through length breadth ratio (-0.103).

4.6.11 Length breadth ratio

Length breadth ratio exhibited a positive direct effect on grain yield (0.3857). The indirect positive effect of length breadth ratio on grain yield was recorded by days to 50 per cent flowering (0.0402) and harvest index (0.0699). However, it exhibited the negative indirect effect *via* days to maturity (-0.0210), plant height (-0.0278), number of tillers per plant (-0.1381), number of productive tillers per plant (-0.0884), panicle length (-0.2032), number of filled grains per panicle (-0.1179), the total number of spikelets per panicle (-0.2470), panicle fertility (-0.0178), test weight (-0.1046) and straw yield (-0.0548).

4.6.12 Straw yield

Straw yield showed a positive direct effect on grain yield (0.234). The positive indirect effect of straw yield on grain yield was observed *via* days to 50 per cent flowering (0.0027), plant height (0.0156), number of tillers per plant (0.0312), number of productive tillers per plant (0.0393), panicle length (0.045), number of filled grains per panicle (0.1178), the total number of spikelets per panicle (0.0640), panicle fertility (0.1219) and test weight (0.0725). However, it showed a negative indirect effect on grain yield through days to maturity (-0.0134), length breadth ratio (-0.0332) and harvest index (-0.0908).

4.6.13 Harvest index

The harvest index showed a positive direct effect on grain yield (0.2926). The positive indirect effect of harvest index on grain yield was observed by days to 50 per cent flowering (0.0459), days to maturity (0.0489), plant height (0.0819), number of tillers per plant (0.0835), number of productive tillers per plant (0.0882), panicle length (0.0810), total number of spikelets per panicle (0.0175), test weight (0.0066) and length breadth ratio (0.0530). However, it showed a negative indirect effect on grain yield through the number of filled grains per panicle (-0.0042), panicle fertility (-0.0260) and straw yield (-0.1136).

4.7 Genetic divergence among grain yield and yield attributing traits

For exploitation of the existing genetic variation in the hybridization programme, it is elementary to find out the genetic divergence among the genotypes. Mahalanobis' generalized distance (D^2) analysis was carried out for thirty rice advanced lines involved in the present investigation.

4.7.1 Clustering pattern of rice advanced lines

Thirty rice advanced lines were grouped into six clusters based on the D^2 statistics. The groups were formed in such a way that the genotypes within each cluster had smaller D^2 values than those between the clusters. The clustering pattern of the rice advanced lines is presented in Table 12.

Clustering pattern revealed that cluster I is the largest cluster carrying seventeen rice advanced lines followed by cluster V with six rice advanced lines; cluster II with three rice advanced lines, cluster III with two rice advanced lines, cluster IV and VI are the smallest clusters with one rice advanced line each.

4.7.2 Intra and inter clusters distance

The distance for the rice advanced lines within the cluster and also the distance of two clusters were assessed. The average D^2 values of intra and inter-clusters distances are presented in Table 13.

The highest intra-cluster distance was shown by cluster III (770.42) followed by cluster I (630.23), cluster II (565.33) and cluster V (541.68). The maximum inter-cluster distances were exhibited between cluster III and cluster IV (4563.99), followed by cluster II and cluster IV (3936.43). The lowest inter-cluster distance was observed between cluster I and cluster II (841.18), followed by cluster II and cluster III (1575.29).

4.7.3 Cluster means analysis

Cluster means for fourteen yield and yield-related traits and two physiological traits were calculated using Tocher's method. Mean recorded for yield and yield-related traits by six clusters are presented in Table 14.

4.7.3.1 Days to 50 per cent flowering

The highest cluster mean for days to 50 per cent flowering was observed for cluster V (131.30), followed by cluster VI (128.71). While lowest cluster mean was found for cluster II (107.08), followed by cluster I (110.15).

4.7.3.2 Days to maturity

The maximum cluster mean for this trait was observed for cluster V (164.29), followed by cluster III (159.65). The minimum cluster mean was observed for cluster IV (137.02), followed by cluster I (144.37).

Table 12: Clustering pattern of rice advanced lines based on D² values

Clusters	No. of genotypes	Cluster members
I	17	KPR2 × IS-9-2-2-2, KPR2 × IS-9-2-2-1, KPR2 × IS × Gandhsali-2-4-4-3, Jyothi × Tunga-4-5, Jyothi × KPR-1BC3F3-1-4, IS × Hyd-3, KPR2 × IS × Gandhsali-2-4-4-2, IS × Hyd-5, Jyothi × Tunga-4-3, KPR2 × IS-1-4-1-2, KHP-11, KPR2 × IS × Gandhsali-2-4-4, Jyothi × KPR-1BC2F6-4-4, Jyothi × KPR-1BC2F6, Gandhsali × Hyd-5-3-4-1-3-4, Jyothi × Tunga-2-4, Jyothi × KPR-1-BC2F6-4-3-2
II	3	Jyothi × Tunga-4-6, Jyothi × Tunga-2-6-1, IS × Hyd-3-2-1-2-2
III	2	Gandhsali × Hyd-5-2-2-4-2-2, Gandhsali × Hyd-5-1-4-1-4
IV	1	Jyothi × KPR-1BC2F6-4-8-2
V	6	Jyothi × KPR-1-BC2F6-2-1-1-1-1-1, KHP-2 × IS, Swarna sub1, FR-13A, KHP-13, KHP-11 × MM-1-3-1
VI	1	Hyd-5 × ISBC3F5-5-2-1-2

Table 13: Inter and intra-cluster distances for yield and its component characters in rice advanced lines

	I	II	III	IV	V	VI
I	630.23	841.18	1619.11	2262.41	2074.74	2147.66
II		565.33	1575.29	3936.43	2496.99	3652.63
III			770.42	4563.99	1918.44	2162.61
IV				0	3790.19	1766.34
V					541.68	1727.13
VI						0

Table 14: Cluster means for yield and yield attributing traits in rice advanced lines

	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄
I	110.15	144.37	108.72	19.23	17.66	22.64	120.21	150.22	79.37	24.23	3.21	31.83	46.49	4628.67
II	107.08	145.10	124.22	20.41	18.41	24.08	119.92	179.29	73.35	28.08	2.54	29.35	49.48	4522.25
III	120.11	159.65	98.25	14.90	11.40	21.23	94.88	148.89	48.34	12.83	2.99	20.09	48.05	2742.00
IV	114.60	137.02	117.48	12.06	11.06	16.75	61.07	90.49	48.35	21.65	4.46	25.28	52.28	5022.00
V	131.30	164.29	125.77	22.88	22.53	23.34	127.17	165.41	79.89	30.40	3.24	30.67	54.34	5643.88
VI	128.71	157.16	89.58	12.04	10.04	15.95	80.30	92.94	66.39	15.75	4.15	32.69	43.54	2489.25

Where,

X ₁ = Days to 50 per cent flowering	X ₆ = Panicle length (cm)	X ₁₁ = Length breadth ratio
X ₂ = Days to maturity	X ₇ = number of filled grains per panicle	X ₁₂ = Straw yield (g)
X ₃ = Plant height (cm)	X ₈ = Total number of spikelets per panicle	X ₁₃ = Harvest index
X ₄ = number of tillers per plant	X ₉ = Panicle fertility (%)	X ₁₄ = Grain yield (kg/ha)
X ₅ =Number of productive tillers per plant	X ₁₀ = Test weight (g)	

4.7.3.3 Plant height

The highest cluster mean value for plant height was observed for cluster V (125.77), followed by cluster II (124.22). Whereas, lowest cluster mean was observed for cluster VI (89.58) followed by cluster III (98.25).

4.7.3.4 Number of tillers per plant

The number of tillers per plant showed the highest cluster mean in cluster V (22.88), followed by cluster II (20.41). While lowest cluster mean was found for cluster VI (12.04), followed by cluster IV (12.06).

4.7.3.5 Number of productive tillers per plant

The maximum cluster value for the number of productive tillers per plant was observed for cluster V (22.53) followed by cluster II (18.41). Whereas, the lowest cluster means for this trait was observed for cluster VI (10.04) followed by cluster IV (11.06).

4.7.3.6 Panicle length

The highest cluster mean value for panicle length was observed by cluster II (24.08), followed by cluster V (23.34). However, the lowest cluster means were observed for cluster VI (15.95), followed by cluster IV (16.75).

4.7.3.7 Number of filled grains per panicle

The maximum cluster means for this trait were observed by cluster V (127.17) followed by cluster I (120.21). Whereas, lowest cluster mean was observed for cluster IV (61.07) followed by cluster VI (80.30).

4.7.3.8 Total number of spikelets per panicle

The highest cluster mean for this trait was observed by cluster II (179.29) followed by cluster V (165.41). Whereas, lowest cluster mean was observed for cluster IV (90.49) followed by cluster VI (92.94).

4.7.3.9 Panicle fertility

The maximum cluster mean for panicle fertility was observed by cluster V (79.89) followed by cluster I (79.37). However, the lowest cluster mean was observed for cluster III (48.34), followed by cluster IV (48.35).

4.7.3.10 Test weight

The highest cluster mean for test weight was observed by cluster V (30.40) followed by cluster II (28.08). Whereas, lowest cluster mean was marked by cluster III (12.83) followed by cluster VI (15.75).

4.7.3.11 Length breadth ratio

The maximum cluster mean for this trait was found for cluster IV (4.46), followed by cluster VI (4.15). However, the lowest cluster mean was found in cluster II (2.54), followed by cluster III (2.99).

4.7.3.12 Straw yield

The highest cluster mean for this character was observed for cluster VI (32.69), followed by cluster I (31.83). Whereas, lowest cluster mean was observed for cluster III (20.09) followed by cluster IV (25.28).

4.7.3.13 Harvest index

Harvest index manifested the highest cluster mean in cluster V (54.34), followed by cluster IV (52.28). Whereas, the lowest cluster mean for this trait was observed by cluster VI (43.54) followed by cluster III (48.05).

4.7.3.14 Grain yield

Grain yield recorded the highest cluster mean in cluster V (5643.88), followed by cluster IV (5022.00). While, the lowest cluster mean was observed for cluster VI (2489.25), followed by cluster III (2742.00).

4.7.4 Contribution of different characters towards divergence

The percentage contribution of the studied characters towards genetic divergence was observed and presented in Table 15.

From all the above-studied characters, days to 50 per cent flowering (29.80 %) contributed the highest for diversity among the genotypes followed by length breadth ratio (26.10 %), test weight (20.44 %), grain yield (11.82 %), harvest index (4.68 %), panicle fertility (3.20 %), straw yield (1.98 %), days to maturity (0.99 %), number of filled grains per panicle (0.74 %) and number of tillers per plant (0.25 %).

Table 15: Per cent contribution of yield and yield-related traits towards genetic divergence

Sl. No	Characters	% Contribution
1	Days to 50 per cent flowering	29.80
2	Length breadth ratio	26.10
3	Test weight (g)	20.44
4	Grain yield (kg/ha)	11.82
5	Harvest index	4.68
6	Panicle fertility (%)	3.20
7	Straw yield (g)	1.98
8	Days to maturity	0.99
9	Number of filled grains per panicle	0.74
10	Number of tillers per plant	0.25

4.8 Molecular diversity studies in rice advanced lines using SSR markers linked to submergence tolerance

Fifteen SSR markers were screened across thirty rice advanced lines and two parents to assess the molecular diversity. Out of all the markers screened, polymorphism was found for nine SSR markers, while the remaining six were monomorphic. The number of alleles, highest frequency allele and Polymorphism Information Content (PIC) values found among thirty rice advanced lines and two parents for nine SSR markers were recorded using Power marker software Version 3.25 (Table 16).

A total of 25 alleles were detected at the loci of nine microsatellite markers across thirty rice advanced lines. These nine markers showed distinct polymorphisms among the rice advanced lines studied. Among the polymorphic markers, RM2 produced five alleles, RM140, RM170, RM58 and RM10890 produced three alleles each. While, RM583, RM212, RM3825 and RM6463 produced two alleles each. The number of alleles per locus ranged from five to two alleles with an average of 2.78 alleles across 25 loci. The major allele frequency at each locus ranged from 31.03 per cent to 75.86 per cent.

Polymorphism Information Content (PIC) value is a reflection of allele diversity and frequency among varieties. PIC values ranged from 0.1570 to 0.5553 with an average of 0.3694. The highest PIC value was observed for RM10890 with 0.5553 and the lowest PIC was observed for RM212 with 0.1570.

4.8.1 Clustering analysis of rice advanced lines with SSR markers

Genotyping data generated by screening the thirty rice advanced lines with nine SSR markers was subjected to estimate Jaccard's similarity coefficient and construction of genetic similarity matrix using unweighted pair group method (UPGMA) and analysis using NTSYS statistical package version 2.2. The details of clusters are presented in Table 17.

The highest genetic distance was found between farthest clusters I and VIII. The rice advanced lines of these clusters, cluster I (KPR2 × IS-9-2-2-2, Gandhsali × Hyd-5-2-2-4-2-2, Jyothi × KPR-1-BC2F6-4-8-2, KPR2 × IS × Gandhasali-2-4-4, Jyothi × KPR-1-BC3F3-1-4, IS × Hyd-5) and cluster VIII (Jyothi × Tunga-2-6-1, Swarna sub1, Jyothi × KPR-1-BC2F6-2-1-1-1-1-1) can be used as parents in the introgression breeding programs for the development of superior varieties or hybrids.

Table 16: Estimates of the number of alleles, major allele frequency and polymorphism information content (PIC) values among rice advanced lines

Sl. No	Marker	No. of alleles	Major allele frequency	PIC
1	RM140	3	62.0690	0.4661
2	RM170	3	72.4138	0.3496
3	RM58	3	65.5172	0.3867
4	RM583	2	31.0345	0.4281
5	RM10890	3	51.7241	0.5553
6	RM2	5	68.9655	0.4590
7	RM212	2	75.8621	0.1570
8	RM3825	2	55.1724	0.2200
9	RM6463	2	65.5172	0.3032
Mean		2.78	60.91953	0.3694

Table 17: Grouping rice advanced lines based on molecular diversity using SSR markers

Clusters	Number of genotypes	Genotypes
Cluster I	6	KPR2 × IS-9-2-2-2, Gandhsali × Hyd-5-2-2-4-2-2, Jyothi × KPR-1-BC2F6-4-8-2, KPR2 × IS × Gandhasali-2-4-4, Jyothi × KPR-1-BC3F3-1-4, IS × Hyd-5
Cluster II	3	Jyothi × Tunga-4-3, Jyothi × Tunga-4-6, Jyothi × Tunga-2-4
Cluster III	4	Jyothi × KPR-1BC2F64-4, Jyothi × KPR-1BC2F64, Jyothi × KPR-1-BC2F6-4-3-2, KHP-11
Cluster IV	5	KPR2 × IS-9-2-2-1, Gandhsali × Hyd-5-1-4-1-4, KPR-2 × IS × Gandhasali 2-4-4-3, KPR-2 × IS-1-3, KHP-11 × MM-1-3-1
Cluster V	4	KPR-2 × IS × Gandhasali 2-4-4-2, KHP-13, FR-13A, Gandhsali × Hyd-5-3-4-1-3-4
Cluster VI	3	KPR2 × IS-1-4-1-2, Jyothi × Tunga-4-5, IS × Hyd-3-2-1-2-2
Cluster VII	2	IS × Hyd-3, HYD-5 × IS-BC3F5-5-2-1-2
Cluster VIII	3	Jyothi × Tunga-2-6-1, Swarna SUB 1, Jyothi × KPR-1-BC2F6-2-1-1-1-1-1

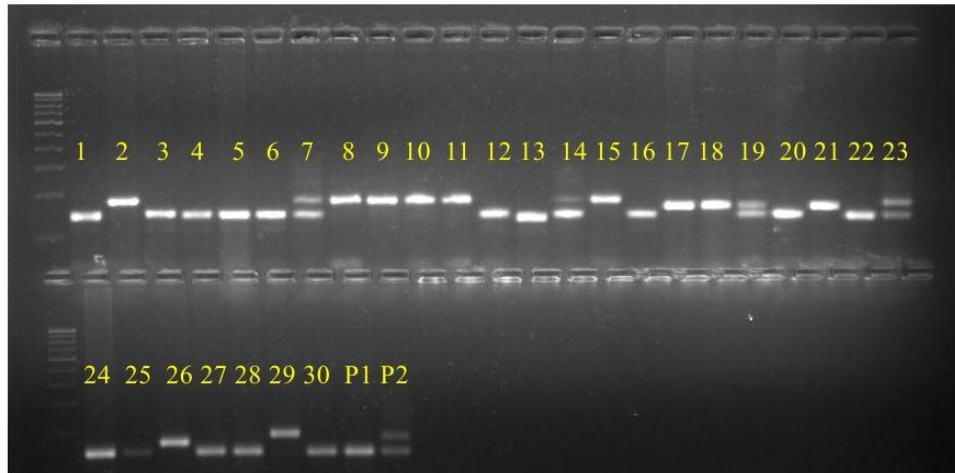


Plate 3: Amplification of RM140 marker in rice advanced lines and two parents

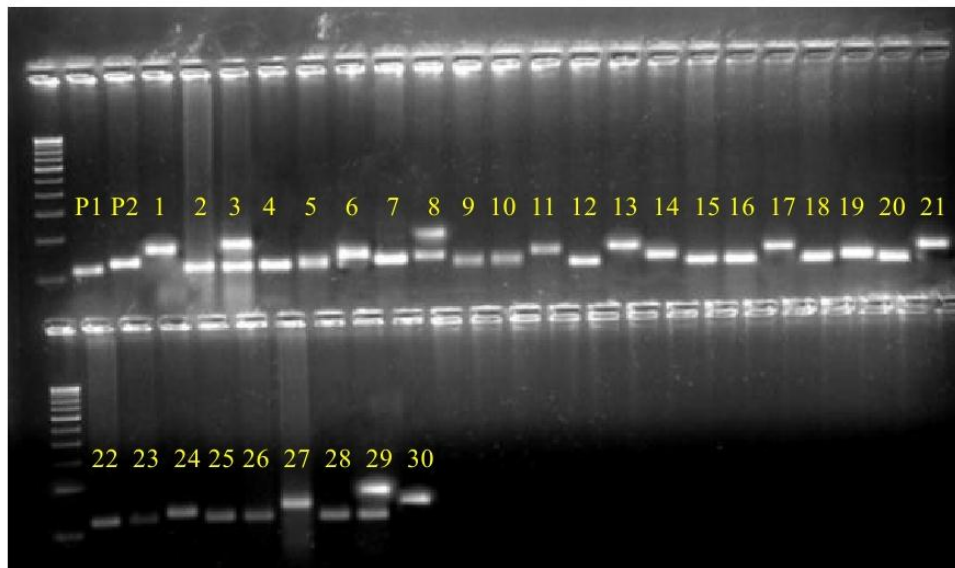


Plate 4: Amplification of RM10890 marker in rice advanced lines and two parents

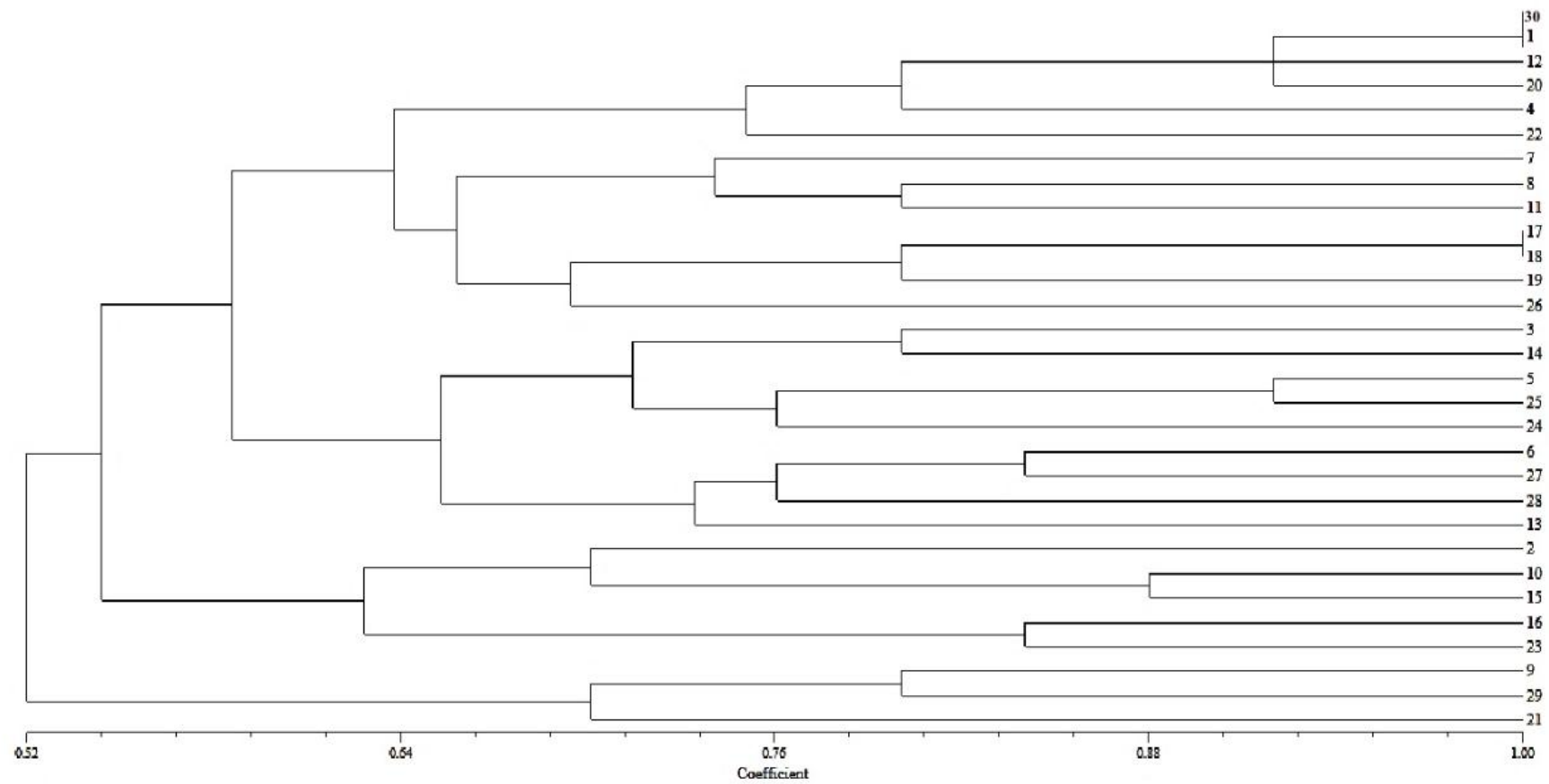


Plate 5: Dendrogram resulting from UPGMA cluster analysis of the rice advanced lines

4.9 Superior rice advanced lines identified for yield and yield attributing traits

The top five superior rice advanced lines were selected based on grain yield and its related traits and are presented in Table 18. KHP-11 × MM-1-3-1 recorded highest yield (6637.50 kg/ha), number of tillers per plant (30.37), panicle length (24.80 cm), total number of spikelets per panicle (182.78), panicle fertility (85.54 %), test weight (33.25 g) and harvest index (55.48) followed by IS × Hyd-3-2-1-2-2 which recorded grain yield (6534 kg/ha), number of tillers per plant (22.50), panicle length (25.80 cm), total number of spikelets per panicle (178.415), panicle fertility (95.84 %), test weight (27.55 g) and harvest index (64.24). They were followed by KPR-2 × IS-1-3 which recorded grain yield (5925 kg/ha), number of tillers per plant (25.57), panicle length (22.48 cm), total number of spikelets per panicle (183.12), panicle fertility (63.54 %), test weight (29.35 g) and harvest index (55.90). Jyothi × KPR-1-BC2F6-4-3-2 recorded grain yield (5707.50 kg/ha), number of tillers per plant (21.12), panicle length (23.95 cm), total number of spikelets per panicle (122.19), panicle fertility (89.34 %), test weight (30.65 g) and harvest index (54.78) and KPR2 × IS-1-4-1-2 recorded grain yield (5460 kg/ha), number of tillers per plant (19.32), panicle length (21.45 cm), total number of spikelets per panicle (174.27), panicle fertility (75.03 %), test weight (27.55 g) and harvest index (35.66).

Table 18: Performance of top five rice advanced breeding lines for yield and yield-related traits

Sl. No.	Genotypes	Number of tillers per plant	Panicle length	Total number of spikelets per panicle	Panicle fertility	Test weight	Harvest index	Grain yield (kg/ha)
1	KHP-11 × MM-1-3-1	30.37	24.80	182.78	85.54	33.25	55.48	6637.50
2	IS × Hyd-3-2-1-2-2	22.50	25.80	178.415	95.84	27.55	62.24	6534.00
3	KPR-2 × IS-1-3	25.57	22.48	183.12	63.54	29.35	55.90	5925.00
4	Jyothi × KPR-1-BC2F6-4-3-2	21.12	23.95	122.19	89.34	30.65	54.78	5707.50
5	KPR2 × IS-1-4-1-2	19.32	21.45	174.27	75.03	27.55	35.66	5460.00
	Checks							
	KHP 11	21.85	23.00	187.98	76.27	29.50	58.90	5610.00
	KHP 13	18.74	22.55	189.04	68.67	31.10	59.21	5160.00
	Swarna SUB 1	24.85	24.49	142.46	94.02	27.65	56.86	5547.00
	FR13 A	18.75	21.38	157.03	86.66	31.40	53.18	5548.50
	CD (5%)	4.53	2.05	22.67	13.22	1.82	8.49	877.40
	CD (1%)	6.11	2.77	34.62	17.84	2.46	11.46	1183.60
	CV (%)	11.44	4.48	8.23	8.58	3.59	8.53	9.24

DISCUSSION

V DISCUSSION

Rice is an indispensable crop as it is the staple food for most of the population worldwide, especially in Southeast Asia. More than 1,20,000 rice cultivars have been improved by breeding to match human demands like high yield potential, stresses tolerance, superior quality and increased nutritional value. Although the above developments had astonishing outcomes in the recent past of rice production, the demand for this crop surpasses production because of exponential population growth and the decline in arable land available for the crop to expand on account of global warming. Rice cultivation and production in abiotic stresses such as seasonal flooding, mainly during the monsoon season is unpredictable, particularly in South and Southeast Asia.

The landrace FR13A (also called ‘Dhalaputia’ in Orissa, India) has been identified as a true submergence tolerant genotype by NRRI, Cuttack. Extensive work has been done using this landrace on different mechanisms of submergence tolerance. Similar outcomes have been used in the present research to screen the rice advanced lines for submergence tolerance.

Extensive screening of the rice advanced lines under 50 to 60 cm depth of water for about 14 days interval or more is the foremost requirement to breed for submergence tolerance. The above-screened material can be utilized further based on the information regarding the amount of variability as well as the character association present between them.

In the present study, twenty-six rice advanced lines were screened for submergence tolerance along with four checks and the genotypes were further studied for morphological and physiological studies. Together, genetic parameters, variability studies, diversity studies, correlation and path analysis of different yield and yield attributing characters were also studied.

The results obtained on the aspects mentioned earlier are discussed under the following sub-headings.

- 5.1 Evaluation of rice advanced lines for submergence tolerance
- 5.2 Morphological and physiological studies of rice advanced lines
- 5.3 Phenotypic correlation studies among physiological parameters with grain yield
- 5.4 Genetic variability parameters for grain yield and yield attributing characters
- 5.5 Phenotypic correlation among yield and yield attributing traits
- 5.6 Path coefficient analysis for grain yield and yield attributing characters
- 5.7 Genetic divergence among grain yield and yield attributing traits

5.8 Molecular diversity studies in rice advanced lines using SSR markers linked to submergence tolerance

5.9 Superior rice advanced lines identified for yield and yield attributing traits.

5.1 Evaluation of rice advanced lines for submergence tolerance

Evaluation of the genotypes under stress conditions will accelerate the selection of superior genotypes during the crop improvement program through the selection of the genotypes which thrive better under the stressful environment to which they are subjected. The study of survival percentage of the rice advanced lines revealed that higher survival percentage was recorded in the case of KHP-11 × MM-1-3-1, IS × Hyd-3-2-1-2-2 and KPR-2 × IS-1-3. Whereas the lower survival percentage was recorded by Hyd-5 × ISBC3F5-5-2-1-2, Gandhasali × Hyd-5-1-4-1-4, KPR × IS × Gandhasali-2-4-4-2, KPR2 × IS-9-2-2-2, etc., which show their susceptibility to submergence.

Sarkar *et al.* (2009), Linh *et al.* (2013), Nishanth *et al.* (2017), Gautam *et al.* (2018) and Nugraha *et al.* (2013) obtained similar results where the lines introgressed with *Sub1* and FR13A showed higher survival percentage and performed well in severe submerged conditions. The above rice advanced lines also showed significant variation and diverse range of survivability for the survival percentage.

5.2 Morphological and physiological studies of rice advanced lines

The prerequisite sign for any genotype to be tolerant to a submerged condition is its survival percentage and its re-emergence after being subjected to a brief period of submergence. The highest survival per cent was recorded in KHP-11 × MM-1-3-1 followed by IS × Hyd-3-2-1-2-2 and KPR-2 × IS-1-3. Many rice advanced lines recorded lower survival percentages which included Hyd-5 × ISBC3F5-5-2-1-2, Gandhasali × Hyd-5-1-4-1-4, KPR × IS × Gandhasali-2-4-4-2, KPR2 × IS-9-2-2-2, etc., showing their susceptibility to submergence. Similar results were obtained by Sarkar *et al.* (2009), Linh *et al.* (2013), Nishanth *et al.* (2017), Gautam *et al.* (2018) and Nugraha *et al.* (2013).

The highest stem elongation was recorded in Gandhsali × Hyd-5-1-4-1-4 followed by Jyothi × KPR-1-BC2F6-2-1-1-1-1 and the lowest stem elongation percentage was recorded by KPR2 × IS-9-2-2-2 followed by HYD-5 × ISBC3F5-5-2-1-2. In the study, most of the rice advanced lines showed higher stem elongation to survive under submergence conditions. But the rice advanced lines with high stem elongation percentage did not yield better because they utilized all the non-structural carbohydrates for their survival and elongation in order to obtain

oxygen. It was observed that the submergence tolerant rice advanced lines had recorded a moderate level of stem elongation to thrive under submergence and also to yield better.

Das *et al.* (2005), Sarkar and Bhattacharjee *et al.* (2011), Singh *et al.* (2014) and Oladosu *et al.* (2018), achieved similar results when they studied the behaviour of rice genotypes under submergence conditions. Their outcomes revealed that most often, the genotypes with moderate or limited elongation capacity showed submergence tolerance.

High PCV and GCV were observed for survival percentage and stem elongation percentage. There was high heritability coupled with high genetic advance observed for the above traits. Adilakshmi and Rani (2012) and Kumari *et al.* (2019) reported similar results that survival percentage and shoot elongation percentage recorded high GCV and PCV as well as high heritability coupled with high genetic advance. But, Nishanth *et al.* (2017) reported low GCV, PCV, high heritability and moderate genetic advance for survival percentage.

The results reveal an immense amount of variability in the rice advanced lines. The characters are highly heritable. Hence, they can be further utilized by selection in future breeding programmes.

5.3 Phenotypic correlation studies among physiological parameters with grain yield

Under submergence conditions, survival percentage showed a significant positive correlation with harvest index and grain yield. Whereas, it showed a significant negative correlation with stem elongation percentage.

Adilakshmi and Rani (2012), Vergara *et al.* (2014) and Kumari *et al.* (2019) achieved similar results. Whereas, Panda and Sarkar *et al.* (2013) reported that increased elongation correlated positively with survival percentage.

Stem elongation percentage showed a negative non-significant correlation with harvest index and grain yield.

Similar results for stem elongation percentage were obtained by Kawano (2009) and Adilakshmi and Rani (2012). But, Kato *et al.* (2014) reported that a moderate level of stem elongation percentage was positively related to grain yield.

Harvest index reported a significant positive correlation with grain yield. A similar result was reported by Afrin *et al.* (2017) and Kumari *et al.* (2019). Pradhan *et al.* (2015) proposed a positive correlation of harvest index with grain yield under both submergence and control conditions.

The results reveal that the characters like survival percentage, stem elongation percentage and harvest index are the important contributors to the grain yield under submerged conditions. They should be given more importance while developing submergence tolerance cultivars.

5.4 Genetic variability parameters for grain yield and yield attributing characters

The presence of variability in genotypes is of prime importance in breeding programmes for improving the crop plants for desired characters. Hence, assessing the magnitude of variability available in the gene pool is the first and foremost step in the breeding programme. The analysis of variance for various characters studied reported the presence of significant difference among the rice advanced lines for those characters showing that they were genetically diverse and selection will be effective. Similar results were proclaimed by Afrin *et al.* (2017), Sudeepthi *et al.* (2020) and Bhargava *et al.* (2021).

Low PCV and GCV were recorded for days to 50 per cent flowering and days to maturity. Similar results were obtained for both the characters by Saha *et al.* (2019) and Rashid *et al.* (2017). Sumanth *et al.* (2017) got similar results for days to 50 per cent flowering. Low estimates of GCV and PCV imply that the selection based on these characters will be inappropriate for the crop improvement program.

Moderate PCV and low GCV were obtained for panicle length. Similar results were obtained by Idris *et al.* (2012). The low estimates of GCV indicate the presence of more environmental influence on the character hence the selection based on this trait will not be useful for further breeding programmes.

Moderate GCV and PCV were obtained for plant height, length breadth ratio and harvest index. Similar results were obtained by Prasad *et al.* (2017) and Sumanth *et al.* (2017) for plant height, Singh and Verma (2018) for length breadth ratio, Abebe *et al.* (2017) and Srujana *et al.* (2017) for harvest index.

High PCV and moderate GCV were observed for the number of filled grains per panicle, the total number of spikelets per panicle, panicle fertility and straw yield per plant. Similar results were found by Abebe *et al.* (2017) for the number of filled grains per panicle, the total number of spikelets per panicle and straw yield per plant. Prasad *et al.* (2017) recorded similar results for panicle fertility.

High PCV and GCV were recorded for the number of tillers per plant, total number of productive tillers per plant, test weight and grain yield. Similar results were obtained by Saha

et al. (2019) for all the characters, Kumari *et al.* (2017) for the number of tillers per plant, Abebe *et al.* (2017), Srujana *et al.* (2017) and Sumanth *et al.* (2017) for grain yield.

High magnitudes of GCV and PCV infer a negligible influence of the environment on the characters. Hence, the selection of the genotypes based on these traits will be helpful in crop improvement programmes.

PCV estimates were higher than the corresponding estimates of GCV for all the traits under study. Chuchert *et al.* (2018) and Girma *et al.* (2018) have also reported higher estimates of PCV than GCV for all the characters considered for the investigation. There is a narrow difference between PCV and GCV, indicating less environmental influence and significant contribution of genetic factors for the variability in these characters.

Although GCV and PCV give information about the extent of variability present in the genotypes for the characters studied along with the environmental influence, they cannot provide a relevant estimate of the extent of the inheritance of the traits. Hence, the heritability of the character will allow the plant breeder to determine the degree of selection pressure to be applied for a particular environmental condition in the crop improvement program. High heritability in broad sense coupled with high genetic advance as per cent mean act as direct selection parameters as they provide the estimates of transmissibility of the characters, which will indicate the effectiveness of the selection in improving the characters (Johnson *et al.*, 1955).

All the characters recorded high heritability under study, *i.e.*, 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, the total number of grains per panicle, panicle fertility, test weight, length breadth ratio, straw yield, harvest index and grain yield. Bandi *et al.* (2018) obtained similar results of high heritability for days to 50 per cent flowering, days to maturity, plant height, number of tillers per plant, the total number of spikelets per panicle, test weight, length breadth ratio and harvest index. Divya *et al.* (2018) gave an account of high heritability for the number of productive tillers per panicle and panicle length. Prasad *et al.* (2017) obtained high heritability for the total number of spikelets per panicle. High heritability for panicle fertility was reported by Sandeep *et al.* (2018). The straw yield was reported as a highly heritable character by Gour *et al.* (2017). Similar results were obtained by Yadav *et al.* (2017) for the harvest index.

Genetic advance as per cent of mean explains the measure of genetic gain under selection. High genetic advance as per cent mean was found in all most all of the characters like plant height, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, the total number of spikelets per panicle, panicle fertility, test weight, length breadth ratio, straw yield, harvest index and grain. Whereas, moderate GAM was observed for days to 50 per cent flowering, days to maturity and panicle length. Similar results were observed by Prasad *et al.* (2017) like moderate GAM for days to 50 per cent flowering, days to maturity and panicle length, high GAM for plant height, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, test weight and grain yield. Pratap *et al.* (2018) gave an account of similar results for the total number of spikelets per panicle and length breadth ratio. Saha *et al.* (2019) obtained a similar result for panicle fertility. Gour *et al.* (2017) gave a similar account on days to 50 per cent flowering, days to maturity, plant height, number of tillers per plant, number of filled grains per panicle, straw yield, harvest index and grain yield.

All the traits like plant height, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, the total number of spikelets per panicle, panicle fertility, test weight, length breadth ratio, straw yield, harvest index and grain yield which have exhibited high heritability coupled with high genetic advance as per cent mean along with high to moderate GCV and PCV indicating the preponderance of additive gene action can be employed in selection and crop improvement program.

5.5 Phenotypic correlation among yield and yield attributing traits

5.5.1 Correlation of grain yield with other characters

A significant positive association was found between grain yield with plant height, number of tillers per plant, number of productive tillers per plant, panicle length, number of filled grains per panicle, the total number of spikelets per panicle, panicle fertility, test weight, straw yield and harvest index. The positive non-significant association of grain was found with days to 50 per cent flowering and days to maturity. These correlation estimates infer the possibility of increasing yield through the selection of these characters. A negative non-significant association was found for length breadth ratio with grain yield, indicating that it cannot be used for selection.

The results obtained were following the results of Singh *et al.* (2018), who got a significant positive association of panicle fertility, test weight, straw yield, harvest index and negative non-significant association of length breadth ratio with grain yield. Lakshmi *et al.* (2014) recorded a significant positive association of grain yield with plant height and the number of productive tillers per plant. Dhavaleshwar *et al.* (2019) observed a positive association of the number of tillers per plant, days to 50 per cent flowering and days to maturity with grain yield. Similar results of a significant positive association of panicle length with grain yield was reported by Singh *et al.* (2020). A significant positive association of the number of filled grains per panicle was reported by Babu *et al.* (2012) and the total number of grains per panicle by Zahid *et al.* (2006) with grain yield.

5.5.2 Correlation among yield components

Days to 50 per cent flowering exhibited a significant positive correlation with days to maturity and non-significant positive correlation with plant height, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, the total number of spikelets per panicle, test weight, length breadth ratio, straw yield, harvest index. At the same time, the non-significant negative association between panicle length and panicle fertility was manifested. Similar results were reported by Singh *et al.* (2020) of positive association for days to maturity and grains per panicle, Singh *et al.* (2018) for plant height, productive tillers per plant, panicle fertility, test weight, L/B ratio and straw yield. Afrin *et al.* (2017) for tillers per plant, fertile grains per panicle and harvest index. Dhavaleshwar *et al.* (2019) reported a positive association for grain yield and Saha *et al.* (2019) proposed a negative association for panicle length.

Days to 50 per cent flowering exhibited a significant positive correlation with days to maturity. Non-significant positive correlation for days to maturity was exhibited by plant height, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, the total number of spikelets per panicle, test weight and harvest index. A non-significant negative association of days to maturity was observed with panicle length, panicle fertility, length breadth ratio and straw yield. Similar results of significant positive association with days to 50 per cent flowering, productive tillers per plant and grains per panicle were reported by Singh *et al.* (2020). Dhavaleshwar *et al.* (2019) reported a positive association with plant height, test weight and grain yield, negative association with panicle fertility. A positive association of tillers per plant was recorded by Oladosu *et al.* (2018). Similar results

for panicle length and filled grains per panicle were reported by Saha *et al.* (2019), L/B ratio and harvest index by Surek and Beser (2003) and biological yield by Panwar *et al.* (2007).

Plant height was significantly positively associated with the number of productive tillers per plant, panicle length, the total number of spikelets per panicle, test weight, and harvest index. A non-significant positive association was observed with days to 50 per cent flowering, days to maturity, number of tillers per plant, number of filled grains per panicle, panicle fertility and straw yield. A non-significant negative correlation was found with the length breadth ratio. Similar positive association results were observed for days to 50 per cent flowering, productive tillers per plant, panicle fertility and straw yield, the negative association for L/B ratio was reported by Singh *et al.* (2018). Dhavaleshwar *et al.* (2019) reported a positive association for days to maturity, Singh *et al.* (2020) for panicle length, test weight and grain yield. Kumari *et al.* (2019) for tillers per plant, Afrin *et al.* (2017) for filled grains per panicle, Saha *et al.* (2019) for total grains per panicle and Panwar *et al.* (2007) for harvest index.

The number of tillers per plant showed a significant positive correlation with the number of productive tillers per plant, panicle length, number of filled grains per panicle, the total number of spikelets per panicle, panicle fertility, test weight and harvest index. Whereas the non-significant positive correlation was found with days to 50 per cent flowering, days to maturity, plant height and straw yield. Plant height was negatively significantly correlated with length breadth ratio. Afrin *et al.* (2017) reported a positive association of days to 50 per cent flowering and grain yield. Oladosu *et al.* (2018) reported a similar positive association with days to maturity, panicle length, filled grains per panicle and test weight. Kumari *et al.* (2019) reported similar results for plant height. Significant positive association for productive tillers and panicle fertility was recorded by Dhavaleshwar *et al.* (2019), for grains per panicle and biological yield by Panwar *et al.* (2007), harvest index by Sarawgi *et al.* (1997) and significant negative association with L/B ratio by Surek and Beser (2003).

A significant positive association of the number of productive tillers per plant was exhibited with plant height, number of tillers per plant, panicle length, number of filled grains per panicle, the total number of spikelets per panicle, panicle fertility, test weight and harvest index. Whereas, the positive non-significant association was found with days to 50 per cent flowering, days to maturity and straw yield. The negative non-significant correlation was observed with the length breadth ratio. Similar results of positive association with days to 50 per cent flowering, plant height, test weight, straw yield, grain yield and negative association

with L/B ratio was reported by Singh *et al.* (2018). Singh *et al.* (2020) reported a similar positive association for days to maturity and grains per panicle, Dhavaleshwar *et al.* (2019) recorded for tillers per plant and panicle fertility. Similar significant positive associations were recorded for panicle length by Oladosu *et al.* (2018), filled grains per panicle by Singh *et al.* (2019) and harvest index by Sarawgi *et al.* (1997).

Panicle length showed a significant positive correlation with plant height, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, the total number of spikelets per panicle, panicle fertility, test weight and harvest index. A non-significant positive correlation was found to be with straw yield. Whereas, the non-significant negative association was manifested with days to 50 per cent flowering, days to maturity. A significant negative association was observed for the length breadth ratio. The results were in harmony with Saha *et al.* (2019) for days to 50 per cent flowering and days to maturity. Singh *et al.* (2020) reported a significant positive association with plant height, number of grains per panicle and yield per plant. Similarly, Oladosu *et al.* (2018) reported a significant positive association for the number of tillers and productive tillers per plant, Afrin *et al.* (2017) for filled grains per panicle, Bhutta *et al.* (2019) for panicle fertility, Dhavaleshwar *et al.* (2019) for test weight and harvest index, Singh *et al.* (2018) for straw yield. Surek and Beser (2003) reported a significant negative association of the L/B ratio.

A significant positive correlation with the number of filled grains per panicle was accompanied by the number of tillers per plant, number of productive tillers per plant, panicle length, straw yield, the total number of spikelets per panicle, panicle fertility, test weight and straw yield. Whereas, the non-significant positive association was accompanied by days to 50 per cent flowering, days to maturity and plant height. A non-significant negative association was found with the harvest index. While a significant positive association was observed for the length breadth ratio. Similar significant positive results were obtained by Afrin *et al.* (2017) for days to 50 per cent flowering, plant height and panicle length. Positive association for days to maturity and number of grains per panicle were recorded by Saha *et al.* (2019), for the number of tillers per plant, test weight and yield per plant by Oladosu *et al.* (2018), productive tillers per panicle by Singh *et al.* (2019), panicle fertility and harvest index by Sarawgi *et al.* (1997) and straw yield by Dhavaleshwar *et al.* (2019). A significant negative association of the L/B ratio was reported by Surek and Beser (2003).

A significant positive correlation with the total number of spikelets per panicle was accompanied by plant height, number of tillers per plant, number of productive tillers per plant, panicle length, number of filled grains per panicle and straw yield. A non-significant positive association was found with days to 50 per cent flowering, days to maturity, panicle fertility, test weight and harvest index. Whereas, a significant negative association was observed for the length breadth ratio. Similar results were reported by Singh *et al.* (2020) for days to 50 per cent flowering, days to maturity, productive tillers per plant and panicle length, Saha *et al.* (2019) for plant height and filled grains per panicle, Panwar *et al.* (2007) for the number of tillers per plant, Singh *et al.* (2018) for panicle fertility, test weight, L/B ratio, straw yield and grain yield. Dhavaleshwar *et al.* (2019) recorded similar results of positive association for harvest index.

Panicle fertility had a significant positive association with the number of tillers per plant, number of productive tillers per plant, panicle length, number of filled grains per panicle, test weight and straw yield. A non-significant positive association was exhibited by plant height and the total number of spikelets per panicle. Whereas, the non-significant negative correlation with panicle fertility was shown by days to 50 per cent flowering, days to maturity, length breadth ratio and harvest index. Similar results were reported by Singh *et al.* (2018) for days to 50 per cent flowering, plant height, the total number of grains per panicle, test weight, L/B ratio and yield per plant. Dhavaleshwar *et al.* (2019) recorded similar results for days to maturity, the number of tillers and productive tillers per plant. Bhutta *et al.* (2019) found similar recordings for panicle length, Sarawgi *et al.* (1997) for filled grains per panicle and harvest index, Panwar *et al.* (2007) for straw yield per plant.

Significant positive association with test weight was shown by plant height, number of tillers per plant, number of productive tillers per plant, panicle length, number of filled grains per panicle, panicle fertility and straw yield. Non-significant positive association was shown by days to 50 per cent flowering, days to maturity, the total number of spikelets per panicle and harvest index. A significant negative association was found with the length breadth ratio. The results were in harmony with the results of Singh *et al.* (2018) for days to 50 per cent flowering, productive tillers per plant, number of grains per panicle, panicle fertility, L/B ratio, harvest index and grain yield. Similar results were recorded by Dhavaleshwar *et al.* (2019) for days to maturity, panicle length and straw yield, Singh *et al.* (2020) for plant height and Oladosu *et al.* (2018) for number of tillers per plant and number of filled grains per plant.

Non-significant positive association with length breadth ratio of the grains was shown by days to 50 per cent flowering and harvest index. A non-significant negative association was recorded by days to maturity, plant height, number of productive tillers per plant, panicle fertility and straw yield. Whereas, a significant negative association was observed for number of tillers per plant, panicle length, number of filled grains per panicle, total number of spikelets per panicle and test weight. Similar results were obtained by Singh *et al.* (2018) for days to 50 per cent flowering, plant height, productive tillers per plant, number of grains per panicle, panicle fertility, test weight and harvest index. Surek and Beser (2003) observed similar results for days to maturity, number of tillers per plant, panicle length, filled grains per panicle and straw yield per plant. Veni and Rani (2006) recorded similar results for grain yield.

A significant positive correlation with straw yield was exhibited by the number of filled grains per panicle, total number of spikelets per panicle, panicle fertility and test weight. While, a non-significant positive correlation was observed by days to 50 per cent flowering, plant height, number of tillers per plant, number of productive tillers per plant and panicle length. A non-significant negative association was shown by days to maturity and length breadth ratio. Whereas, a significant negative association was found with the harvest index. Similar results were obtained by Singh *et al.* (2018) for days to 50 per cent flowering, plant height, number of productive tillers per plant, panicle length, total number of grains per panicle, L/B ratio and grain yield. Panwar *et al.* (2007) recorded similar results for days to maturity, number of tillers per plant, number of filled grains per panicle and panicle fertility. Dhavaleshwar *et al.* (2019) recorded similar results for test weight and harvest index.

Harvest index was found to have a significant positive association with plant height, number of tillers per plant, number of productive tillers per plant and panicle length. A positive non-significant association was found with days to 50 per cent flowering, days to maturity, total number of spikelets per panicle, test weight and length breadth ratio. A negative non-significant association was found with number of filled grains per panicle, panicle fertility and straw yield. The results obtained were in harmony with that of Surek and Beser (2003) for days to maturity, number of tillers per plant and panicle length, Afrin *et al.* (2017) for days to 50 per cent flowering, Panwar *et al.* (2007) for plant height, Sarawgi *et al.* (1997) for number of productive tillers per plant and panicle fertility. Oladosu *et al.* (2018) recorded similar results for number of filled grains per panicle, Dhavaleshwar *et al.* (2019) for straw yield and total number of grains per panicle, Singh *et al.* (2018) for test weight, L/B ratio and grain yield.

The results revealed that grain yield was significantly positively correlated with plant height, number of tillers per plant, number of productive tillers per plant, panicle length, number of filled grains per panicle, total number of spikelets per panicle, panicle fertility, test weight, straw yield and harvest index. This indicates that the above characters should be given importance during the selection of the plants for crop improvement.

5.6 Path coefficient analysis for grain yield and yield attributing characters

Path coefficient analysis presents the information about the influence of each character which contributes to yield under the study. This splits the correlation coefficient into the estimates of direct and indirect effects. It measures the direct as well as the indirect contribution of the independent variables on a dependent variable viz., yield. Hence, it helps the plant breeders to determine the yield components.

The outcomes of path coefficient analysis disclosed that the test weight followed by number of tillers per plant, harvest index, plant height, straw yield, panicle length, days to maturity, total number of spikelets per panicle, panicle fertility, number of filled grains per panicle manifested direct positive effect on grain yield and also showed a positive correlation with grain yield at phenotypic level indicating that, these characters can be considered as a selection criterion in crop improvement programs for yield. Similar results were reported by Parimala *et al.* (2019), Chhangte *et al.* (2019) and Lakshmi *et al.* (2020).

The highest direct negative effect was exhibited by the number of productive tillers per plant followed by days to 50 per cent flowering. The results were in accordance with the findings of Kishore *et al.* (2018) for number of effective tillers per plant and Gour *et al.* (2017) for days to 50 per cent flowering.

The highest indirect positive effect on grain yield was exhibited by number of tillers per plant through number of productive tillers per plant followed by test weight through number of productive tillers per plant and number of tillers per plant through panicle length.

Hence, the direct selection of the characters which recorded direct effect on grain yield would be greatly rewarding. Also, the indirect selection of the traits which reported indirect effects through other component traits will be of significant importance during crop improvement program for yield.

5.7 Genetic divergence among grain yield and yield attributing traits

Thirty rice advanced lines were grouped into six clusters based on the D^2 statistics. The groups were formed in such a way that the genotypes within each cluster had smaller D^2 statistics than those between the clusters. Clustering pattern revealed that cluster I is the largest cluster carrying sixteen rice advanced lines followed by cluster V with six rice advanced lines; cluster II with three rice advanced lines, cluster III with two rice advanced lines, cluster IV and VI are the smallest clusters with one rice advanced lines each. The results were in accordance with Venkatesan *et al.* (2018), Lahari *et al.* (2017), Kodihalli *et al.* (2014) and Rashid *et al.* (2014).

5.7.1 Average intra and inter clusters distance

The highest intra cluster distance was shown by cluster III followed by cluster I. Hence, the rice advanced lines present in cluster III (Gandhsali $\times$ Hyd-5-2-2-4-2-2, Gandhsali $\times$ Hyd-5-1-4-1-4) and cluster I (KPR2 $\times$ IS-9-2-2-2, KPR2 $\times$ IS-9-2-2-1, KPR2 $\times$ IS $\times$ Gandhsali-2-4-4-3, Jyothi $\times$ Tunga-4-5, Jyothi $\times$ KPR-1BC3F3-1-4, IS $\times$ Hyd-3, KPR2 $\times$ IS $\times$ Gandhsali-2-4-4-2, Jyothi $\times$ Tunga-4-3, KPR2 $\times$ IS-1-4-1-2, KHP-11, KPR2 $\times$ IS $\times$ Gandhsali-2-4-4, Jyothi $\times$ KPR-1BC2F6-4-4, Jyothi $\times$ KPR-1BC2F6, Gandhsali $\times$ Hyd-5-3-4-1-3-4, Jyothi $\times$ Tunga-2-4, Jyothi $\times$ KPR-1-BC2F6-4-3-2 and IS $\times$ Hyd-5) can be used for hybridization programs due to the presence of a greater amount of diversity within themselves.

The maximum inter cluster distances were exhibited between cluster III and cluster IV followed by cluster II and cluster IV. The lowest inter-cluster distance was observed between clusters I and II, followed by clusters II and III.

Cluster III with two rice advanced lines (Gandhsali $\times$ Hyd-5-2-2-4-2-2, Gandhsali $\times$ Hyd-5-1-4-1-4) and cluster IV with one rice advanced line (Jyothi $\times$ KPR-1BC2F6-4-8-2), Cluster II with three rice advanced lines (Jyothi $\times$ Tunga-4-6, Jyothi $\times$ Tunga-2-6-1, IS $\times$ Hyd-3-2-1-2-2) and cluster IV with one rice advanced line (Jyothi $\times$ KPR-1BC2F6-4-8-2) were the most divergent groups with highest inter cluster distances. Clusters which have maximum inter cluster distance infer the wider genetic diversity between the rice advanced lines present in these clusters and these rice advanced lines can be used in the hybridization program. While the clusters which have minimum inter cluster distance manifest the narrow genetic diversity among such genotypes and hybridization between them will not give good results. Hence, it is preferable to select the genotypes which fall under the clusters having greater inter cluster distances for the hybridization purpose in order to develop high-yielding varieties and hybrids.

4.7.3 Cluster means analysis

Cluster V (Jyothi $\times$ KPR-1-BC2F6-2-1-1-1-1, KPR-2 $\times$ IS-1-3, KHP-11 $\times$ MM-1-3-1) exhibited the highest mean values for most of the characters like survival percentage, days to 50 per cent flowering, days to maturity, plant height, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, panicle fertility, test weight, harvest index and grain yield. Hence, the rice advanced lines from this cluster can be selected directly and utilized for the crop improvement program. Whereas, cluster IV (Jyothi $\times$ KPR-1BC2F6-4-8-2) showed maximum cluster mean for stem elongation percentage and L/B ratio, cluster II (Jyothi $\times$ Tunga-4-6, Jyothi $\times$ Tunga-2-6-1, IS $\times$ Hyd-3-2-1-2-2) showed the highest cluster means for panicle length and total spikelets per panicle and cluster VI showed highest cluster mean for straw yield.

Similar results were reported by Rani *et al.* (2013), Chanbeni *et al.* (2012) and Lahari *et al.* (2017) accordingly they suggested that selection of the parents for hybridization program should be from two clusters which have higher inter cluster distance to get maximum variability in the segregating generations and also to obtain transgressive segregants.

5.7.3 Contribution of different characters towards divergence

The maximum contribution to genetic divergence among the genotypes was through length breadth ratio, days to 50 per cent flowering, test weight, grain yield, harvest index and straw yield which accounted for 93.84 per cent of the total divergence. Ranjith *et al.* (2018) and Srinivas *et al.* (2018) reported the contribution of days to 50 per cent flowering, test weight, grain yield and harvest index towards divergence. Hence, these characters should be given more preference during the selection of diverse parents for the hybridization program.

The genotypes belonging to cluster III and cluster IV, cluster II and IV which showed the highest inter cluster distance and the characters like length breadth ratio, days to 50 per cent flowering, test weight, grain yield, harvest index and straw yield should be given more

importance during the selection of parents for hybridization as well as crossing program.

5.8 Molecular diversity studies in rice advanced lines using SSR markers linked to submergence tolerance

Fifteen SSR markers were screened across thirty rice advanced lines and three parents to assess the molecular diversity. Out of all the markers screened, polymorphism was found for nine SSR markers while the remaining six were monomorphic. A total of 25 alleles were detected at the loci of nine microsatellite markers across thirty rice advanced lines. These nine markers showed distinct polymorphisms among the genotypes studied. Among the polymorphic markers, RM2 produced five alleles, RM140, RM170, RM58 and RM10890 produced three alleles each. While, RM583, RM212, RM3825 and RM6463 produced two alleles each.

The major allele frequency was highest in RM212 and the lowest was found in RM583. RM10890 recorded the highest PIC value and the lowest was recorded by RM212.

The results obtained were in accordance with the results obtained by Tarang *et al.* (2020) and Barik *et al.* (2020). They observed similar type of polymorphism and PIC values among the different rice advanced lines.

The unweighted pair group method (UPGMA) clustering system generated eight genetic clusters in the studied rice advanced lines. Cluster I and cluster IV are the biggest clusters with five rice advanced lines each, followed by cluster III and cluster V with four rice advanced lines each, cluster II, cluster VI and cluster VIII with three rice advanced lines each. Cluster VII is the smallest cluster with only two rice advanced lines.

The highest genetic distance was found between farthest clusters I and VIII. The rice advanced lines of these clusters, cluster I (KPR2 × IS-9-2-2-2, Gandhsali × Hyd-5-2-2-4-2-2, Jyothi × KPR-1-BC2F6-4-8-2, KPR2 × IS × Gandhasali-2-4-4, Jyothi × KPR-1-BC3F3-1-4) and cluster VIII (Jyothi × Tunga-2-6-1, Swarna sub1, Jyothi × KPR-1-BC2F6-2-1-1-1-1-1) have highest genetic diversity and can be used as parents in the introgression breeding programs for the development of superior varieties or hybrids. Donde *et al.* (2019) and Asante *et al.* (2019) observed similar results of the clustering patterns by the UPGMA method.

5.9 Superior rice advanced breeding lines identified for yield and yield attributing traits

Among all the rice advanced lines studied, the top-performing rice advanced lines were selected based on grain yield and its related traits which are KHP-11 × MM-1-3-1 (6637.50 kg/ha) followed by IS × Hyd-3-2-1-2-2 (6534 kg/ha), KPR-2 × IS-1-3 (5925 kg/ha) and Jyothi × KPR-1-BC2F6-4-3-2 (5707.50 kg/ha). They recorded higher yield in compared to the checks FR13A (5548.50 kg/ha), Swarna sub1 (5547 kg/ha), KHP-11 (5610 kg/ha), KHP13 (5160 kg/ha). The important traits which contribute to the yield like total number of tillers, panicle length, total number of spikelets per panicle, panicle fertility, test weight and harvest index were also found to be higher in these rice advanced lines when compared to the checks. Hence, these rice advanced lines were identified as superior and can be used to test further under multi-location trails.

Conclusion

- ✓ Thirty rice advanced lines were screened for submergence tolerance which revealed that the three rice advanced lines KHP-11 × MM-1-3-1, IS × Hyd-3-2-1-2-2, KPR-2 × IS-1-3 recorded more than 75 per cent survival.
- ✓ These rice advanced lines were studied for genetic variability, diversity and character association under non-submergence conditions.
- ✓ Analysis of variance revealed the presence of significant difference for all the yield and yield attributing traits characters studied among all the rice advanced lines.
- ✓ Genetic variability studies manifested moderate to high PCV and GCV, high heritability coupled with high genetic advance as per cent mean for the characters like plant height, length breadth ratio, harvest index, number of filled grains per panicle, total number of spikelets per panicle, panicle fertility, straw yield per plant, number of tillers per plant, total number of productive tillers per plant, test weight and grain yield. This may be due to the presence of additive gene action. So, the selection for these characters will be highly effective.
- ✓ Correlation studies revealed that the grain yield exhibited a significant positive correlation with plant height, number of tillers per plant, number of productive tillers per plant, panicle length, number of filled grains per panicle, total number of spikelets per panicle, panicle fertility, test weight, straw yield and harvest index.
- ✓ Path coefficient analysis disclosed that the test weight, number of tillers per plant, harvest index, plant height, straw yield, panicle length, days to maturity, total number of spikelets per panicle, panicle fertility, number of filled grains per panicle manifested direct positive effect on grain yield and also showed a positive correlation with grain yield at phenotypic level indicating that, these characters can be considered as a selection criterion in crop improvement programs for yield.
- ✓ D² analysis revealed that the maximum inter cluster distances was exhibited between cluster III and cluster IV. So, the rice advanced lines belonging to these clusters have wide genetic diversity and this can be used to exploit maximum heterosis by crossing program.
- ✓ Molecular diversity analysis using SSR markers also confirmed the presence of high genetic diversity among the rice advanced lines.

- ✓ The rice advanced lines KHP-11 × MM-1-3-1, IS × Hyd-3-2-1-2-2 and KPR-2 × IS-1-3 performed superior than the checks for yield and yield attributing traits and also showed high survival percentage under submerged condition. Hence, these tolerant lines can be further tested in two years station trials and proposed for multi-locational trials and farm trials in low land situations.

Future line of work

On the basis of the results obtained from the present investigation, the following future line of work can be proposed.

- ✓ The rice advanced lines KHP-11 × MM-1-3-1, IS × Hyd-3-2-1-2-2, KPR-2 × IS-1-3 and Jyothi × KPR-1-BC2F6-4-3-2 manifested higher yield under both submerged and control conditions. They can be confirmed at molecular level by validation of markers linked to submergence and may be advance to multi-location trials and to be proposed for variety release under submerged condition in Zone-9 of Karnataka
- ✓ As there is a high amount of genetic diversity among the rice advanced lines for all the characters studied, they may be utilized for hybridization programme.

SUMMARY

VI SUMMARY

Rice, primary food crop grown all over the world, is subjected to environmental variations and climate changes. Of them, submergence is one of the important hindrances in rice production in high rainfall, low land flood areas because of increasing water levels due to global climate change. In India, about 33.51 m ha is affected by floods annually. Hence, the development of hybrids and varieties tolerant to submergence is becoming increasingly important. Thus, varieties tolerant to submergence should be identified. Also, the genotypes should be evaluated for variability, diversity and association of yield and yield attributing characters and molecular analysis. The present study was focused on the assessment of genetic variability, character association, path coefficient analysis, genetic and molecular divergence for yield and yield attributing characters, and the screening of the genotypes for submergence tolerance.

Twenty-six rice advanced breeding lines and four checks were screened for submergence tolerance during *Kharif* 2020 at the College of agriculture, KSNUAHS, Shivamogga based on survival and stem elongation percentages. The highest survival percentage was observed for KHP-11 $\times$ MM-1-3-1, IS $\times$ Hyd-3-2-1-2-2 and KPR-2 $\times$ IS-1-3. Among checks, Swarna sub 1 recorded the highest survival percentage.

The highest stem elongation percentage was recorded in Gandhsali $\times$ Hyd-5-1-4-1-4 followed by Jyothi $\times$ KPR-1-BC2F6-2-1-1-1-1-1 and the lowest stem elongation percentage was recorded by KPR2 $\times$ IS-9-2-2-2 followed by HYD-5 $\times$ ISBC3F5-5-2-1-2.

Analysis of variance revealed high significant difference among the rice advanced breeding lines for the characters studied under submergence conditions. Genetic variability studies revealed high PCV and GCV for survival percentage and stem elongation percentage. There was high heritability coupled with a high genetic advance for the above traits.

Phenotypic correlation among physiological characters under submergence conditions indicated survival percentage to be significantly positively correlated with harvest index and grain yield. Whereas, it showed a significant negative correlation with stem elongation percentage.

Thirty rice advanced lines including four checks (KHP 11, KHP 13, Swarna sub1, FR13A) were studied under non-submergence conditions for genetic variability, diversity and character association during *Kharif* 2020 in randomized block design with two replications. The observations were recorded on five randomly selected plants per rice advanced line in each replication. Observations recorded are 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, the total number of spikelets per panicle, panicle fertility, test weight, length breadth ratio, straw yield, harvest index, grain yield.

Analysis of variance revealed the presence of high significant difference among the rice advanced lines for all the characters studied. The genetic variability studies revealed high PCV and GCV for the number of tillers per plant, the total number of productive tillers per plant, test weight and grain yield, high PCV and moderate GCV for the number of filled grains per panicle, the total number of spikelets per panicle, panicle fertility and straw yield per plant, moderate GCV and PCV for plant height, length breadth ratio and harvest index, moderate PCV and low GCV for panicle length, low PCV and GCV for days to 50 per cent flowering and days to maturity. All the characters recorded high heritability. High genetic advance as per cent mean was found for plant height, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, the total number of spikelets per panicle, panicle fertility, test weight, length breadth ratio, straw yield, harvest index and grain yield per plant. Moderate GAM was observed for days to 50 per cent flowering, days to maturity and panicle length.

Correlation studies revealed a positive association of plant height, number of tillers per plant, number of productive tillers per plant, panicle length, number of filled grains per panicle, the total number of spikelets per panicle, panicle fertility, test weight, straw yield and harvest index, days to 50 per cent flowering and days to maturity with grain yield.

Path coefficient analysis disclosed that the test weight followed by the number of tillers per plant, harvest index, plant height, straw yield, panicle length, days to maturity, the total number of spikelets per panicle, panicle fertility, number of filled grains per panicle manifested direct positive effect on grain yield per plant and also showed a positive correlation with grain yield per plant at phenotypic level.

Thirty rice advanced lines were grouped into six clusters based on the D^2 statistics. Cluster I is the largest with sixteen rice advanced lines followed by cluster V with six rice advanced lines; cluster II with three rice advanced lines, cluster III with two rice advanced lines, cluster IV and VI are smallest with one rice advanced line each. The highest intra cluster distance was shown by cluster III followed by cluster I. The maximum inter cluster distance was observed between cluster III and cluster IV followed by cluster II and cluster IV. The lowest inter cluster distance was observed between cluster I and cluster II followed by cluster II and cluster III.

Cluster V exhibited the highest mean values for days to 50 per cent flowering, days to maturity, plant height, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, panicle fertility, test weight, harvest index and grain yield per plant. Cluster IV showed the maximum cluster mean for the L/B ratio. Cluster II showed the highest cluster means for panicle length and total spikelets per panicle and cluster VI showed the highest cluster mean for straw yield.

Fifteen SSR markers were screened across thirty rice advanced lines and two parents to assess the molecular diversity. Out of them, polymorphism was found for nine SSR markers and the remaining were monomorphic. A total of 25 alleles were detected at the loci of nine microsatellite markers across 30 rice advanced lines. Among the polymorphic markers, RM2

produced five alleles, RM140, RM170, RM58 and RM10890 produced three alleles each. While RM583, RM212, RM3825 and RM6463 produced two alleles each.

The unweighted pair group method (UPGMA) clustering system generated eight genetic clusters in the studied rice advanced lines. Cluster I is the biggest cluster with six rice advanced lines each. Cluster VII is the smallest cluster with only two rice advanced lines. The highest genetic distance was found between farthest clusters I and VIII.

Among all the rice advanced lines studied, the top-performing rice advanced lines were selected based on grain yield and its related traits. KHP11 × MM-1-3-1 followed by IS × Hyd-3-2-1-2-2, KPR-2 × IS-1-3 and Jyothi × KPR-1-BC2F6-4-3-2 recorded higher yield as well as high survival percentage compared to the checks. The important traits which contribute to the yield, like the total number of tillers, panicle length, the total number of spikelets per panicle, panicle fertility, test weight and harvest index, were also found to be high in these genotypes when compared to the checks.

REFERENCES

VII REFERENCES

- ABEBE, T., ALAMEREW, S. AND TULU, L., 2017. Genetic variability, heritability and genetic advance for yield and its related traits in rainfed lowland rice (*Oryza sativa* L.) genotypes at Fogera and Pawe, Ethiopia. *Adv. Crop Sci. Technol.*, **5**(2): 272.
- ADILAKSHMI, D. AND RANI, M. G., 2012. Variability, character association and path analysis in rice varieties under submergence. *Crop Res.*, **44**(1and2): 146-151.
- AFRIN, W., HOSSAIN, M. A. AND ISLAM, M. M., 2017. Evaluation of yield and yield contributing traits for submergence tolerance of rice. *Progress. Agric.*, **28**(1): 7-11.
- AL JIBOURI., 1958, Genetic variability and correlation studies in chillies. *Prog. Hort.*, **36**: 113-117.
- AKINWALE, M. G., AKINYELE, B. O., ODIYI, A. C., NWILENE, F., GREGORIO, G. AND OYETUNJI, O. E., 2012, Phenotypic screening of Nigerian rainfed lowland mega rice varieties for submergence tolerance. *Proc. Int. Conf. Eng.* **1**: 4-6.
- ANDERSON, J. A., CHURCHILL, G. A., SUTRIQUE, J. E., TANKSLEY, S. D. AND SORRELLS, M. E., 1993, Optimizing parental selection for genetic linkage maps. *Genome*, **36**: 181-186.
- ANONYMOUS, 2018, Climate change and environmental concerns: breakthroughs in research and practice: breakthroughs in research and practice. *Book id: o95PDwAAQBAJ&dq*. (Verified on 14 May 2018).
- ASANTE, M. D., ADJAH, K. L. AND ANNAN-AFFUL, E., 2019. Assessment of genetic diversity for grain yield and yield component traits in some genotypes of rice (*Oryza sativa* L.). *J. Crop. Sci. Biotechnol.*, **22**(2): 123-130.
- ASHRAF, H., HUSAINI, A. M., BHAT, M. A., PARRAY, G. A., KHAN, S. AND GANAI, N. A., 2016. SSR based genetic diversity of pigmented and aromatic rice (*Oryza sativa* L.) genotypes of the western Himalayan region of India. *Physiol. Mol. Biol. Plants.*, **22**(4): 547-555.

- BABU, V. R., SHREYA, K., DANGI, K. S., USHARANI, G. AND SHANKAR, A. S., 2012. Correlation and path analysis studies in popular rice hybrids of India. *Int. J. Sci. Res.*, **2**(3): 1-5.
- BANDI, H. R. K., SATYANARAYANA, P. V., BABU, D. R., CHAMUNDESWARI, N., RAO, V.S. AND RAJU, S.K., 2018. Genetic variability estimates for yield and yield components traits and quality traits in rice (*Oryza sativa* L.). *Journal homepage: <http://www.ijcmas.Com>*, **7**(5): 20.
- BANUMATHY, S., MANIMARAN, R., SHEEBA, A., MANIVANNAN, N., RAMYA, B., KUMAR, D. AND RAMASUBRAMANIAN, G. V., 2010. Genetic diversity analysis of rice germplasm lines for yield attributing traits. *Electron. J. Plant Breed.*, **1**(4): 500-504.
- BARIK, J., KUMAR, V., LENKA, S. K. AND PANDA, D., 2020. Assessment of variation in morpho-physiological traits and genetic diversity in relation to submergence tolerance of five indigenous lowland rice landraces. *Rice Sci.*, **27**(1): 32-43.
- BARIK, J., KUMAR, V., SANGRAM, K., LENKAC. AND PANDAA, D., 2019, Assessment of Variation in Morpho-Physiological Traits and Genetic Diversity in Relation to Submergence Tolerance of Five Indigenous Lowland Rice Landraces. *Rice Sci.*, **27**(1): 2-43, doi: <https://doi.org/10.1016/j.rsci.2019.12.004>
- BHARGAVA, K., SHIVANI, D., PUSHPAVALLI, S. N. C. V. L., SUNDARAM, R. M., BEULAH, P. AND SENGUTTUVEL, P., 2021. Genetic variability, correlation and path coefficient analysis in segregating population of rice. *Electron. J. Plant Breed.*, **12**(2): 549-555.
- BHUTTA, M. A., MUNIR, S. A. N. A., QURESHI, M. K., SHAHZAD, A. N., ASLAM, K. A. S. H. I. F., MANZOOR, H. AND SHABIR, G., 2019. Correlation and path analysis of morphological parameters contributing to yield in rice (*Oryza sativa*) under drought stress. *Pak. J Bot.*, **51**: 73-80.
- BISWAJIT, P., SRITAMA, K. AND SABYASCHI, K., 2017. Genetic variability and character association for yield and yield components in submergence tolerant rice varieties. *Indian J. Agric. Res.*, **51**(3): 239-244.

- BOSE, K. AND PRADHAN, K., 2005. Genetic divergence in deep water rice genotypes. *J. Cent. Eur. Agric.*, [6](#): 4
- BURTON, G. W. AND DEVANE, E. M., 1953, Estimating heritability in tall fescue (*Festuca circunclinaceae*) from replicated clonal material. *Agron. J.*, **45**: 478-481.
- CHANBENI, Y. O., LAL, G. M. AND RAI, P. K., 2012. Studies on genetic diversity in Rice (*Oryza sativa* L.). *J. Agric. Technol*, **8**(3): 1059-1065.
- CHHANGTE, L. AND DEVI, T. R., 2019. Correlation and path analysis studies in aromatic rice germplasm of North-East region of India. *J. Pharm. Innov.*, **8**(10): 01-04.
- CHUCHERT, S., NUALSRI, C., JUNSAWANG, N. AND SOONSUWON, W., 2018. Genetic diversity, genetic variability, and path analysis for yield and its components in indigenous upland rice (*Oryza sativa* L. var. *glutinosa*). *Songklanakarin, J. Sci. Technol.*, **40**(3).
- COCHRAN, W. G. AND COX, G. M., 1957. Experimental designs., 127-131.
- CRRI-VISION 2050, 2013, doi: *ebook_crrivision2050_final_16Jan13.pdf* (verified on 4 July 2021)
- DAS, A. AND UCHIMIYA, H., 2002, Oxygen stress and adaptation of a semi-aquatic plant: rice (*Oryza sativa* L.). *J. Plant Res.*, **115**: 315-320.
- DAS, K. K., SARKAR, R. K. AND ISMAIL, A. M., 2005. Elongation ability and non-structural carbohydrate levels in relation to submergence tolerance in rice. *Plant Sci.*, **168**(1): 131-136.
- DAS, K. K., PANDA, D., SARKAR, R. K., REDDY, J. N. AND ISMAIL, A. M., 2009. Submergence tolerance in relation to variable floodwater conditions in rice. *Environ. Exp. Bot.*, **66**(3): 425-434.
- DEVI, K. R., CHANDRA, B. S., LINGAIAH, N., HARI, Y. AND VENKANNA, V., 2017. Analysis of variability, correlation and path coefficient studies for yield and quality traits in rice (*Oryza sativa* L.). *Agricultural Science Digest-A Research Journal.*, **37**(1): 1-9.

- DEVI, K. R., PARIMALA, K., VENKANNA, V., LINGAIAH, N., HARI, Y. AND CHANDRA, B. S., 2016. Estimation of variability for grain yield and quality traits in rice (*Oryza sativa* L.). *Int. J. Pure App. Biosci*, **4**(2): 250-255.
- DEWEY, P. R. AND LU, K. H., 1959, A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.*, **51**: 515-518.
- DHAMA, N., SAINI, R. K., KUMAR, R., CHAUDHARY, D. P., MAURYA, B. K., SHARMA, M., SEN, R., KUMAR, D., MALIK, P. AND KUMAR, P., 2018. Analysis of genetic diversity in rice (*Oryza Sativa* L.) cultivars using SSR markers. *Bull Environ. Pharmacol. Life Sci.*, **7**(3): 1-7.
- DHANWANI, R. K., SARAWGI, A. K., SOLANKI, A. AND TIWARI, J. K., 2013. Genetic variability analysis for various yield attributing and quality traits in rice (*O. sativa* L.). *The bioscan.*, **8**(4): 1403-1407.
- DHAVALESHWAR, K., IQBAL, T., HUSSAIN, I., AHMAD, N., NAUMAN, M., ALI, M., SAEED, S., ZIA, M. AND ALI, F., 2019. Regular article genetic variability, correlation and cluster analysis in elite lines of rice. *J. Sci. Agric.*, **2**: 85-91.
- DIVYA, J., RAJU, C. D., RAO, L. S. AND APARNA, K., 2018. Genetic Variability Studies in genetically diverse rice genotypes. *Int. J. Curr. Microbiol. App. Sci*, **7**(4): 1169-1172.
- DONDE, R., KUMAR, J., GOUDA, G., GUPTA, M. K., MUKHERJEE, M., BAKSH, S. Y., MAHADANI, P., SAHOO, K. K., BEHERA, L. AND DASH, S. K., 2019. Assessment of genetic diversity of drought tolerant and susceptible rice genotypes using microsatellite markers. *Rice Sci.*, **26**(4): 239-247.
- DOYLE, J. J. AND DOYLE, J. L., 1990, A rapid total DNA preparation procedure for fresh plant tissue. *Focus*, **12**: 13-15.
- FAOSTAT, 2018, FAO official website: www.fao.org
- FIYAZ, R. A., RAMYA, K. T., CHIKKALINGAIAH, A. B., GIREESH, C. AND RS, K., 2011. Genetic variability, correlation and path coefficient analysis studies in rice (*Oryza sativa* L.) under alkaline soil condition. *Electron. J. Plant Breed.*, **2**(4): 531-537.

- GANGASHETTY, P. I., SALIMATH, P. M. AND HANAMARATTI, N. G., 2013. Genetic variability studies in genetically diverse non-basmati local aromatic genotypes of rice (*Oryza sativa* L.). *Rice genomics and genetics.*, **4**(1).
- GAUTAM, A., CHETIA, S. K., MODI, M. K. AND AHMED, T., 2018. Phenotypic Screening and Evaluation of Sub1 Introgressed Lines in Popular Rice Varieties Ranjit and Bahadur of Assam, India. *Int. J. Curr. Microbiol. App. Sci*, **7**(9): 1744-1755.
- GIRMA, B. T., KITIL, M. A., BANJE, D. G., BIRU, H. M. AND SERBESSA, T. B., 2018. Genetic variability study of yield and yield related traits in rice (*Oryza sativa* L.) genotypes. *Adv. Crop. Sci. Tech*, **6**(4): 381.
- GOUR, L., KOUTU, G. K., SINGH, S. K., PATEL, D. D., SHRIVASTAVA, A. AND SINGH, Y., 2017. Genetic variability, correlation and path analyses for selection in elite breeding materials of rice (*Oryza sativa* L.) genotypes in Madhya Pradesh. *J. Pharm. Innov.*, **6**(11): 693-696.
- IDRIS, A. E., JUSTIN, F. J., DAGASH, Y. M. I. AND ABUALI, A. I., 2012. Genetic variability and inter relationship between yield and yield components in some rice genotypes. *J. Exp. Agric. Int.*, 233-239.
- IRRI Standard Evaluation System (SES) for Rice, 1988, Website: www.clrri.org/uploads
- JOHNSON, H. W., ROBINSON, H. F. AND COMSTOCK, R. E., 1955, Estimates of genetic and environmental variability in soybean. *Agron. J.*, **7**(7): 314-318.
- KAR, R. K., MISHRA, T. K., PANDEY, R. K. AND DAS, S. R., 2018. Assessment of genetic variability in lowland sub1 introgressed rice genotypes showing tolerance to submergence and stagnant flooding. *Electron. J. Plant Breed.*, **9**(2): 392-399.
- KATO, Y., COLLARD, B. C., SEPTININGSIH, E. M. AND ISMAIL, A. M., 2014. Physiological analyses of traits associated with tolerance of long-term partial submergence in rice. *AoB Plants.*, **6**.
- KAWANO, N., ITO, O. AND SAKAGAMI, J. I., 2009. Morphological and physiological responses of rice seedlings to complete submergence (flash flooding). *Annals of Botany*, **103**(2): 161-169.

- KHALEQUZZAMAN, M., ISLAM, M. Z., AKTER, K. AND BASHAR, M. K., 2008. Genetic diversity in local rainfed lowland rice (*Oryza sativa* L.) in Bangladesh. *Bangladesh J. Plant Breed. Genet.*, **21**(1): 49-54.
- KISHORE, C., KUMAR, A., PAL, A. K., KUMAR, V., PRASAD, B. D. AND KUMAR, A., 2018. Character association and path analysis for yield components in traditional rice (*Oryza sativa* L.) genotypes. *Int. j. curr. Microbiol. Appl. Sci.*, **7**(3): 283-291.
- KODIHALLI, B. AND DUSHYANTHAKUMAR, B. M., 2014. Genetic Diversity for Grain Yield and its Components in Local Rice (*Oryza sativa* L.) Genotypes under Submergence. *Electron. J. Plant Breed.*, **5**(1): 67-70.
- KUMARI, N., KUMAR, R. AND KUMAR, A., 2019. Genetic variability and association of traits in mutant lines of rice (*Oryza sativa* L.) for submergence tolerance. *Curr. J. Appl. Sci. Technol.*, 1-7.
- LAHARI, G., 2017. Assessment of Genetic Diversity of Rice Genotypes for Submergence Tolerance in Rainfed Lowlands (Doctoral dissertation, University of Agricultural & Horticultural Sciences, Shivamogga).
- LAKSHMI, M. V., SUNEETHA, Y., YUGANDHAR, G. AND LAKSHMI, N. V., 2014. Correlation studies in rice (*Oryza sativa* L.). *Int. J. Genet. Eng. Biotechnol.*, **5**(2): 121-126.
- LAKSHMI, V. I., SREEDHAR, M., GIREESH, C. AND VANISRI, S., 2020. Genetic variability, correlation and path analysis studies for yield and yield attributes in African rice (*Oryza glaberrima*) germplasm. *Electron. J. Plant Breed.*, **11**(02): 399-404.
- LINH, T. H., LINH, L. H., CUC, D. T. K., HAM, L. H. AND KHANH, T. D., 2013. Improving submergence tolerance of Vietnamese rice cultivar by molecular breeding. *J. Plant. Breed. Genet.*, **1**(3): 157-168.
- LIU, K. AND MUSE, S. V., 2005, Power Marker: an integrated analysis environment for genetic marker analysis. *Bioinformatics*, **21**: 2128-2129
- LUSH, J. L., 1949, Heritability of quantitative characters in farm animals. *Proc. 8th Congr. Genet. Hereditas*, **35**: 356-375.

- MAHALANOBIS, P. C., 1936, On the generalized distance in statistics. *Proc. Nat. Inst. Sci. India.*, **2**: 49-55.
- MALLIK, S., LAKHE, C. R., MITRA, N. K. AND MANDAL, B. K., 1988, Breeding for submergence tolerance. *Int. Rice Res. Notes.*, **4**(13): 12-13.
- MANJUNATHA, B. AND KUMARA, B. N., 2019. Genetic variability analysis for quantitative traits in rice (*Oryza sativa* L.). *J. Exp. Agric. Int.*, 1-4.
- NATH, S. AND KOLE, P. C., 2021. Genetic variability and yield analysis in rice. *Electron. J. Plant Breed.*, **12**(1): 253-258.
- NI, J., COLOWIT, P. M. AND MACKILL, D. J., 2002. Evaluation of genetic diversity in rice subspecies using microsatellite markers. *Crop sci.* **42**(2): 601
- NIROULA, R. K., PUCCIARIELLO, C., HO, V. T., NOVI, G., FUKAO, T. AND PERATA, P., 2012. SUB1A-dependent and-independent mechanisms are involved in the flooding tolerance of wild rice species. *Plant J.*, **72**(2): 282-293.
- NISHANTH, G. K., DUSHYANTHAKUMAR, B. M., GANGAPRASAD, S., GOWDA, T. H., NATARAJU, S. P. AND SHASHIDHAR, H.E., 2017, Screening and Genetic Variability Studies in Submergence Tolerance Rice Germplasm Lines under Flood Prone Lowlands of Hill Zone of Karnataka. India. *Int. J. Curr. Microbiol. App. Sci.*, **6**(7): 1254-1260, doi: <https://doi.org/10.20546/ijcmas.2017.607.1>
- NUGRAHA, Y., VERGARA, G. V., MACKILL, D. J. AND ISMAIL, A. B., 2013. Response of Sub1 introgression lines of rice to various flooding conditions. *Indones. J. Agric. Sci.*, **14**(1): 15-26.
- OLADOSU, Y., RAFII, M. Y., AROLU, F., CHUKWU, S. C., MUHAMMAD, I., KAREEM, I., SALISU, M. A. AND AROLU, I. W., 2020. Submergence tolerance in rice: Review of mechanism, breeding and, future prospects. *Sustainability*, **12**(4): 1632.
- OVUNG, C. Y., LAL, G. M. AND RAI, P. K., 2012. Studies on genetic diversity in rice (*Oryza sativa* L.). *J. Agric. Technol.*, **8**(3): 1059-1065.
- PANDA, D. AND SARKAR, R. K., 2013. Characterization of leaf gas exchange and anti-oxidant defense of rice (*Oryza sativa* L.) cultivars differing in submergence tolerance

- owing to complete submergence and consequent re-aeration. *Agricultural Res.*, **2**(4): 301-308.
- PANDEY, P., ANURAG, P. J., TIWARI, D. K., YADAV, S. K. AND KUMAR, B., 2009. Genetic variability, diversity and association of quantitative traits with grain yield in rice (*Oryza sativa* L.). *J. bio-science*, **17**: 77-82.
- PANWAR, L. L. AND ALI, M., 2007. Correlation and path analysis of yield and yield components in transplanted rice. *Oryza*, **44**(2): 115.
- PARIMALA, K. AND DEVI, R. K., 2019. Estimation of Variability and Genetic Parameters in Indica and Japonica Genotypes of Rice (*Oryza sativa* L.). *Int. J. Curr. Microbiol. App. Sci.*, **8**(3): 1138-1142.
- PATEL, J. R., SAIYAD, M. R., PRAJAPATI, K.N., PATEL, R. A. AND BHAVANI, R. T., 2014. Genetic variability and character association studies in rainfed upland rice (*Oryza sativa* L.). *Electron. J. Plant Breed.*, **5**(3): 531-537.
- PRADHAN, B., MISHRA, T. K. AND DAS, S. R., 2015. Genetic Basis of yield variations in lowland rice. *International Journal of Sciences: Basic. Appl. Res.*, **19**(2): 306-318.
- PRASAD, K. R., RADHA-KRISHNA, K. V., BHAVE, M. H. V. AND SUBBA-RAO, L. V., 2017. Genetic variability, heritability and genetic advance in boro rice (*Oryza sativa* L.) germplasm. *Int. J. Curr. Microbiol. Appl. Sci.*, **6**(4): 1261-1266.
- PRATAP, A., BISEN, P., LOITONGBAM, B. AND SINGH, P. K., 2018. Assessment of Genetic Variability for Yield and Yield Components in Rice (*Oryza sativa* L.) Germplasms. *Int. J. Bio-resource Stress Management.*, **9**(1): 87-92.
- PRATAP, N., SINGH, P. K., SHEKHAR, R., SONI, S. K. AND MALL, A. K., 2012. Genetic variability, character association and diversity analyses for economic traits in rice (*Oryza sativa* L.). *SAARC J. Agric.*, **10**(2): 83-94.
- RAHMAN, M. M., RASAUL, M. G., HOSSAIN, M. A., IFTEKHARUDDAULA, K. M. AND HASEGAWA, H., 2012. Molecular characterization and genetic diversity analysis of rice (*Oryza sativa* L.) using SSR markers. *J. crop improv.*, **26**(2): 244-257.

- RANAWAKE, A. L., AMARASINGHE, U. G. S. AND SENANAYAKE, S. G. J. N., 2014. Submergence tolerance of some modern rice cultivars at seedling and vegetative stages. *J. Crop Weed*. **10**(2): 240-247.
- RANI, M. G., ADILAKSHMI, D., SATYANARAYANA, P. V. AND SURYANARAYANA, Y., 2013. Genetic diversity of rice genotypes for submergence tolerance. *Crop Research*, **45**(1to3): 74-78.
- RANJITH, P., SAHU, S., DASH, S. K., BASTIA, D. N. AND PRADHAN, B. D., 2018. Genetic diversity studies in Rice (*Oryza sativa* L.). *J. Pharmac. Phytochem*. **7**(2): 2529-2531.
- RAM, B. J., BABU, G. S., LAVANYA, G. R., KUMAR, K. M. AND SPANDANA, B., 2017. Genetic variability for yield attributing traits of elite rice germplasm (*Oryza sativa* L.). *J. Pharmacog. Phytochem.*, **6**(3): 832-834.
- RAO, C. R., 1952, Advance statistical methods in biometric research. John Wiley and Sons Inc., New York.
- RASHID, K. A. S. H. I. F., KAHLIQ, I., FAROOQ, M. O. AND AHSAN, M. Z., 2014. Correlation and cluster analysis of some yield and yield related traits in Rice (*Oryza sativa*). *J. Recent Advances Agric.*, **2**(6): 271-276.
- RASHID, M. M., NURUZZAMAN, M., HASSAN, L. AND BEGUM, S. N., 2017. Genetic variability analysis for various yield attributing traits in rice genotypes. *J. Bangladesh Agricul. Univ.*, **15**(1): 15-19.
- ROBINSON, H. F., COMSTOCK, R. E. AND HARVEY, P. H., 1949, Estimation of heritability and degree of dominance in Corn. *Agron. J.*, **41**:353-359.
- SAHA, S. R., HASSAN, L., HAQUE, M. A., ISLAM, M. M. AND RASEL, M., 2019. Genetic variability, heritability, correlation and path analyses of yield components in traditional rice (*Oryza sativa* L.) landraces. *J. Bangladesh Agric. Univ.*, **17**(1): 26-32.
- SANDEEP, S., SUJATHA, M., SUBBARAO, L. V. AND NEERAJA, C. N., 2018. Genetic variability, heritability and genetic advance studies in rice (*Oryza sativa* L.). *Int. J. Curr. Microbiol. App. Sci.*, **7**: 3719-3727

- SARAWGI, A. K., RASTOGI, N. K. AND SONI, D. K., 1997. Correlation and path analysis in rice accessions from Madhya Pradesh. *Field Crops Res.*, **52**(1-2): 161-167.
- SARKAR, R. K. AND BHATTACHARJEE, B., 2011, Rice genotypes with *SUB1* QTL differ in submergence tolerance, elongation ability during submergence and re-generation growth at re-emergence. *Rice*, **5**(7):1-11.
- SARKAR, R. K., PANDA, D., REDDY, J. N., PATNAIK, S. S. C., MACKILL, D. J. AND ISMAIL, A. M., 2009. Performance of submergence tolerant rice (*Oryza sativa*) genotypes carrying the Sub1 quantitative trait locus under stressed and non-stressed natural field conditions. *Indian J. Agric. Sci.*, **79**(11): 876-83.
- SEETHARAM, K., THIRUMENI, S. AND PARAMASIVAM, K., 2009. Estimation of genetic diversity in rice (*Oryza sativa* L.) genotypes using SSR markers and morphological characters. *African J. Biotechnol.*, **8**(10).
- SHIVASUBRAMANIAN, S. AND MENON, N., 1973, Heterosis and inbreeding depression
- SINGH, A., MUKUL, J. M., RAM, M., ARYA, M. AND SINGH, P. K., 2015. Screening and evaluation of rice cultivars for submergence tolerance using SSR markers. *The Ecoscan*, **9**(1&2): 255-259.
- SINGH, K. S., SUNEETHA, Y., KUMAR, G. V., RAO, V. S., RAJA, D. S. AND SRINIVAS, T., 2020. Variability, correlation and path studies in coloured rice. *Int. J. Chem. Stud*, **8**(4): 2138-2144.
- SINGH, N. AND VERMA, O. P., 2018. Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) under salt stressed soil. *J. Pharmacog. Phytochem.*, **7**(3): 3114-3117.
- SINGH, R. K. AND CHAUDHARY, B. D., 1977, Biometrical methods for quantitative genetic analysis, *Kalyani Publishers, New Delhi.*, 378.
- SINGH, R., YADAV, V., MISHRA, D. N. AND YADAV, A., 2018. Correlation and path analysis studies in rice (*Oryza sativa* L.). *J. Pharmacog. Phytochem.*, 2084-2090.
- SINGH, S., MACKILL, D. J. AND ISMAIL, A. M., 2014. Physiological basis of tolerance to complete submergence in rice involves genetic factors in addition to the SUB1 gene. *AoB Plants.*, **6**.

- SINGH, T. V. J., MOHAN, Y. C., DAMODARRAJU, C. H., JAGADESHWAR, R. AND BALRAM, M., 2019, Character association and path coefficient studies in rice (*Oryza sativa* L.). *Int. J. Pharmacogn.*, **8**(3): 383-387.
- SRAVAN, T., RANGARE, N. R., SURESH, B. G. AND KUMAR, S. R., 2012. Genetic variability and character association in rainfed upland rice (*Oryza sativa* L.). *J. Rice Res.*, **5**(1): 2.
- SREEDHAR, S. AND REDDY, U. R., 2019. Association studies for yield and its traits in rice (*Oryza sativa* L.) genotypes. *Int. J. Current Microbiol. Appl. Sci.*, **8**(1): 2337-2342.
- SRINIVAS, T., 2018. Genetic diversity studies in rice (*Oryza sativa* L.). *Electron. J. Plant Breed*, **9**(4): 1335-1341.
- SRUJANA, G., SURESH, B. G., LAVANYA, G. R., JALANDHAR RAM, B. AND SUMANTH, V., 2017, Studies on Genetic Variability, Heritability and Genetic advance for yield and quality components in rice (*Oryza sativa* L.). *Int. J. Pharmacogn.*, **6**(4): 564-566.
- SUDEEPTHI, K., SRINIVAS, T., KUMAR, B. R., JYOTHULA, D. P. B. AND UMAR, S. N., 2020. Assessment of genetic variability, character association and path analysis for yield and yield component traits in rice (*Oryza sativa* L.). *Electron. J. Plant Breed.*, **11**(01): 144-148.
- SUMANTH, V., SURESH, B. G., RAM, B. J. AND SRUJANA, G., 2017. Estimation of genetic variability, heritability and genetic advance for grain yield components in rice (*Oryza sativa* L.). *J. Pharmacog. Phytochem.*, **6**(4): 1437-1439.
- SÜREK, H. and BEŞER, N., 2003. Correlation and path coefficient analysis for some yield-related traits in rice (*Oryza sativa* L.) under thrace conditions. *Turkish J. Agric. Forestry.*, **27**(2): 77-83.
- TARANG, A., KORDROSTAMI, M., KUMLEH, A. S., CHALESHTORI, M. H., SARAVANI, A. F., GHANBARZADEH, M. AND SATTARI, M., 2020. Study of genetic diversity in rice (*Oryza sativa* L.) cultivars of Central and Western Asia using

- microsatellite markers tightly linked to important quality and yield related traits. *Genetic Res. Crop Evol.*, **67**(6): 1537-1550.
- TIWARI, D. N., TRIPATHI, S. R., TRIPATHI, M. P., KHATRI, N. AND BASTOLA, B. R., 2019. Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. *Advances in Agric.* **21**(4): 77-78
- TRIPATHI, S., SINGH, S. K., SRIVASHTAV, V., KHAIRE, A. R., VENNELA, P. AND SINGH, D. K., 2020. Molecular diversity analysis in rice (*Oryza sativa* L.) using SSR markers. *Electron. J Plant Breed.*, **11**(03): 776-782.
- UPADHYAY, P., NEERAJA, C. N., KOLE, C. AND SINGH, V. K., 2011. Population structure and genetic diversity in popular rice varieties of India as evidenced from SSR analysis. *Biochem. Genetics.*, **50**(9): 770-783.
- VANAJA, T. AND BABU, L. C., 2007. Variability in grain quality attributes of high yielding rice varieties (*Oryza sativa* L.) of diverse origin. *J. Trop. Agric.*, **44**: 61-63.
- VENI, B. K. AND RANI, N. S., 2006. Association of grain yield with quality characteristics and other yield components in rice. *Oryza.*, **43**(4): 320.
- VENKATESAN, M., SOWMIYA, C. A. AND ANBARASI, B., 2016, Studies on genetic diversity of rice (*Oryza sativa*) under submergence. *Plant. Arch.*, **16**(2): 617-620
- VENKATESAN, M., SOWMIYA, C. A. AND ANBARASI, B., 2018. Studies on genetic diversity of rice (*Oryza sativa*) under submergence. *Plant Archives*, **16**(2): 617-620.
- VERGARA, G. V., NUGRAHA, Y., ESGUERRA, M. Q., MACKILL, D. J. AND ISMAIL, A. M., 2014, Variation in tolerance of rice to long term stagnant flooding that submerges most of the shoot will aid in breeding tolerant cultivars. *AoB plants*, **6**:1-16.
- VU, H. T. T., NGUYEN, H. T. T., TRAN, K. D., KHUAT, T. H. AND NAKAMURA, C., 2016. Genetic diversity of Vietnamese lowland rice germplasms as revealed by SSR markers in relation to seedling vigour under submergence. *Biotech. Biotechnol. Equip.*, **30**(1): 17-25.
- WEBER, C. R. AND MURTHY, B. R., 1952, Heritable and non-heritable relationships and variability for oil content and agronomic characters in the F₂ generation of soybean crosses. *Agron. J.*, **44**: 202-209.

- WENING, R. H., RUMANTI, I. A., PURWAKO, B. S., SUWARNO, W. B. AND KHUMADIA, N., 2019, Screening of Submergence Tolerant Rice under Artificial Condition Based on Multiple Selection Indices. *Plant Breed. Biotech.*, **7**: 360-374
- WRIGHT, S., 1921, Correlation and causation. *J. Agric. Res.*, **20**: 557-587.
- YADAV, R., RAJPOOT, P., VERMA, O. P., SINGH, P. K., SINGH, P. AND PATHAK, V., 2017. Genetic variability, heritability and genetic advance in Rice (*Oryza sativa* L.) for grain yield and its contributing attributes under sodic soil. *J. Pharmacogn. Phytochem.*, **6**(5): 1294-1296.
- ZAHID, M. A., AKHTER, M., SABAR, M., MANZOOR, Z. AND AWAN, T., 2006. Correlation and path analysis studies of yield and economic traits in Basmati rice (*Oryza sativa* L.). *Asian J. Plant Sci.*, **5**(4): 643-645.

APPENDICES

VII APPENDIX

Appendix I: Mean values for sixteen traits of the rice advanced lines

Sl. No	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄	X ₁₅	X ₁₆
1	5	16.19	114.62	149.61	116.46	15.19	14.63	22.13	109.60	134.94	67.83	21.80	3.48	25.72	57.05	5137.50
2	45	35.01	116.56	149.57	104.29	19.32	17.82	21.45	120.92	174.27	75.03	27.55	2.68	43.31	35.66	5460.00
3	60	26.93	111.62	145.56	122.92	19.10	17.60	22.65	134.39	156.29	85.97	26.35	3.04	42.49	45.35	5260.50
4	25	38.28	107.94	142.56	97.45	20.74	19.74	23.40	115.70	134.87	94.28	31.70	3.51	36.44	49.38	5322.00
5	35	32.78	109.68	143.62	106.87	19.00	16.64	22.40	88.73	129.33	54.19	12.65	3.48	24.55	52.95	4149.75
6	10	43.53	107.13	143.58	111.11	22.94	18.44	22.35	98.72	152.16	64.92	12.20	3.26	25.42	48.75	4454.25
7	40	44.52	110.83	145.77	147.82	17.18	19.18	22.15	138.95	151.36	92.01	32.50	3.23	34.49	39.95	5175.00
8	55	39.60	109.79	146.62	125.40	18.66	16.66	23.50	131.01	202.78	64.56	30.80	2.26	34.39	41.53	3659.25
9	15	44.67	106.82	141.61	90.69	20.06	16.06	22.95	93.54	156.69	59.65	25.90	2.32	27.06	44.66	3329.25
10	45	26.26	107.61	142.59	106.85	14.65	14.65	24.60	156.36	158.22	98.74	26.25	3.49	35.10	40.41	5340.00
11	35	34.26	104.82	139.57	95.10	21.59	16.59	22.45	124.83	150.50	83.04	28.80	2.94	26.96	46.78	3578.25
12	30	26.36	123.61	158.59	106.48	18.75	13.25	24.30	104.25	202.20	51.56	14.20	2.46	25.29	46.07	3202.50
13	45	27.89	105.21	137.64	102.88	17.60	13.10	23.55	127.49	189.30	67.73	14.20	3.38	32.40	46.24	4188.00
14	10	55.32	116.61	160.71	90.03	11.05	9.55	18.15	85.50	95.58	45.12	11.45	3.53	14.90	50.03	2281.50
15	85	49.20	104.62	147.08	156.56	22.50	22.50	25.80	135.22	178.42	95.84	27.55	3.04	26.59	62.24	6578.25
16	35	47.69	110.81	145.73	92.31	19.68	16.68	23.95	158.32	171.46	92.46	12.65	3.32	40.59	47.22	3618.75
17	30	41.27	105.12	138.94	111.31	24.85	24.85	22.20	82.00	132.22	62.19	25.30	3.08	24.23	52.02	3940.50
18	25	50.97	104.63	137.58	110.70	14.91	14.91	23.35	93.94	121.43	77.41	26.95	3.27	27.49	46.56	3601.50
19	55	25.04	104.09	139.51	105.68	21.12	17.80	23.95	109.17	122.19	89.34	30.65	3.18	31.40	54.78	5706.75
20	15	46.23	114.60	137.02	117.48	12.06	11.06	16.75	61.06	90.50	48.35	21.65	4.48	25.28	52.28	5022.00
21	30	52.44	133.07	167.52	133.67	19.00	19.00	24.34	111.64	138.06	80.90	30.25	2.96	33.00	45.42	5045.25
22	55	27.57	118.07	152.61	101.48	18.03	18.03	18.61	121.13	137.00	88.46	28.70	3.20	32.68	21.84	3516.00
23	15	20.97	128.71	157.16	89.58	12.04	10.04	15.95	80.30	92.94	66.40	15.75	4.14	32.69	43.54	2489.25
24	100	28.17	124.67	156.58	114.59	30.37	29.37	24.80	137.86	182.78	85.54	33.25	3.30	35.50	55.48	6637.5
25	45	35.25	115.69	149.81	112.77	19.31	17.82	22.40	116.46	152.24	75.19	24.74	3.21	30.33	48.63	4637.38
26	75	29.62	139.56	166.54	153.07	25.57	25.57	22.48	114.52	183.12	63.53	29.35	3.30	31.17	55.90	5925.00
27	85	30.07	123.67	155.55	106.36	21.85	21.85	23.00	143.12	187.98	76.26	29.50	2.92	26.09	58.90	5610.00
28	75	25.42	129.66	161.55	134.35	18.74	18.74	22.55	130.00	189.04	68.67	31.10	3.30	23.71	59.21	5160.00
29	85	33.89	127.57	161.04	112.22	24.85	24.85	24.49	133.62	142.46	94.02	27.05	3.42	28.06	56.86	5547.00
30	100	22.10	133.31	172.52	106.75	18.75	17.64	21.38	135.37	157.02	86.66	31.40	3.18	32.59	53.18	5548.5
Mean	45.52	35.25	115.69	149.81	112.77	19.31	17.82	22.40	116.46	152.24	75.19	24.74	3.21	30.33	48.63	4637.38

Where,

X ₁ = Survival percentage	X ₇ = Number of productive tillers per plant	X ₁₃ = Length breadth ratio
X ₂ = Stem elongation percentage	X ₈ = Panicle length	X ₁₄ = Straw yield
X ₃ = Days to 50% flowering	X ₉ = Number of filled grains per panicle	X ₁₅ = Harvest index
X ₄ = Days to maturity	X ₁₀ = Total number of spikelets per panicle	X ₁₆ = Grain yield per plant
X ₅ = Plant height	X ₁₁ = Panicle fertility	
X ₆ = Number of tillers per plant	X ₁₂ = Test weight	